us-09-909-164-5.rag

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- protein search, using sw model OM protein June 10, 2003, 13:24:45; Search time 31.3571 Seconds (without alignments) 46.744 Million cell updates/sec Run on:

US-09-909-164-5 52 Title: Perfect

score:

1 EEVVPXGMSYS 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched: Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result / No.	Score	% Query Match	% Query Match Length DB	DB	ID	Description
	1	50	96.2	11	23	ABB80521	Hepatitis C virus
	7	20	96.2	11	23	ABB80522	Hepatitis C virus
4	3	20	96.2	11	23	ABB80525	Hepatitis C virus
۷	4	20	96.2	11	23	ABB80526	Hepatitis C virus
~	2	20	96.2	11	23	ABB80559	Hepatitis C virus
	9	20	96.2	11	23	ABB80563	Hepatitis C virus
	7	20	96.2	11	23	ABB80564	Hepatitis C virus
	8	50	96.3	11	23	ABB80565	Hepatitis C virus
	9	20	96.2	11	23	ABB80566	Hepatitis C virus
	10	20	96.2	11	23	ABB80567	Hepatitis C virus
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ALIGNMENTS

RESULT 1 ABB80521 ID ABB80521 standard; peptide; 11 AA.

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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                            'note= "N-terminal acetyl"
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                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                 Hepatitis C Virus NS3/NS4a serine protease inhibitor peptide #1.
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    Length 11;
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Best Local Similarity
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    residue 7"
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                                                                                                                                                                                                                                                                                                                              otide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
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19-JUL-2001; 2001WO-US23169
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                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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         (CORV-) CORVAS INT INC
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Claim 17; Page 65; 69pp; English.
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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Pred. No. 0.0011;
0; Mismatches 0; Indels
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ABB80566 standard; peptide; 11 AA
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tive 0;
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                            "Alpha-propynyl-glycinyl-carbonyl residue forming a keto-amide linkage with residue 7"
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                                                                                                                                                                                                                       "(s,s)allothreonyl carbonyl residue forming a keto-amide linkage with residue 7"
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virucide.
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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Pred. No. 0.0075;
0; Mismatches 1; Indels
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                                                                                                                                      Claim 17; Page 64; 69pp; English.
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Best Local Similarity 90.9
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 Lim-wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80529;
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                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                                                         The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                          peptide compound having hepatitis C virus protease inhibitory
ty useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 23;
Pred. No. 0.0075;
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                                                                                                                                      Brunck TK;
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90.9%;
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                                 19-JUL-2001; 2001WO-US23169.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                      Lim-wilby M, Levy OE,
                                                                                                    (CORV-) CORVAS INT INC
                                                                                                                                                                    WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AA;
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                                                                                                                                                                                                                                          virus protease
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31-JAN-2002
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RESULT 13 ABB80528

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Synthetic
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                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                               Gaps
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                                                                                                                             Length 11;
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                                                                                                                           Score 46; DB 23;
Pred. No. 0.0075;
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                 Claim 17; Page 64; 69pp; English.
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                                                                                                                           88.5%;
90.9%;
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                                                                                                                                   Local Similarity
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                                                                                                         11 AA;
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virus protease
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                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                           virucide.
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
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Pred. No. 0.0075;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80562 standard; peptide; 11
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90.9%;
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                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                           Gaps
                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Ity useful for treating disorders associated with hepatitis C
 is useful for treating disorders associated with hepatitis C virus.
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                                               Score 46; DB 23;
Pred. No. 0.0075;
); Mismatches 1,
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90.9%;
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                                                                                                                 1 EEVVPXGMDYS 11
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                                                                                                   1 EEVVPXGMSYS
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                                                          Local Similarity
ses 10; Conserv
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                         Sequence
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                                                                                                                                                                                                                  ABB80523;
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                                               Query Match
                                                                                                                                                                                                                                                                                                        virucide
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                                                                          Matches
                                                                                                                                                                  RESULT 17
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                            virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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Pred. No. 0.012;
0; Mismatches 1; Indels
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                                                                                                                                                                   ABB80527 standard; peptide; 11 AA
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90.9%;
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les 10; Conservative
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EEVVPXGMHYS 11
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ABB80535
ID ABB80
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Gaps

Indels

Conservative

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                                                                                             "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
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Pred. No. 0.012;
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                                                              note= "N-terminal acetyl"
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                                                                                                                                                                            "C-terminal amide"
                                                                                                                                            "D-form residue"
                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                           TK;
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90.9%;
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                           Misc-difference
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                                             Modified-site
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Synthetic.
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                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #15.
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                                                                                                                                                                                                                                                                                     11
/note= "C-terminal amide"
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus protease
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Modified-site
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        ABB80535;
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(CORV-) CORVAS INT INC
                                                                                                                                    virus protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Norvalyl carbonyl forming keto-amide linkage with residue 7\,\mathrm{m}
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                  Score 45; DB 23; Length 11;
Pred. No. 0.012;
0; Mismatches 1; Indels
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                         /note= "C-terminal amide"
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        'note= "D-form residue"
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                                                                                                                                     Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80540 standard; peptide; 11 AA.
                                                                                                                                                                                                            Claim 17; Page 65; 69pp; English.
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                    (CORV-) CORVAS INT INC
                                                                                                                                     Lim-wilby M, Levy OE,
                                                                                                                                                      WPI; 2002-361643/39.
Misc-difference 8
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ABB80540
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    residue 7"
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Pred. No. 0.012;
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                                                                                                                                                              Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80558 standard; peptide; 11
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90.9%;
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19-JUL-2001; 2001WO-US23169.
                                                     21-JUL-2000; 2000US-220101P.
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                                                                                                                                                                 Levy OE,
                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                                                                                                    WPI; 2002-361643/39
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AA;
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Gaps

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Score 45; DB 23; Length 11; Pred. No. 0.012; 0; Mismatches 1; Indels

English.

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat discorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                          86.5%;
90.9%;
                                                           65; 69pp;
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nes 10; Conserv
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                                                                                                                                                                      11 AA;
                                      virus protease
                                                          Claim 17; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                   ABB80544;
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                                                                                                                                                                                          Query Match
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                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have a reactivity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                        Gaps
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                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
            Levy OE, Brunck TK;
                                                                                                                                                                                                                                                                                                                                                 ABB80560 standard; peptide; 11 AA.
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                                                                                              Claim 17; Page 65; 69pp; English.
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90.9%;
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                                WPI; 2002-361643/39.
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                                                                                                                                                                                                                                        1 Similarity
10; Conserv
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                                                                           virus protease
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                                                                                                                                                                                                                              Query Match
Best Local 9
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Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C btease -
                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Norvalyl
ABB80544 standard; peptide; 11
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                                                                                                                                (first entry)
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CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;
Query Match
Best Local Similarity 90.9%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Indels 0; Gaps 0;
I EEVVPXGMSYS 11
Db 1 EEVVPXGTSYS 11
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Search completed: June 10, 2003, 13:39:05 Job time: 32.3571 secs

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June 10, 2003, 13:31:45; Search time 9.64286 Seconds (Without alignments) 33.564 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                          262574 seqs, 29422922 residues
                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                            US-09-909-164-5
52
1 EEVVPXGMSYS 11
                                                                                                                                                                              Title:
Perfect score:
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                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                            Searched:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Segmenter 73 April	336	Seguence 236, App	236.	5177	S	N _O	S	99	.99	Sequence 23, Appl	4	. 4	4	,	Sequence 21, Appl	2	21,	21,	22,	22,	22,	22,	6, 2	9	4	4
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SOFTERSTES	ID	US-09-228-986-73	-08-637-759R-23	-08-871-355A-2	-09-201-945-236	771	5177197-1	5177197-30	US-09-357-952-66	-09	US-09-168-888-66	US-08-580-988A-23	US-08-460-694-4	US-08-460-744-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	US-08-246-361A-21	US-08-463-772-21	PCT-US93-05000-21	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22	US-08-464-517-6	US-08-463-772-6	08-24	PCT-US93-05000-4
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PCT - US93 US - 08 - 46 US - 08 - 24 US - 08 - 24 US - 08 - 46 PCT - US93 US - 07 - 94	US-08-464-517-19 US-08-464-517-20 US-08-246-316A-20 US-08-246-316A-20 US-08-463-772-19 US-08-463-772-19 US-08-463-772-20 US-08-463-772-20 US-08-463-772-40 US-08-464-517-44 US-08-464-517-44 US-08-464-517-44 US-08-770-761A-3 US-08-770-761A-3 US-08-770-761A-5 US-08-770-761A-5 US-08-770-761A-5 US-08-770-761A-5 US-08-770-761A-5 US-08-770-761A-5 US-08-770-761A-5 US-08-770-761A-7 US-08-770-761A-7 US-08-770-761A-7 US-08-770-761A-7 US-08-78-78-78-78-78-78-78-78-78-78-78-78-78	US-08-834-776A-2
	2000 2000 2000 2000 2000 2000 2000 200	
61. 61. 61. 61.		57.
	337 344 440 440 440 440 440 440 440	

ALIGNMENTS

Sequence 73, Application US/09228986
Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions in the Modification of Plant Cell Signalling;
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 73
LENGTH: 947 ; TYPE: PRT; ORGANISM: Pinus radiata US-09-228-986-73 US-09-228-986-73 RESULT 1

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63.5%; Score 33; DB 3; Length 45; 60.0%; Pred. No. 5.1;
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                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5.1;
1; Mismatches
                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PADS: PATICA L.
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street
                  STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
  Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
, MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-236
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Best Local Similarity
                                                                                                           COUNTRY: USA
ZIP: 30309-3450
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ZIP: 30309-3450
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STATE: Georgia
COUNTRY: USA
                                                                 CITY: Atlanta
STATE: Georgia
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ADDRESSEE:
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65.4%; Score 34; DB 4; Length 947; 66.7%; Pred. No. 1e+02;
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                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/637,759B
FILING DATE: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 236, Application US/08871355A
Patent No. 6015669
GNERAL INFORMATION:
GNERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          Sequence 236, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                       Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 6; Conservative
                                            6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEISPLGWSY 10
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686 VMPSGISYS 694
                                                                                         3 VVPXGMSYS 11
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                  Best_Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-871-355A-236
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US-08-637-759B-236
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  Query Match
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US-09-357-952-66
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LENGTH: 10
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                                                                                                                       ; Patent No.
                                                                                                      5177197-30
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"WENNSTEDT, CHRISTER, HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
"LENDIN, CARL-HENRIK
"TILL OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
"HUMAN TEANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KANZAKI, TETSUTO:OLOFSSON, ANDERS;MOREN, ANITA;
;WERNSTEDT, CHRISTER;HELLMAN, ULF;MIXAZONO, KOHEI;CLAESSON-WELSH,
;LDA,HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
;HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 33; DB 6; Length 410; 45.5%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                Score 33; DB 4; Length 45; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5%; Score 33; DB 6; Length 65; 45.5%; Pred. No. 7.8; 1ve 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                      3; Indels
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APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEC ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                 NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                  63.5%;
60.0%;
                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0.
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Best Local Similarity 45.55
Matches 5; Conservative
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                                                                                                                                                                                        LENGTH: 45 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
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52 KEICPGGMGYT 62
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Matches 5; Conserv
                                                                                                                                                                                                                                              linear
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Patent No. 5177197
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LENGTH: 65
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APPLICANT: Zhang, Han-Zhong
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Tang, Wu
APPLICANT: Tang, Wu
APPLICANT: Tang, Wu
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prot
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
CURRENT APPLICATION WHEER: US/09/357,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER RILING DATE: 21-UUL-1998
NUMBER OF SEQ ID NOS: 139
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                                                                                                                                                                                         HENSTEDT, CHRISTER, HELLMAN, ULF; MIYAZONO, ANDERS; MOREN, ANITA; WERNSTEDT, CHRISTER, HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, LENA; HELLLIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 6; Length 1394;
Pred. No. 2.6e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 66, Application US/09357952; Patent No. 6248904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%;
45.5%;
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Best Local Similarity 45.5
Matches 5; Conservative
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399 KEICPGGMGYT 409
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399 KEICPGGMGYT 409
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1 EEVVPXGMSYS 11
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; LENGTH: 1394
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US-09-521-650-66
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Sequence 23, Application US/08580988A
Patent No. 585661
GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh operaring System, macintosh operaring System, macintosh SOFTWARE: Microsoft Word for Macintosh APPLICATION DATA: US/08/580,988A FILING DATE: January 3,1996 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-460-694-4; Sequence 4, Application US/08460694; Patent No. 5858655; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 amino acids
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APPLICATION NUMBER:
FILING DATE:
                                         1 DDIVPCSMSY 10
                 1 EEVVPXGMSY 10
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Best Local Similarity
These 6; Conservat
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STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: 1
; ORIGINAL SOURCE:
US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 77071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                      US-08-580-988A-23
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                                                                                                                                  RESULT 11
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APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Exema, John F.W.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: Heir Applications for Whole-Cell Fluorescent Reporter Molecules and
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: UNBER: US/09/168,888
CURRENT FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-10-09
SOFTWARE: PAPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SSOTUMBE: PatentIn Ver. 2.0

EARLIER PAPLICATION OF THE CASPAGE
SEQ ID NO 66
                                                                                      TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the TITLE OF INVENTION: USE THEREOF TITLE OF INVENTION: USE THEORY FLUE REFERENCE: 1735.0290002

CURRENT APPLICATION NUMBER: US/09/521,650

CURRENT FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
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US-09-168-888-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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3; Mismatches
                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 09/168,888
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-10
EARLIER FILING DATE: 1997-10-10
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 66, Application US/09168888
Patent No. 6342611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserva
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RESULT 15
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Pred. No. 33;
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TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: O2-JUM-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCONATHY, EVelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0609.4070005
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NAME: MCCONATHY, EVELYN
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPPHONE: 202-371-2600
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 60.0
Matches 6; Conservative
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                                                                             Washington
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ZIP: 20005
                                                                                                                                                                                         20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-460-694-4
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                                                                                                                                                       COUNTRY:
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                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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Pred. No. 33;
1; Mismatches 3; Indels
                                                                                                                       Score 32; DB 3; Length 152;
Pred. No. 33;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Pradl Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ANDESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,711B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1991
108/07/667,711B
11-MAR-1991
108. 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/07667711B; Patent No. 6110700; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08193977
Patent No. 5625031
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
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60.0%;
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60.0%;
                                                                                                        Query Match
Query Match
Best Local Similarity 60.00.
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TYPE: amino acid
STRANDEDNESS: single
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not relevant
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Best Local Similarity 60...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: not relevar; MOLECULE TYPE: peptide US-07-667-711B-4
                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-460-744-4
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APPLICANT: WEBSTER,
APPLICANT: COLEMAN,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                              US-07-667-711B-4
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    P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN PAPILLOMAVIRUS E7 ONCOPROTEIN
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Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%; Score 32; DB 1; Length 173; 60.0%; Pred. No. 38; 1tive 1; Mismatches 3; Indels
                                                                                                       AUDRESSEE: REED & ROBINS

CITY: PALO ALTO
STATE: G15 BRYANT STREET
CITY: PALO ALTO
STATE: CALLFORNIA
COUNTRY: UNITED STATES OF AMERICA
21P: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/POCKET UNBER: 33,208
REFERENCE/POCKET UNBER: 5998-0016
TELEFNA: (415) 617-8999
TELEFNA: (415) 617-8999
TELEFNA: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7;
SEQUENCE CHARACTERISTICS:
LENGTH: 173 antho acids
TVER: LENGTH: 173 antho acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
TITLE OF INVENTION: P34C
TITLE OF INVENTION: PAPI
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.5
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 EEVFPLAMNY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Bosto
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-464-517-21
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Sequence 21, Application US/08246361A
Sequence 21, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHLVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 2; Length 189;
Pred. No. 42;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 19-MAY 1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION WABER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY 1991
ATTORNEY AGENT INFORMATION:
                    APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECHOMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 227-5641
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-464-517-21
                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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74 EEVFPLAMNY 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: B
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RESULT 20
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Sequence 21, Application US/08463772

Patent No. 6066501

GENERAL INFORMATION:
APPLICANT: BERCH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                        Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 3; Length 189;
                                                                        DB 2;
                                                                                       Pred. No. 42;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 42;
1; Mismatches
                                                                         Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATORICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 21, Application PC/TUS9305000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFRAX: (617) 227-5941
INPERMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                        61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.5
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                        Conservative
               ; MOLECULE TYPE: peptide US-08-246-361A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                            1 EEVVPXGMSY 10
                                                                                                                                                                                74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserva
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                        JS-08-463-772-21
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APPLICANT: MITOTIX TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
UNDER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 189;
                                                                                                                                                                 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ced. No. 42;
Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US93/05000 FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-WAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          %5-08-464-517-22
; Sequence 22, Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 616-861-9540 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 189 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 60. و
المالية والمالية والمالية
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05000-21
                                                                                                                                                                                                                                                                                                        Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02109
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                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE 6 COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 2;
Pred. No. 54;
FILING DATE: 16-CL. 17-18

APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATE: APPLICATION NUMBER: US 07/701,514

FILING DATE: 16-MAY-1991

ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709

RESTRANDE/ACCENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 227-7400

TELEFAN: (617) 227-7400

TELEFAN: (617) 227-740

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: Single
STRANDEDNESS: Single
STRANDEDNESS: Single
US-08-464-517-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFWARE: ASCII(text)
CURRENT APPLICATION DATA:
PROFILE APPLICATION DATA:
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/886,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTONNEY, AGENT INFORMATION:
MANAW: MATTHONEY APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 61.5
Best Local Similarity 60.0
Matches 6; Conservative
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20 EEVFPLAMNY 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
STATE:
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Sequence 22, Application US/08463772
Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INFORMATION:
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: BOSTON
                                                                                                                       DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 236;
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Pred. No. 54;
1; Mismatches
                                                                                                                   Score 32; DB 2
Pred. No. 54;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk-
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     61.5%;
60.0%;
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60.0%;
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ATTORNEY/AGENT INFORMATION:
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-246-361A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0.
                                                                                                                                                      Conservative
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MOLECULE TYPE: peptide

US-08-463-772-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                        1 EEVVPXGMSY 10
                                                                                                                                                                                                           20 EEVFPLAMNY 29
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Best Local Similarity
Matches 6; Conserva
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USA
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Patent No. 5869640
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                        TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 5; Length 236;
Pred. No. 54;
1; Mismatches 3; Indels
                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: US
ZID: 02173
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY, AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REPRENCE/POCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
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COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Sequence 22, Application PC/TUS9305000 GENERAL INFORMATION: APPLICANT: MITOTIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 236 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 616-861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-05000-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 02109
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PCT-US93-05000-22
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                                                                                                                                                                                 CITY: I
STATE:
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Gaps
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Sequence 6, Application US/08463772
Sequence 6, Application US/08463772
Patent No. 606501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCES: 0
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: BOSTON
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 2; Length 280;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                      APPLICATION NUMBER: US 0/790,300
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: APPLICATION acids
TYPE: APPLICATION acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-007-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
SOFTWARE: ASCII(text)
APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MII-004C
                            US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-517-6
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-OCT-
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSY 10
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CLASSIFICATION: 435
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us-09-909-164-5.rai

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                                                                                                                            Query Match 61.5%; Score 32; DB 3; Length 280; Best Local Similarity 60.0%; Pred. No. 65; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                             Search completed: June 10, 2003, 13:51:31
Job time: 11.6429 secs
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-772-6
                                                                                                                                                                                                  1 EEVVPXGMSY 10
||| | |:|
75 EEVFPLAMNY 84
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein . protein search, using sw model

June 10, 2003, 13:46:50 ; Search time 15 Seconds (Without alignments) 75.710 Million cell updates/sec Run on:

1 EEVVPXGMSYS 11 US-09-909-164-5 52 Perfect score: Sednence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: 392085 seqs, 103240269 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 75 summaries Match 100% Maximum

Database :

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/cgn2_6/ptodate/2/pubpaa/USO0_NEW_PUB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1061, Appl Sequence 1061, Appl Sequence 4, Appli Sequence 4, Appli Sequence 73, Appl Sequence 73, Appl Sequence 108, Appl Sequence 208, Appl Sequence 208, Appl Sequence 208, Appl Sequence 66, Appl Sequence 53, Appl Description US-10-037-801-4 US-10-101-464A-73 US-10-101-464A-73 US-09-924-340-108 US-09-924-600A-108 US-09-926-600A-108 US-10-000-489-108 US-10-000-986-108 US-10-000-986-108 US-10-986-108 US-09-919-497-54 US-09-925-300-1061 US-09-923-304-4 US-10-024-066-2 US-10-024-066-4 US-10-027-806-4 SUMMARIES 10 10 9 Query Match Length DB 63.5 63.5 63.5 63.5 63.5 61.5 61.5 61.5 61.5 61.5 61.5 Score Result Š.

Sequence 2, Sequence 105 Sequence 107 Sequence 117 Sequence 117 Sequence 117 Sequence 117 Sequence 107 Sequence 2, Asquence 513 Sequence 5, Asquence 618 Sequence	Sequence 359, App Sequence 444, App Sequence 359, App
US-09-925-731-00-05-136-4 US-10-092-136-8 US-10-092-136-8 US-10-092-136-8 US-09-738-626-6 US-09-738-626-6 US-09-738-626-6 US-09-738-626-6 US-09-738-626-6 US-09-738-626-6 US-09-738-626-6 US-09-738-626-6 US-09-915-139-2 US-09-738-626-6 US-09-915-242-1 US-09-915-242-1 US-09-915-242-1 US-09-915-020-1 US-09-915-050-1	US-09-989-735-359 US-09-989-735-359 US-09-990-444-359 US-09-990-446-359 US-09-991-181-359 US-09-993-687-359 US-09-983-744-359 US-09-983-78-444 US-10-175-737-444 US-10-175-737-444 US-10-175-738-444 US-10-175-738-444 US-10-175-738-444 US-10-176-757-444 US-10-176-757-444 US-10-176-757-444 US-10-180-552-444 US-10-180-552-444 US-10-180-552-444 US-09-990-562-359 US-09-990-562-359 US-09-990-562-359 US-09-990-562-359 US-09-990-562-359 US-10-173-706-444
1377 110 2799 99 2799 99 53 10 53 10 53 10 53 10 163 99 1053 10 14053 10 14063 10 14063 10 1406 10 1406 10 151 10 121 10 121 10	
611.5 611.5	57. 57. 57. 57. 57. 57. 57. 57. 57. 57.
325 335 337 337 337 337 337 337 337 337 33	
00000000000000000000000000000000000000	55 57 57 57 57 57 57 57 57 57

ALIGNMENTS

Sequence 4, Application US/10027806
Patent No. US20020160476A1
GENERAL INFORMATION:
APPLICANT: Sender N. Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP 002A
CURRENT APPLICATION NUMBER: US/10/027,806 US-10-027-806-4 RESULT 1

Sequence 4, Appli

US-10-101-921-4

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Sequence 4, Application US/10034623

Publication No. US20020198365A1

GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: UNCLEC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILER REFERENCE: DCORP.002A

CURRENT APPLICATION NUMBER: US/10/034,623

CURRENT PILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FEASTED for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCRAILION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Scaleger, Christa
TITLE Schleger, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT APPLICATION NUMBER: BAPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NO 4
LENGTH: 3472
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020 PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3472;
                                                                                                                                                                                                                                        Score 38; DB 9; Length 3472;
Pred. No. 1.2e+02;
4; Mismatches 1; Indels
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54.5%; Pred. No. 1.2e+02;
tive 4; Mismatches 1; Indels
                                                     NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/10027801
; Publication No. US20030054364A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRGANISM: Cenarchaeum symbiosum
US-10-027-801-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Cenarchaeum symbiosum US-10-034-623-4
                                                                                                                                                    TYPE: PRT ; OKGANISM: Cenarchaeum symbiosum US-10-027-806-4
                                                                                                                                                                                                                                                Query Match 73.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5
Matches 6; Conservative
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LENGTH: 3472
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US-LU-IU1-404A-/3

Sequence 73, Application US/10101464A

Publication No. US20030046728A1

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.10262

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT APPLICATION NUMBER: 09/704,302

PRIOR PILING DATE: 2000-11-01

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-10-12

SPRIOR FILING DATE: 1999-11-01

SPRIOR FILING DATE: 1900-01-11

NUMBER OF SOI ID NOS: 989

SOFTWARE: FastSEQ for Windows Version 4.0

SEQUENCE: 100-01-13
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TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
FILE REFERENCE: CA1138
CURRENT APPLICATION NUMBER: US/10/214,766
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,734
PRIOR PILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
SEQ ID NO 43
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  Length 3472;
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66.7%; Pred. No. 1.8e+02;
Score 38; DB 9; I
pred. No. 1.2e+02;
4; Mismatches 1;
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; Publication No. US20030084473A1
; GENERAL INFORMATION:
            73.1%;
54.5%;
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Best Local Similarity 60...
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                                    Best Local Similarity 54.5
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
                                                                                                      1 EEVVPXGMSYS 11
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686 VMPSGISYS 694
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              Query Match
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1 EEVVPXGMSY 10

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APPLICANT: Tanaka, Hiroaki
IITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
Indels
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60.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <UNKNOWN>
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-746-783-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MIASINCIC, Debra J.
REGISTRATION UNBER: 46,931
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 108, Application US/10000489
Publication No. US20030092011A1
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
                                                                                                                                                                                                                                                                                                                                        Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 184:
                                                                                                                                                                                       Sequence 184, Application US/09746783; Publication No. US20030044935A1
GENERAL INFORMATION: APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                          McCoy, John M.
LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                  Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140
COMPUTER READABLE FORM:
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Matches 6; Conservative
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STATE: MA
    6; Conservative
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                                                                                 239 EVAPAGASYN 248
                                         2 EVVPXGMSYS 11
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US-10-000-489-108
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      Matches
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                                                                                                                         Sequence 108, Application US/09924340

Sequence 108, Application No. US20030027248A1

GENERAL INFORMATION.

APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hircaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.USZ.REG
CURRENT APPLICATION NUMBER: US/09/924,340

CURRENT APPLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-06-55

NUMBER OF SEQ ID NOS: 112

SOFTWARE: JPACENT.
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 9; Length 478; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 478;
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CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
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PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 108, Application US/09992600A Publication No. US20030027161A1 GENERAL INFORMATION: Stephane APPLICANT: Benjanin, Stephane APPLICANT: Tanaka, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%;
60.0%;
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Matches 6; Conservative
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SOFTWARE: JPatent
SEQ ID NO 108
LENGTH: 478
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        223 EFVIPAGOSY 232
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Best Local Similarity
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                                                                                                              US-09-924-340-108
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Gaps
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Fechtel, Kim TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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US-09-820-843A-26

Sequence 26, Application US/09820843A

Publication No. US20030039963A1

Sequence 26, Application No. US20030039963A1

SEQUENCE AND INTERPRATION:

APPLICANT: Council of Scientific and Industrial Research

TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES

FILE REFERENCE: Q63915 ANTI-INFECTIVES

CURRENT APPLICANTION NUMBER: US/09/820,843A

CURRENT APPLICANTION NUMBER: US/09/820,843A

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 26

SEQ ID NO 26

LENGTH: 653
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Sequence 66, Application US/09947387

Sequence 66, Application US/09947387

Sequence 66, Application Sequence 66, Application Sequence 66, Applications:

APPLICANT: Where, Ed., Sui Xiong

APPLICANT: Cai, Sui Xiong

APPLICANT: Cai, Sui Xiong

APPLICANT: Drewe, John A.

APPLICANT: Drewe, John A.

TITLE OF INVENTION: No. US20020150885Alel Fluorogenic or Fluorescence

TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

TITLE OF INVENTION: USCREEN TO 100-07

TITLE OF INVENTION: USCREEN TO 100-07

FILE REFERENCE: 1735.0290005

CURRENT APPLICATION NUMBER: US 60/061,582

PRIOR APPLICATION NUMBER: US 60/061,582

PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1998-10-09

NUMBER OF SEQ ID NOS: 142

SEGTWARE: Patentin Ver. 2.0

SEGTWARE: Patentin Ver. 2.0
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CTHER INFORMATION: iron(III) ABC transporter, permease protein

NAME/KEY: misc_feature

CTHER INFORMATION: gi|9654609

US-09-820-843A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 3.5;
3; Mismatches 2
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Vibrio cholerae FEATURE:
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Best Local Similarity 50.00
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LENGTH: 10
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| Publication No. US20030096247A1
| GENERAL Incomarian No. US20030096247A1
| GENERAL Incomarian Stephane | APPLICANT: Benjanin, Stephane | APPLICANT: Benjanin, Stephane | TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF CURRENT APPLICATION HUMBER: US/10/000,986 | USPUT OF ILLING DATE: 2001-11-14 | PRIOR APPLICATION NUMBER: US 09/924,340 | PRIOR PILING DATE: 2001-08-06 | PRIOR PLICATION NUMBER: PCT/IB01/01715 | PRIOR PLICATION NUMBER: US 60/305,456 | PRIOR PLICATION NUMBER: US 60/305,456 | PRIOR FILING DATE: 2001-06-15 | PRIOR FILING DATE: 2001-06-15 | PRIOR PLICATION NUMBER: US 60/298,698 | PRIOR FILING DATE: 2001-06-15 | PRIOR PLICATION NUMBER: US 60/293,574 | PRIOR 
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Pred. No. 1.4e+02;
1; Mismatches 3; Indels
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                          CURRENT PELLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR PAPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR PELLING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/202,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PELLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PELLING DATE: 2001-06-15
PRIOR PELLING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
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60.0%;
FILE REFERENCE: 91.US6.DIV
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Matches 6; Conservative
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Matches 6; Conserv
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LENGTH: 478
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RESULT 16
US-09-919-497-54
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                                                                                                                                 APPLICANT: KHOSRAVI, Rami et al.

ITTLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT PILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
SPRIOR FILING DATE: 2000-03-29
SPRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
LENGTH: 254
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APPLICANT: F1eld, Loren J.
APPLICANT: F1eld, Loren J.
APPLICANT: F1eld, Loren J.
APPLICANT: F1eld, Loren J.
APPLICANT: Pasumarthi, Kishore Babu S.
APPLICANT: PASUMARTHI, Kishore Babu S.
TITLE OF INVENTION: CANDOMYCOYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: CANDOMYCOYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: CANDOMYCOYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
THILD OF TOOR OF THE STATE 
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pred. No. 1.1e+02;
1; Mismatches 3; Indels
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Pred. No. 1.3e+02;
1; Mismatches 3; Indels
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                                  Sequence 53, Application US/09778927A Patent No. US20020068342A1
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; Patent No. US20020166134A1
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60.0%;
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60.0%;
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Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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73 EEVFPLAMNY 82
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                                                                                                              GENERAL INFORMATION:
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US-09-778-927A-53
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US-10-024-066-2
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US-10-024-066-4
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Sequence 4, Application US/10024066
Patent No. US20020166134A1
SERURAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Field, Loren J.
TITLE OF INVENTION: CARDIOMYCOTTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
CURRENT APPLICATION NUMBER: 60/139,942
PRIOR FILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-18
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTING VENTION NUMBER: 2010-06-19
NUMBER OF SEQ ID NOS: 8
LENGTH: 289
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| Patent No. US20020106662A1
| Patent No. US20020106662A1
| GENERAL INFORMATION
| TILE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
| FILE REFERENCE: B0801/725
| CURRENT APPLICATION NUMBER: US/09/919,497
| CURRENT FILING DATE: 2001-07-31
| PRIOR APPLICATION NUMBER: US 60/221,735
| PRIOR PILING DATE: 2000-07-31
| NUMBER OF SEQ ID NOS: 100
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 54
| LENGTH: 289
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Patent No. US20020151681A1

GENERAL INFORMATION:
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101

CURRENT APPLICATION UNDBER: US/09/925,300

CURRENT PILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08
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60.0%; Pred. No. 1.3e+02;
tive 1; Mismatches 3;
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Matches 6; Conservative
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Matches 6; Conservative
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US-09-919-497-54
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 691

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                                                                                                                                                                                                    LOCATION: (243)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/FEY: SITE
LOCATION: (277)
                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-300-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09923304
Patent No. US20020081612A1
Patent No. US20020081612A1
APPLICAMT: MATEL NUTH
APPLICAMT: JIANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
FILE REPERENCE: UTSC.658US
CURRENT APPLICATION NUMBER: US/09/923,304
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10101921
| Publication No. US20030022199A1
| GENERAL INFORMATION:
| APPLICANT: Nezu, Jun-Ichi
| APPLICANT: See, Asuka
| APPLICANT: Tsuji, Akira
| APPLICANT: Tsuji, Akira
| TTLE OF INVENTION: TRANSPORTER GENES OATP-B, C, D, AND E
| TILE REFRENCE: 06501-104US1
| CURRENT FILING DATE: 2002-06-28
| PRIOR APPLICATION NUMBER: PCT/JP00/06416
| PRIOR APPLICATION NUMBER: PCT/JP00/06416
| PRIOR APPLICATION NUMBER: PCT/JP00/06416
| PRIOR RILING DATE: 1999-09-21
| NUMBER OF SEQ ID NOS: 38
| SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2.46+02;
2; Indels
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VEF. 2.0
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                 NAME/KEY: SITE
                                                                                 SEQ ID NO 1061
LENGTH: 295
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US-09-923-304-4
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APPLICANT: Yanamotto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVEWTION: Identification of Essential Genes in
TITLE OF INVEWTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,727
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                     1; Indels
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62.5%; Pred. No. 3.2e+02;
ive 2; Mismatches 1; Indels
                                                                                         Score 32; DB 9; 1
Pred. No. 3.2e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: AMBROSE, HELEN JEAN
APPLICANT: CRESWELL, CARL JOHN
APPLICANT: DUDLEY, ADAM JESTON
TITLE OF INVENTION: CHEMICAL COMPOUNDS
FILE REFERENCE: DJB/009901/0282795
CURRENT APPLICATION NUMBER: 0S/09/925,731
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/226,909
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10384, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ADEOKUN, ANTHONI MONISOLA
                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/09925731
; Patent No. US20020090622A1
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                       61.5%;
62.5%;
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                                                                                  Query Match 61.5
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-921-4
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188 IVPLGLSY 195
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ORGANISM: Homo sapiens
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188 IVPLGLSY 195
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                                                                                                                                                                                                                                                                                   RESULT 20
US-09-925-731-2
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APPLICANT:
APPLICANT:
APPLICANT:
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Wed Jun 11 15:44:03 2003

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APPLICANT: Callaghan, Michelle J.
APPLICANT: Callaghan, Michelle J.
APPLICANT: Sutherland, Lindfield
APPLICANT: Sutherland, Lindfield
APPLICANT: Witherland, Lindfield
APPLICANT: Witherland, Lindfield
CURRENT: WATTON: No. US20020192160Alel Human Tumour Suppressor GeneFILE REFERENCE: RICE-010CON
CURRENT APPLICATION NUMBER: US/10/151,736
CURRENT APPLICATION NUMBER: US/403,402
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030054375A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION:

FILE REFERENCE: PC009C1

CURRENT FILIGO DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 2003

Prior Application removed - See File Wrapper or Palm

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 878

LENTH: 53
                                                                                                                                                                                                                                                                                                                           Score 32; DB 10; Length 1377;
Pred. No. 6.7e+02;
4; Mismatches 2; Indels (
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE FEASTERD FOR Windows Version 4.0
SEQ ID NO 10384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10151736 Publication No. US20020192160A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           Query Match 61.5%;
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                      ; ORGANISM: Escherichia coli US-09-815-242-10384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:| |||:
2096 EVLPTKMSYA 2105
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
US-10-092-154-878
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LENGTH: 2799
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FEATURE:

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                                ; OTHER INFORMÁTION: Xaa equals any of the naturally occurring L-amino acids 0S-10-092-154-878
                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                             Sequence 878, Application US/09764847

Patent No. US20020132767A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 2003

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 878

LENGTH: 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 10; Length 59;
Pred. No. 37;
3; Mismatches 3; Indels
                                                                                                     Length 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ANDERSEN, CARSTEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BAUDIT2, PETER
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/09/948,080
CURRENT FILING DATE: 2001-09-06
PRIOR FILING DATE: 1997-11-04
                                                                                                       6
                                                                                                   59.6%; Score 31; DB 66.7%; Pred. No. 33; ative 1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-948-080-14; Sequence 14, Application US/09948080; Patent No. US20020102702A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT;
CRGANISM: Enterococcus faecalis
US-09-948-080-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.68;
45.58;
                                                                                  Ouery Match
Best Local Similarity 66.7.
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Best Local Similarity 45.5
Matches 5; Conservative
NAME/KEY: misc_feature
LOCATION: (7)
                                                                                                                                                                                       3 VVPXGMSYS 11
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                          RESULT 24
US-09-764-847-878
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1 EEVVPXGMSYS 11 |::| |: || 38 EKHIPGGLEYS 48

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Search completed: June 10, 2003, 14:35:40 Job time: 16.0714 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 94.297 Million cell updates/sec June 10, 2003, 13:31:15; Search time 11.2143 Seconds Run on:

US-09-909-164-5 52

Title:

1 EEVVPXGMSYS 11 Scoring table: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 75 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical 367K	probable sulfate p	sulfate permease -	V1 protein - tobac	DNA segregation AT	hypothetical prote	hypothetical prote	zinc finger protei	topoisomerase IV s	DNA-binding protei	hypothetical prote	cell division inhi	probable ABC subst	hypothetical prote	┛	hypothetical prote		hypothetical prote	hypothetical prote	beta-ketoacyl-ACP	hypothetical prote	3-phosphoshikimate	cdc37 protein - fi	iron(III) ABC tran	bacteriocin BCN5 -	ATP-dependent DNA	conserved hypothet	transforming growt	DNA-directed RNA p
SUMMARIES	ID	T31308	T39116	T40413	A42452	B97355	S57810	T24111	S22293	H82691	A34203	S54619	H69491	C82900	140758	E90544	D69493	C81374	T34536	S75817	T47670	F72281	D82163	T43653	D82352	A30481	AF3286	D87046	A35626	G82336
	DB	5	7	•	7			~	•	•	C)		•	7	7		7				•						~	•	N	7
	Length DB	3472	840	877	102	1498	225	425	670	749	2717	156	252	544	94	116	165				298		426	466	653	890	1028	1152	1394	1401
dф	Query	73.1	71.2	71.2	69.2	69.2	67.3	67.3	67.3	67.3	67.3	65.4	65.4	65.4	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5		•		•	63.5	•	63.5	63.5
	Score	38	37	37	36	36	35	35	35	35	35	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
	Result No.	1	7	æ	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

thetical and protein protein of p	rhas protein precurbs protein in rh RhsH core protein in rh rhsC protein in rh rhsC protein in rh rhsA core protein rhsB protein precurbsB protein rhsB protein precurgen 1-1 protein trans-regulatory s hypothetical prote probable cobh probable pourQ prote probable pourQ prote probable purQ prote
104456 A38261 P000616 T01453 T01451 B72481 B72481 L58372 A41984 A41984 A41984 A41984 A41984 A41984 A41984 A55523 J02342 B55120 B55120 B55120 B55120 B6604 A56523 A56523 A56523 A56523 A56523 A56523 A56523 A56523 A56523 A56523 A56523 A56523 A56523 A56523 A6600	C61159 C66159 C66159 C661634 A95570 A95570 P91187 P91187 VKLC31 A71173 A71173 G707044 F87186
	00000000000000
1144 1712 1744 1744 1744 1744 1744 1744	1377 13377 13397 13397 1440 1399 1394 137 137 137 137 137 137 137 137 137 137
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88888888888444444444888888888888888888	000 000 000 000 000 000 000 000 000 00

ALIGNMENTS

RESULT 1

Typothetical 367K protein - Cenarchaeum symbiosum C; Species: Cenarchaeum symbiosum Species: Cenarchaeum symbiosum C; Species: Cenarchaeum symbiosum C; Species: Cenarchaeum symbiosum C; Species: Cenarchaeum symbiosum C; Species: Canarchaeum symbiosum C; Species: Canarchaeum Species: C; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V. J. Bacteriol. 180, 5003-5009, 1998
R; Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V. J. Bacteriol. 180, 5003-5009, 1998
R; Schleper: Z20994; MUID: 98422450; PMID: 9748430
A; Reference number: Z20994; MUID: 98422450; PMID: 9748430
A; Accession: T31308
A; Accession: T31308
A; Accession: T31308
A; Accession: T31308
A; Cossion: T31308
A; Cossion:

Gaps ; 0 Score 38; DB 2; Length 3472; Pred. No. 59; 1; Indels 4; Mismatches 1; Indels Ouery Match 73.1%; Best Local Similarity 54.5%; Matches 6; Conservative

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1 EEVVPXGMSYS 11

Gaps

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Length 102;

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C.Species: Clostridium acetobutylicum
C.Species: Clostridium acetobutylicum
C.Species: L4-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C.Accession: B97355
R.Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.;
J. Bacteriol. 183, 4823-4833, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B9735
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 11-498 KKUR>
A;Cross-references: GB:Ab001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA segregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein precursor (clone TPP11) - tomato
C; Species: Lycopersicon esculentum (tomato)
C; Deteis: Lycopersicon esculentum (tomato)
R; Milligan, S. B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A; Title: Nature and regulation of pistil-expressed genes in tomato.
A; Title: Nature and regulation of pistil-expressed genes in tomato.
A; Reference number: S57808; MUID:95375233; PMID:7647301
A; Reference number: S57810
A; Accession: S57810
A; Molecule type: mRNA
A; Residues: 1-225 cMIL>
A; Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:9924626
C; Superfamily: plant Kunitz-type proteinase inhibitor
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hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
R;Percy, C.
           A; Cross-references: GB: M81103; NID: 9335283; PIDN: AAA47947.1; PID: 9335284
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63;
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Pred. No. 13;
3; Mismatches 2; Indels
                                                                                  Score 36; DB 2;
Pred. No. 3.5;
3; Mismatches
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Pred. No. 63;
2; Mismatches
                                                                                  69.28;
60.08;
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60.0%;
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54.5%;
                                            Query Match
Best Local Similarity 60.00
Best Local 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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1276 EQKIPMGMSY 1285
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32 DEVVPNGKTYA 42
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B97355
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C; Species: tobacco yellow dwarf virus
C; Spacession: A42452
R; Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Viroloyy 187, 633-642, 1992
A; Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
A; Reference number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                              probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T39116
R; Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, November 1999
A; Reference number: 221829
A; Reference number: 221829
A; Reference number: 221829
A; Residue; preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-840 CHUN>
A; Cass-references: EMBL: AL132779; PIDN: CAB60015.1; GSPDB: GN00066; SPDB: SPAC869.05c
A; Experimental source: strain 972h-; cosmid c869
C; Genetics: SPDB: SPAC869.05c
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A;Experimental source: strain 972h-; cosmid c3H7
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Sacession: T40413
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Submitted to the EMBL Data Library, August 1998
A;Reference number: Z21926
A;Reference number: Z2
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Pred. No. 21;
1; Mismatches 1
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Pred. No. 22;
1; Mismatches 1
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77.8%;
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77.88;
| :|:| |:|:|
2294 EDVIPRGISFS 2304
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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A;Gene: SPDB:SPBC3H7.02
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A; Residues: 1-102 <MOR>
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T40413
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A42452
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67.3%;
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77.8%;
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Best Local Similarity 7/...
Ref. Local 7; Conservative
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Matches 6; Conservative
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A; Residues: 1-156 <DEH>
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C; Species: Xylella fastidiosa
C; Species: Sylella fastidiosa
C; Species: He2501
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature; The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Residues: I-749
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Residues: I-749
A; Cross-references: GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84162.1; GSPDB:GN001
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.J.S.
Submitted to Genbank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Rattus norvegicus (Norway Tat)
C; Species: Rattus norvegicus (Norway Tat)
C; Date: 29-dan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C; Accession: S22293; 178656
R; Mitchelmore, C.; Traboni, C.; Cortese, R.
R; Mitchelmore, C.; Traboni, C.; Cortese, R.
R; Mitchelmore, C.; Traboni, C.; Cortese, R.
A; Mitchelmore, C.; Traboni, C.; Traboni, T.; A; Tithe: Solation of two Conas encoding zinc finger proteins which bind to the alpha 1-A; Reference number: 158280; MUID:91187610; PMID:1901405
                  A; Reference number: 219842
A; Accession: T24111
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-425 < WILL>
A; Cross-references: EMBL: 281109; PIDN: CAB03241.1; GSPDB: GN00023; CESP: R10D12.10
A; Experimental source: clone R10D12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S22293
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-670 cMIT>
A; Cross-references: EMBL:X54250; NID:957519; PIDN:CAA38151.1; PID:957520
A; Note: the authors did not translate the codon for residue 1
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription regulation; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        67.3%; Score 35; 50.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zinc finger protein AT-BP2 - rat (fragment)
                                                                                                                                                                                                                                                                                                                          A; Introns: 23/3; 56/3; 113/3; 257/2
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Best Local Similarity 60...
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMSYS 11
                                                                                                                                                                                                                                      C,Genetics:
A,Gene: CESP:R10D12.10
A,Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
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chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martir A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; San A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.C.R.; da Silva, F.R.; da Silva, A.C.R.; da Silva, A.R.; Sulva Jr., M.A.; da Silva, A.R.; Sulva Jr., W.A.; da Silva, A.R.; Sulva Jr., M.A.; Asterence number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: XF1353
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Fan, C.M.; Maniatis, T.
Genes Dev. 4, 29-42, 1990
A;Title: A DNA-binding protein containing two widely separated zinc finger motifs t.
A;Reference number: A34203; MUID:90169514; PMID:2106471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNÅ
A; Residues: 1.217 FRNA
A; Cross-references: EMBL:X51435; NID:938017; PIDN:CAA35798.1; PID:938018
R; Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
Mol. cell. Biol. 10, 1406-1414, 1990
A; Fitle: A large protein containing zinc finger domains binds to related sequence e
A; Reference number: A34779; MUID:90205817; PMID:2108316
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A. Cross-references: GB:M32019
C. Superfamily: HIV-EP2 enhancer-binding protein
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hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
hypothetical protein O2612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; S66879
C;Accession: S54619; S66879
By Bublitted to the EMBL Data Library, May 1995
A;Reference number: S54617
A;Reference number: S54617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C;Accession: A34203; A34779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
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Pred. No. 1.9e+02;
2; Mismatches 1; Indels
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48;
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Pred. No.
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Gaps

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hypothetical protein 1 - Campylobacter jejuni (fragment)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140758; 2472, 1995
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine amic A;Reference number: 140758; MUID:95247673; PMID:7730270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90544
R;Chambaud, I:, Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer,
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A;Reference number: A99512; MUID:21267165; PMID:11353084
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D69493
hypothetical protein AF1949 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar*2000
C;Accession: D69493
R;Riens D69493
R;Riens H. H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dou.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, J. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes.
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A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50S ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: 236940; NID: 9535805; PIDN: CAA85392.1; PID: 9535806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.5%; Score 33; DB 2; Length 116; Best Local Similarity 77.8%; Pred. No. 17; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%; Score 33; DB 2; Length 94; ilarity 55.6%; Pred. No. 13; Conservative 2; Mismatches 2; Indels
                             Indels
                         5;
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A;Genetic code: SGC3
C;Superfamily: Escherichia coli ribosomal protein L20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                             Mismatches
                         1;
                    7; Conservative
                                                                                                                                                                                135 EEVVPHYLSY 144
                                                                                                1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMSYS 11
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Best Local Similarity
Laca 5; Conserva
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A;Molecule type: DNA
A;Residues: 1-116 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA A; Residues: 1-94 <RES>
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                Matches
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                                                                                                                 A;Molecule type: DNA
A;Residues: 1-156 <DEW>
A;Residues: 1-156 <DEW>
A;Cross-references: EMBL:274920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Accession: H69491
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.
F; Felschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A;Attle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A; Reference number: A69250; MuID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-252 <KLES
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R.Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A.Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A.Reference number: A82870
A.Refe
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C;Superfamily: cell division inhibitor minD
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 34; DB 2; Length 156; .66.7%; Pred. No. 14;
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submitted to the Protein Sequence Database, July 1996
A;Reference number: 866877
A;Accession: 866879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 2;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                           A; Map position: 15R
C; Superfamily: hypothetical protein YOR013w
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70.0%;
                                                                                                                                                                                                                                                                                                                          A; Cross-references: SGD:S0005539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 66.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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Best Local Similarity
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Best Local Similarity
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A;Gene: ABCsbp-5; UU359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Accession: C81374
R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A; Fitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A; Reference number: A81250; MUID:20150912; PMID:10688204
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: D69493
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                               A,Molecule type: DNA
A,Residues: 1-165 <KLE>
A,Cross-references: GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89307.1; PID:g264859
C,Superfamily: Archaeoglobus fulgidus hypothetical protein AF1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Cross-references: GB:AL139076; GB:AL111168; NID:96868128; PIDN:CAB73246.1; PID:9686842
A; Experimental source: serotype O2, strain NCTC 11168
C; Genetics:
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, Submitted to the Protein Sequence Database, October 1999
A;Reference number: 221540
A;Accession: T34536
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Pred. No. 39;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                 Length 165;
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A; Molecule type: mRNA
A; Residues: 1-259 <POU>
A; Cross-references: EMBL:AL122063
A; Experimental source: adult testis; clone DKF2p434C031
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein DKFZp434C031.1 - human (fragment)
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40;
                                                                                                                                                                                                                               Score 33; DB 2;
Pred. No. 25;
1; Mismatches
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55.6%;
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ilarity 60.0%;
Conservative
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                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-253 <PAR>
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Best Local Similarity
Matches 6; Conserv
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III I III. EVAPAGASYN 31

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Ciprocies: Synechocystis sp.
A; Variety: PCC 6803
C; Accession: S7-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; Accession: S75817
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Y. A; A; I) 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechoc
                                                                                                                                                                                                                                                                                                               A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S75817
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DMA
A; Residues: 1-284 <KAN>
A; Residues: 1-284 <KAN>
A; Residues: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18276.1; PID:d1
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nilternate names: protein T26112190
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
C; Accession: T47670
B: Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, K submitted to the Protein Sequence Database, February 2000
A; Reference number: 224471
A; Reference number: 224471
A; Reference number: BNA
A; Residues: 1-298 < MON>
A; Residues: 1-298 < MON>
A; Residues: 1-298 < MON>
C; Genetics: C; Genetics: Columbia; BAC clone T26112
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72281
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; H
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 25/3
A; Note: T26112.190
C; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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hypothetical protein slr1275 - Synechocystis sp. (strain PCC 6803)
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47;
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Pred. No.
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55.6%;
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Matches 5; Conservative
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187 IVPGGLAYS 195
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Best Local Similarity
Matches 5; Conserv
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iron(III) ABC transporter, permease protein VC0203 [imported] - Vibrio cholerae (str. C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: 18-aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: D8-200
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller J. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 200
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833; PMID: 10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-653 <HEI>A;Cross-references: GB:AE004110; GB:AE003852; NID:g9654600; PIDN:AAF93379.1; GSPDB:GA;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics:
                              A; Cross-references: EMBL: AL049769; PIDN: CAB42371.2; GSPDB: GN00067
                                                                                                                                                                                                                                                                                                                                                                                                      Length 466;
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Pred. No. 1.1e+02;
2; Mismatches 1;
                                                                                                                                                                 A; Accession: T43654
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-466 < WE2>
                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 2;
Pred. No. 76;
2; Mismatches
                                                                                                                                                                                                                                                     A)Cross-references: EMBL:AJ132377; PIDN:CAB38758.1
C;Genetics:
                                                         A; Experimental source: strain 972h-; cosmid c9B6
                                                                       R;Westwood, P.K.; Preston, N.C.; Fantes, P.A. submitted to the BMBL Data Library, March 1999 A;Description: Schizosaccharomyces pombe cdc37 A;Reference number: 222603
                                                                                                                                                                                                                                                                                                                                                                                                      63.5%;
50.0%;
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Matches 5; Conservative
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98 DSAIPGGMSY 107
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A:Introns: 8/2; 17/2; 21/1
                                                                                                                                                                                                                                                                                                         A; Gene: cdc37; SPAC9B6.10
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les 6; Conserv
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       A; Residues: 1-466 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: DNA
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A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: D82352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: VC0203
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D82352
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Matches
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                                                                                                               GB:AE000512; NID:94981757; PIDN:AAD36291.1; PID:9498176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-phosphoshikimate 1-carboxyvinyltransferase VC1732 [imported] - Vibrio cholerae (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 1
C;Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG37 protein - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Date: 21-Jan.2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C.Accession: T43653; T40791; T43654
R.Westwood, P.K.; Preston, N.C.; Fantes, P.A.
Submitted to the EMBL Data Library, March 1999
A.Description: Schizosaccharomyces pombe cdc37 cDNA.
A.Accession: T43653
A.Scession: T43653
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-466 < WES.
A.Cross-references: EMBL.AJ32376; PIDN:CAB38757.1
R.Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
Submitted to the EMBL Data Library, May 1999
A.Reference number: Z21875
A.Accession: T40791
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
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                A Accession: F72281
A Status: preliminary
A Molecule type: Day
B A Molecule type: Day
B A Residues: 1.368 CARN>
A Cross-references: GB: AE001778; GB: AE000512; NID: 94981757;
A PEXPERIMENTAL SOURCE: Strain MSB8
C ; Genetics:
A ; Gene: TM1216
C; Superfamily: NADH dehydrogenase (ubiquinone) 49K protein
A; Reference number: A72200; MUID: 99287316; PMID: 10360571
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                                                                                                                                                                                                                                                         DB 2;
59;
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Pred. No. 59;
3; Mismatches
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Pred. No. 69;
1; Mismatches
                                                                                                                                                                                                                                                         63.5%;
55.6%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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294 IVPKGMAYA 302
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Matches 5; Conserv
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Dacteriocin BCN5 - Clostridium perfringens plasmid pIP404
C;Species: Clostridium perfringens
C;Date: 31-Mar-1992 #text_change 24-Nov-1999
C;Date: 31-Mar-1992 #text_change 24-Nov-1999
C;Accession: A30481; S03779
R;Garnier, T.; Cole, S.T.
J Bacteriol. 168, 1189-1196, 1986
A;Title: Characterization of a bacteriocinogenic plasmid from Clostridium perfringen A;Reference number: J70354; MUID:87057020; PMID:2877971
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-890 <GAR>
A;Cross-references: GB:M32882; GB:J03309; NID:g150738; PIDN:AAA98249.1; PID:g150739
C;Genetics:
A;Gene: bcn
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Gaps

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A; Genome: plasmid
C; Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5
C; Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin
C; Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5
C; Superfamily: G5.5%; Score 33; DB 2; Length 890;
Best. Local Similarity G6.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 EVVPXGMSY 10
| | | | | | | | |
Db 170 EVVPGGFTY 178
Search completed: June 10, 2003, 13:49:09
Job time: 13.2143 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:25:04; Search time 4.5 Seconds (without alignments) 101.387 Million cell updates/sec Run on:

1 EEVVPXGMSYS 11 US-09-909-164-5 52 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description		_		Q04351 clostridium	P15822 homo sapien	-		_	-			Q9nzm5 homo sapien						Q04827 rattus norv	P30279 homo sapien		Q90459 brachydanio		_	P53782 xenopus lae	_	-	2	~	80	7	homo i	homo	P52384 numan nerpe
SUMMARIES		TI.	CARB_FUSNN	SULH_SCHPO	Y11K_TYDVA	Y1A9_CLOAB	ZEP1_HUMAN	CY14_NEUCR	A10C_HUMAN	RL20_MYCPU	Y990_CAMJE	AROA_VIBCH	CC37_SCHPO	GSR2_HUMAN	BCN5_CLOPE	LTBS_HUMAN	RPOC_VIBCH	LTBL_HUMAN	LTB1_RAT	CGD2_RAT	CGD2_HUMAN	CGD2_MOUSE	CGD1_BRARE.	CGD1_XENLA	CGD2_CHICK	CGD2_XENLA	CGD1_CHICK	CGD3_HUMAN	CGD1_HUMAN	CGD1_MOUSE	CGD1_RAT	TOLB_HAEIN	ENP3_HUMAN	OAT6_HUMAN	PRTP_HSV6U
		8 : BB :	Н	-	-	Н	-		7	-	Н	Н	Н	-	-	-	_	-	Н	-	1	Н	Н	-	Н	-	,	-	Н	Н	П	Н	7	, ,	-
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,	% Query	Match	73.1	71.2	69.2	69.5	67.3	65.4	65.4	m	63.5	63.5		٠	63.5				٠		٠	٠	61.5	•	•	•	•	61.5	•	61.5	٠		٠	61.5	6.1d
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	Result	No.	7	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	. 26	27	28	29	30	31	32	3,5

		Q9uey8 homo sapien . Q9qyb5 mus musculu Q61586 mus musculu P97564 rattus norv O94489 schirosacch P00577 escherichia Q9ueg0 caenorhabdi p19102 senorhabdi	028825 archaeoglob 09uhf0 homo sapien 06903 aquifex aeo 09rgy0 lactobacill 026270 methanobact 092pil rhizobium m P57489 buchnera ap 059042 methanococc 09zle3 helicobacte P5606 helicobacte P5606 helicobacte P58233 rattus norv P87033 ustilago ma P28331 salmonella
	REV_SIVCZ 1 CODB, MYCTU PURO_PYRHO PURO_MYCTU PURO_MYCLE PURO_MYCLE PURO_MYCLE 1 PURO_MYCLE 1 PURO_MYCLE 1 PURO_MYCLE 1 PURO_MYCLE 1 PURO_MYCLE 1 PURO_MYCLE 1 PURO_MYCLE 1 PURO_REATH 1 Y939_METJA 1 VHAI_CRYPA 1 PURA_YEAST 1 NOM2_PSEAE		
	24888444469846 200088444460846 248884446098646		
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34 35 37 39 40	7444444444 0000000000000000000000000000	54 55 57 50 50 60 60	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

STRAINFATCC 25586;
MEDLINE-21886394; PubMed=11889109;
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ARCC 25586.";
J. Bacteriol. 184:2005-2018(2002).
-: CATALYITC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + CARB_COSNN STANDARD, PRT, 1058 AA.

GARGG6;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 41, Last annotation update)
phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-CARB OR FN0422. Fusobacterium nucleatum (subsp. nucleatum). Bacteria; Fusobacteria; Fusobacterium. NCBI_TaxID=76856; CARB_FUSNN RESULT 1

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3 VVPXGMSYS 11
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                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                       -I- PATHWAY: Pyrimidine biosynthesis; first step.
-I- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manganese; Complete proteome.

1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

12 546 OLIGOMERIZATION DOMAIN.

1929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

1058 ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
ATP-binding; Manganese; Complete proteome.
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Pred. No. 6.2;
3; Mismatches 1; Indels
phosphate + L-glutamate + carbamoyl phosphate.
-!- COFACTOR: Binds three manganese ions (By similarity).
-!- PATHWAY: Arginine biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPBC3H7.02.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                  EMBL; AE010554; AAL94625.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005483; CPSse_L.
InterPro; IPR005483; CPsse_L.D2.
InterPro; IPR005480; CPsse_L.D3.
InterPro; IPR005481; CPsse_L.D3.
InterPro; IPR00481; CPsse_L.D3.
InterPro; IPR004852; MGS_like.
Pfam; PF00289; CPssse_L.Chain; 2.
Pfam; PF02786; CPssse_L.D2; 2.
Pfam; PF02781; CPssse_L.D3; 1.
Pfam; PF02142; MGS; 1.
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60.08;
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190 EIVPNGLNYS 199
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832 83
1058 AA;
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NCBI_TaxID=4896;
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ID SULH_SCHPO
AC 074377;
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NP_BIND
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MEDLINE-21848401; PubbWed=11859360;

RA Squirs=9/4.

RA Squirs J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Squirs J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Squirs J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgon G.,

RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgon G.,

RA Gentles S., Mungall N., Murphy L., Niblett D., Odell C.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Monoby P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Nutherford K., Rutter S., Sanders D., Quall M.A., Rabbinowitsch E.,

RA Rutherford K., Rutter S., Sanders D., Stevens K.,

RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Woestl D., Hilbert H., Nochlardt R., Pohl T.M.,

RA Gabel C., Fuchs M., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dimeno S., Gloux S., Lelaure V., Mottler S.,

Lucas M., Rochet M., Gaillardin C., Honce K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Manstrong J., Forsburg S.L.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Paulsen I., Potashkin J.,

RA Gerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Dominguez A., Revuelte J.L., Moren S., Armstrong J., Potashkin J.,

RA Rayler Walls Shapavovski G.V., Ussery D., Barrell B.G., Nurse P.,

Rayler Walls Shapavovski G.V., Barrell B.G., Nurse P.,

Rayler Walls Shapavovski G.V., Barrell B.G., Nurse P.,

Raylor R., Rayler M., Raylard R., Rayler M., Rayler M., Rayler W., Rayler M., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLUTAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
-!- SIMILARITY: CONTAINS 1 STAS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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InterPro; IPR001902; Sulfate_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00316; Sulfate_transp; 1.
Pfam; PF01740; STAS; 1.
TGRFAMS; TIGRO0815; Sulp; 1.
PROSITE; PS01130; SLC26A; 1.
PROSITE; PS50801; STAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96373 MW;
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461
484
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877 AA;
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NP_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                            MEDLINE=92188538; PubMed=1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; the nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyladonous plants."; Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; Length 102;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l protein.
102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                              Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                              102 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002621; Gemini_mov. Pfam; PF01708; Gemini_mov; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein CAC3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.2%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||| |::||
7 QVVPSGINYS 16
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148 VVPQGMSYA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A42452; A42452.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                              NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                             Y11K_TYDVA
P31619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                 Y11K_TYDVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-EP1) (Major histocompatibility complex binding protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                             to frameshifts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High-resolution three-dimensional structure of a single zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                              Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: BELONGS TO THE FISK/SPOILIE FAMILY.
-!- CAUTION: Ref. 2. sequence differs from that shown due to frameshif in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fan C.M., Maniatis T.;
"A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92232684; PubWed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "High-resolution solution structure of the double Cys2His2 zinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 1498;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL).
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MEDLINE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X65276; CAA46379.1; ALT_FRAME.
InterPro; IPR002543; FtsK.SpoIIIE.
Pfam; PF01580; FtsK_SPOIIIE.
Hypothetical protein; ATP-binding; Complete proteome.
MP_BIND 675 682 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from a human enhancer binding protein in solution.";
Biochemistry 29:9324-9334(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
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60.0%;
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRDII-BF1)
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15-JUN-2002 (Rel. 41, Last annotation update)

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                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Gaps
                                                                                                        -!- SUBCELLULAR LOCATION: Nuclear.
-!- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
-!- DOMAIN: CONTAINS TWO SETS OF 2 ZING-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZING-FINGER IN-BETWEEN.
-!- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00355; ZnF_C2H3; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Transcription regulation; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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Pred. No. 70;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C2HC-TYPE (POTENTIAL).
ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2H2-TYPE
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                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000822; Znf_C2H2. Pfam; PF00096; zf-C2H2; 5. PRINTS; PR00048; ZINCFINGER.
                                                                                                                                                                                                                                                                                   EMBL; X51435; CAA35798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.78;
                                                                                             T-CELL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:4920; HIVEP1.
MIM; 194540; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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2405 VVPAGLTYS 2413
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2088
2092
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                                                                                                                                                                                                                                                                                                       PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
TRANSFAC; T00497; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                PIR; A34203; A34203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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2099
2109
2115
2123
2123
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P23622;
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ZN_FING
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ZN_FING
DOMAIN
ZN_FING
ZN_FING
ZN_FING
STRAND
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                                                                                                                                                                                                                    Gaps
                                                                                                                      Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.; "Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
4FC604B60798CE77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 788;
Pred. No. 32;
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InterPro; IPR001902; Sulfate_transp.
Pfam, PF00916; Sulfate_transp; 1.
TIGRPAMS; TIGR00815; Sulp; 1.
PROSITE; PS01130; SLC26A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M59167; AAA33615.1; ALT_SEQ.
                                                                                               SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
                                                                                                                                                                                                             MEDLINE=94188926; PubMed=8140616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred
                                                                                                                                                                        Biochemistry 30:1780-1787(1991).
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060312; 096914;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%;
66.7%;
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6; Conservative
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            Sulfate permease II.
                                                                                                                                                                                                PROBABLE REVISIONS.
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                                     Neurospora crassa.
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FRANSMEM
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Best Local
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ID A10C_HU
AC 060312;
DT 30-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     small intestine.

SINCE AND STATES THE ATPLOCE MAY BE A CAUSE OF ANGELMAN SYNDROME (AS), also known as 'happy puppet syndrome'.

SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21225279; PubMed-11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saltoh S.
                                                                                                                                                                                            ....... maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; att. Genet. 28:19-20(2001).
                                 (EC 3.6.3.1) (ATPVC)
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-21313119; PubMed-11353404;
Herzing L.B.K., The Name S.-J., Cook E.H. Jr., Ledbetter D.H.;
Herzing L.B.K., The human aminophospholipid-transporting ATPase gene ATP10C maps adjacent to UBB3A and exhibits similar imprinted expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kidney, followed by lung, brain, prostate, testis, ovary, and
                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Potential phospholipid-transporting ArPase VC Aninophospholipid translocase VC).
ATPLOC OR ATPVC OR KIAA0566.
                                                                                                                                                                                                                                                                                                                                       J. Hum. Genet. 68:1501-1505(2001).
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JOINED.
JOINED.
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JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB051358; BAB47392.1; -.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 337-1499 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK33100.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY029502; AAK33100.1;
AY029503; AAK33100.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK33100.1;
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                                                                           Homo sapiens (Human).
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY029488;
AY029489;
AY029490;
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                                                                                                                                                                                                                                                                                                                                                                                 rissue-Brain;
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"The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis."; Nucleic Acids Res. 29:2145-2153(2001).

-I- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL SUBDUIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS OF THAT SUBDUIT (BY SIMILARITY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F., Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                   PRINTS; PRO0119; CATATPASE.
NOSOSITE; PSO0154; APPASE_B1_E2; 1.
Hydrolass; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=2107;
                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
PADSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 1; Length 1499;
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                > R (IN REF. 3).
D4996A4D0635A68D CRC64;
                                                                                                                                                                                                                                                                                          POTENTIAL. EXTRACELLULAR (POTENTIAL).
                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                            CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                CYTOPLASMIC (POTENTIAL)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                    POTENTIAL
                  Interpro; IPR001757; Arpase_E1-E2.
Interpro; IPR001454; Hlgnase/hydrlase.
Pfam; PF00702; Hydrolase; 1,
                                                                                                                                                                                                                                                POTENTIAL
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MEDLINE=21267165; PubMed=11353084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                  65.4%;
                                                                                                                                                                                                                                                                                                                                                                                            167687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Last
15-JUN-2002 (Rel. 41, Last
50s ribosomal protein L20.
RPLT OR MYPU_2610.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEVVPRGGSVS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMSYS 11
                                                                                                                                                                                      11087
11108
11119
11140
11170
11228
11228
11292
11499
1427
10331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma pulmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           427
427
1031
1035
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193
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                                                                                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                               223
        105830;
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Q98QV0;
                                                                                                          TRANSMEM
DOMAIN
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TRANSMEM
DOMAIN
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qq
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. EMBL; Z36940; CAA85392.1; -. Hypothetical protein; Complete proteome. SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;

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MEDLINE-20150912; PubMed=10688204;
MEDLINE-20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 43431 / TGH 9011;
MEDILINE=95247673; PubMed=7730270;
Hani E.K., Chan V.L.;
"Expression and characterization of Campylobacter jejuni
benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mypuaco.
InterPro: IRR001081; Ribosomal_L20; 1.
Pfam; PF00453; Ribosomal_L20; 1.
PRINTS; PR00062; RIBOSOMALL20; 1.
ProDom; PD002389; Ribosomal_L20; 1.
IIGREAMS; TIGRE01032; Pp1T_bact; 1.
PROSITE; PS00937; RIBOSOMAL_L20; 1.
Ribosomal protein; IRNA-binding; Complete protecome.
CROTENCE 116 AA; 13565 MW; C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y990_CAMJE STANDARD; PRT; 253 AA. P4548; O9PNV0; O1-NOV-1995 (Rel. 32, Created) CCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein Cj0990c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No
                                                                                                                                                                                                                                                                                                                                                                     reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 177:2396-2402(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 77.8
nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SERAIFEI TOT NIG961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                               enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODUCT PRODUCT PROPERTY PRODUCT PRODUCT PRODUCT PRODUCT PROPERTY PRODUCT PROPERTY PROBLEM PROSTIE; PS000867; EPSP_SYNTHASE_1; 1.

PROSITE; PS000867; EPSP_SYNTHASE_2; 1.

Aromatic amino acid blosynthesis; Transferase; Complete proteome. SEQUENCE 426 As; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
                 63.5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 16; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1; Length 426;
Pred. No. 27;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                      426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001986; EPSP_syntase.
                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE004251; AAF94882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%;
60.0%;
Query Match
Best Local Similarity 55.v.
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 EFVIPAGQSY 232
                                                                                                                             185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMSY 10
                                                                                         2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sixth step.
                                                                                                                                                                                                                                                                                                                                                AROA OR VC1732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VC1732;
                                                                                                                                                                                                                   AROA_VIBCH
Q9KRB0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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RRC STRANN-972,

RAM MEDIINE-21848401; PubbHed=11859360;

RA MEDLINE-21848401; PubbHed=11859360;

RA God V., Gwilliam R., Hayles J., Baker S., Basham D., Bowann S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Mongall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Ritherford K., Rutter S., Saudres R., Seeger K., Sharp S.,

RA Stelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Goffeau A., Cadlelu E., Dreano S., Gloux S., Lelaure V., Mortler S.,

RA Golfeau R., Cadleu E., Dreano S., Gloux S., Lelaure V., Mortler S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Spakovski G.V., Ussery D., Barrell B.G., Nurse P.,

RA Spakovski G.V., Ussery D., Barrell B.G., Nurse R.,

RA Shapavorski G.V., Ussery D., Barrell B.G., Nurse P.,

RH The genome sequence of Schizosaccharomyces pombe.";

Rature 415:871-880(2002).

C. ''Subbases, Cresulting in stabilization and promotion of their activity (By similarity).

L'Inseel R., Linker R., Willed R., R., Palsen I., Subbases R., Lesulting in stabilization and promotion of their stabilization activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
HSp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDc37 OR SPAC9B6.10.
                                                                                                                                                                                                                                                                                                                                                                                                            Westwood P.K., Preston N.C., Fantes P.A.; "Schizosaccharomyces pombe cdc37 gene."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ132377; CAB38758.1; -.
EMBL; AJ132376; CAB38757.1; -.
EMBL; AL049769; CAB42371.2; -.
CABPERONE; CELL division; Cell cycle.
SEQUENCE 466 AA; 52554 MW; 647238B34CABB3C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinases (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: BELONGS TO THE CDC37 FAMILY.
                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                          Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                             STANDARD;
                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                             CC37_SCHPO
094740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=972;
                    CC37_SCHPO
RESULT 11
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Nuclear.
-:- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
-:- SIMILARITY: BELONGS TO THE GLISCR2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20175430; PubMed-10708517;
MEDLINE-20175430; PubMed-10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ueki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Schetthauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 199-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
                                         ;
                                                                                                                                                                                                                               Q9NZM5; Q9NPD1; Q9NPR4; Q9UF12; Q9BTC6; Q9HAX6; 16-CTT-2001 (Rel. 40, Created) 116-CCT-2001 (Rel. 40, Last sequence update) 15-UVN-2002 (Rel. 41, Last annotation update) Glioma tumor suppressor candidate region gene 2 protein (p60).
   Length 466;
                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andreu N., Estivill X., Escarceller M., Sumoy L.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                           Mismatches
   Score 33; DB Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF182076; AAF62873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC004229; AAH04229.1; -. EMBL; BC006311; AAH06311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 218-477 FROM N.A.
63.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 12-478 FROM N.A.
 Query Match 63.5
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 64:44-50(2000).
                                                                                                                   98 DSAIPGGMSY 107
                                                                               1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Testis;
                                                                                                                                                                                                                   GSR2_HUMAN
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                                                                                                                                                                                             GSR2_HUMAN
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D -> H (IN REF. 3).
PEGNIINDREKSFQRRNMIEPRERAKFKRYKVKLVEKRAF
                                                                                                                                                                                                                                                                            EGNIIRDREKSFORRNMIEDRERAKFRKKKKVKLVEKRAFR
EIQL -> RGQHSFETGSRAFRGGI (IN REF. 3).
7F18923E348CB52B CRC64;
                                                                                                                                                         RRKEQLWEKLAKQGELPREVRRAQARLLNPSATRAKPGPQD
                                                                                                                                                                     TVERP -> SGRSSYGRSWPSRASSPGGAQGPSPVAQPFCN
                                                                                                                                                                                                                                                       REIQ -> VLTVSCRGAPCPVMTPSLLPVPPRGYGRHHGCP
WAGPVGPMPRG (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                KGPNPAPCHRIAA (IN REF. 3).
SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWFGCLFPG (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; Plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garnler T., Cole S.T.; "Studies of UV-inducible promoters from Clostridium perfringens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garnier T., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium perfringens and molecular genetic analysis of the bacteriocin-encoding gene.;
J. Bacteriol. 168:1189-1196(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                         R -> Q.
/FTId-VAR_011486.
GGS -> HEG (IN REF. 2; AAH04229).
G -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                DB 1; Length 478; 30;
                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN'1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
Bacteriocin BCN5.
                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                               Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
EMBL; ACS96124; AR410095.1; EMBL; ACS96124; AG30413.1; EMBL; AL359335; CAB94786.1; EMBL; AL122063; CAB94787.1; EMBL; AL122063; CAB94787.1; EMBL; AL122063; CABS942.1; Genew; HGNC.4333; GLTSCR2.
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MEDLINE=88336297; PubMed=2901768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87057020; PubMed=2877971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89039249; PubMed-2460717;
                                                                                             Nuclear protein; Polymorphism.
                                                                                                                                                                                                                                                                                                    478 AA; 54417 MW;
                                                                                                                                                                                                                                                                                                                             63.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium perfringens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                  239 EVAPAGASYN 248
                                                                                                                                6
9
191
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                                                                                                                                                                                             215
                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sarnier T., Cole S.T.;
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                             9
                                                                                                                                                                                                                  235
                                                                                                                                                                                                                                                                              434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1502;
                                                                                                                                                                                           198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pIP404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CPN50
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ID BCN5_CLOPE
AC P08696;
                                                                                                                                             CONFLICT
                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                               CONFLICT
                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                                                                                                                                                                             Query Match
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETAL FROM PLATELETS IS COMPOSED OF THE TGF-BETAL MOLECULE NONCOVALENTLY ASSOCIATED WITH A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETAL PRECURSOR AND A THIRD COMPONENT DENOTED TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA1-BP. TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.
-!- ALTERNATIVE PRODICTS: 2 isoforms; a short form (shown here) and a long form (AC Q14706); are produced by alternative splicing.
-!- PTM: CONTAINS HYDROXILATED ASPARAGINE RESIDUES.
-!- PTM: The N-terminus is blocked.
-!- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Fibroblast, and Platelet;
MEDLINE-90275601; Pubmed-2150783;
Kanzaki T., Olofsson A., Worren A., Wernstedt C., Hellman U.,
Miyazono K., Claesson-Welsh L., Heldin C.-H.;
"TGF-beta 1 binding protein: a component of the large latent complex of TGF-beta 1 with multiple repeat sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUC-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1S precursor
(Transforming growth factor beta binding protein 1) (TGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 890; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                             DOMAIN 815 869 HYDROPHOBIC.
SEQUENCE 890 AA; 96699 MW; F4E5E8971C31C6C6 CRC64;
              MOI. Microbiol. 2:607-614(1988).
-!- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-!- INDUCTION: BY UV IRRADIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                     EMBL; M14481; AAA98248.1; -.
EMBL; M32882; AAA98249.1; -.
PIR; A30481; A30481.
Interpro; IPR003646; SH3_bac.
SMART; SM00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 EVVPGGFTY 178
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vivo and in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                LTBS_HUMAN
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REPEAT C.

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15.

EGF-LIKE 15.

EGF-LIKE 15.

EGF-LIKE 15.

EGF-LIKE 15.

EGF-LIKE 16.

EGF-LIKE 17.

EGF-LIKE 17.

EGF-LIKE 16.

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EGF-LIKE 16.

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EGF-LIKE 17.

EGF-LIKE 16.

EGF-LIKE 16.

EGF-LIKE 16.

EGF-LIKE 16.

EGF-LIKE 17.

EGF-LIKE 16.

EGF-
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EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                              PROSITE; PS00010; ASX_HYDROXYL; 13.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 11.
GROWTH Factor binding: Repeat; EGF-like domain; Hydroxylation; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL) REPEAT C.
                                                                                                                                                                                                                                                                                                                                                                                                  EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL) REPEAT A.
                                                                                                                                                                                                                                                                                                                                                                 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                           InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002212; Fibril-assoc.
Pfam; PF00008; EGF; 15.
                                                                                                                                                                                               Pfam; PF00683; TB; 4.
SMART; SM00179; EGF_CA; 13.
SMART; SM00001; EGF_like; 4.
               EMBL; M34057; AAA61160.1;
                                                                          Genew; HGNC:6714; LTBP1.
MIM; 150390; -.
                                                HSSP; P00750; 1TPG.
3lycoSuiteDB; P22064; -.
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3339
3339
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1084
1139
1262
1180
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1379
849
                  PIR; A35626; A35626.
HSSP; P00750. 1
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SIGNAL
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DISULFID
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SEQUENCE FROM N.A.

STRAIN=El Tor N16961,

MEDLINE=2040683; PubMed=10952301;

MEDLINE=2040683; PubMed=10952301;

Medicalberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CETACLY: DATA DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES (By similarity).

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).
RPOC OR VC0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW; DFFCA81A40B2C7D1 CRC64;
BY SIMILARITY.
BY SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId-CAR_000184
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Pred. No.
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45.5%;
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Q9KV29;
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CARBOHYD
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-! - SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE

[RNA](N).

us-09-909-164-5.rsp

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                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBBNIT: THE LARGE LATENT COMPLEX OF TGF-BETAL FROM PLATELETS IS COMPOSED OF THE TGF-BETAL MOLECULE NONCOVALENTLY ASSOCIATED WITH A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPEFILDE OF THE TGF-BETAL PRECURSOR AND A THIRD COMPONENT BENOTED TGF-BETAL-BP. TGF-BETAL-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETAL. ALTERNATIVE PRODUCTS: 2 isoforms; a short form (AC P22064) and a long form (shown here); are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1L precursor (Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Efficient association of an amino-terminally extended form of human latent transforming growth factor-beta binding protein with the extracellular matrix.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Fibroblast, and Platelet,
MEDLINE-90275601; PubMed-2350783;
Manzaki T., Olofsson A., Moren A., Wernstedt C., Hellman U.,
Miyazono K., Claesson-Welsh L., Heldin C.-H.;
"TGF-beta 1 binding protein: a component of the large latent complex of TGF-beta 1 with multiple repeat sequences.";
Cell 61:1051-1061(1990).
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN (BY similarity).
-1. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olofsson A., Ichijo H., Moren A., ten Dijke P., Miyazono K., Reldin C.-H.;
                                                                                                                                                                                                                                                                                                   DB 1; Length 1401;
                                                                                                                                                                                                                 Pfam; PF00623; RNA_pol_A; Pfam; Pfam; PF01854; RNA_pol_A2; 2.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                       1401 AA; 155021 MW; DFDB0F2B5514504F CRC64;
                                                                                                                                                                                                                                                                                                Score 33; DB 1
Pred. No. 93;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1595 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 270:31294-31297(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96125117; PubMed=8537398;
                                                                                                                                                                                        InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
                                                                                                                                                      EMBL; AE004121; AAF93502.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 347-1595 FROM N.A.
                                                                                                                                                                                                                                                                                               63.5%;
50.0%;
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                                                                                                                                                                                                                                                                                                           Best_Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  ::|{ |: ||
581 QIVPKGLPYS 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                   HSSP; Q9KWU6; 1HQM.
TIGR; VC0329; -.
                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 1401 AA
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Q14766;
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OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF_like.
InterPro; IPR000212; Fibril-assoc.
InterPro; IPR002212; Fibril-assoc.
InterPro; IPR002212; Fibril-assoc.
InterPro; IPR002212; Fibril-assoc.
InterPro; IPR00212; Fibril-assoc.
InterPro; IPR00181; EGF; 15.
IPROSITE; PS00010; Asx_HYDROXYL; 13.
IPROSITE; PS001186; EGF_2; 11.
IPROSITE; PS011186; EGF_2; 11.
IPROSITE; PS011187; EGF_CA; 15.
IPROSITE; PS01187; 
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EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
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EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL)
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-!- TISSUE SPECIFICITY: The long isoform is found in fibroblasts.
-!- PTM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1L.
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EMBL; M34057; AAA61160.1; ALT_INIT.
HSSP; P08709; 1BF9.
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SIGNAL 1 23 POTENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.

EGF-LIKE 1.

EGF-LIKE 2.

INTERNEL REPEAT 1.

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

INTERNEL REPEAT 2.

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-LIKE 17.
EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like domain; Hydroxylation; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE (POTENTIAL).
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EGF-LIKE 17.
-!- SIMILARITY: CONTAINS 18 EGF-LIKE DOMAINS
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SMART; SM00001; EGF_Like; 5.
PROSITE; PS000010; ASX_HYDROXYL; 13.
PROSITE; PS010022; EGF_L; 2.
PROSITE; PS01186; EGF_2; 10.
PROSITE; PS01187; EGF_CA; 15.
Growth factor binding; Repeat; EGF_1:
                                                                                                                                                                                                                         EMBL; M55431; AAA42235.1; -.
PIR; A38261; A38261.
H$SP; PL6109; IFSB.
InterPro: IPR000152; Asx hydroxyl.
InterPro: IPR001581; EGF-like.
InterPro: IPR001881; EGF_Ca.
InterPro: IPR002121; Fibril-assoc.
Pfam; PF00008; EGF; I6.
Pfam; PF00683; TB; 4.
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1 precursor (Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-1) (Transforming growth factor beta-1 masking protein, large subunit).
LYBP1.
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-1- SUBUNT: THE LARGE LATENT COMPLEX OF TGF-BETAL FROM PLATELETS IS
COMPOSED OF THE TGF-BETAL MOLECULE NONCOYALENTLY ASSOCIATED WITH
A MASKING PROTEIN CONSISTING OF A DISULFIDE-BONDED COMPLEX OF A
DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETAL PRECURSOR AND
A THIRD COMPONENT DENOTED TGF-BETAL-BP (OR MP LARGE SUBUNIT).
TGF-BETAL-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=91062373; PubMed=2247454;
Tsuji T., Okada F., Yamaguchi K., Nakamura T.;
"Molecular cloning of the large subunit of transforming growth factor type beta masking protein and expression of the mRNA in various rattissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
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N-LINKED (GLCNAC. .) (POTENTIAL).
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Pred. No. 1.1e+02;
3; Mismatches 3; Indels
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KEICPGGMGYT 610
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                                                     -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZIME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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MEDLINE-93205384; PubMed-8455931;
Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;
"Cyclins D1 and D2 are differentially expressed in human B-lymphoid cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92347851; PubMed=1386336; Xiong Y., Menninger J., Beach D., Ward D.C.; "Molecular cloning and chromosomal mapping of CCND genes encoding
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Pred. No. 2
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Interpro; IPR004367; Cyclin_Cterm.
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Pfam; PF02984; cyclin, 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
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60.0%;
                          Oncogene 8:1661-1666(1993).
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Genomics 13:575-584(1992).
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6; Conservative
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73 EEVFPLAMNY 82
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             cyclin D2
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxiD=10116;
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MEDLINE=93275661; PubMed=8502486;
Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
Francke U., Jolicoeur P.;
"The Vin-1 gene, identified by provirus insertional mutagenesis,
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Pred. No. 1.1e+02;
3; Mismatches 3; Indels
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01-0cr-1993 (Rel. 27, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
CCND2 OR VIN-1.
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718 KEICPGGMGYT 728
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  G1/S-specific cyclin D2
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                                                              Mus musculus (Mouse).
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                                                                                                                                             NCBI_TaxID=10090;
                             CCND2 OR CYL-2
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Q90459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                              EDLINE=92347850; PubMed=1386335; ..
.naba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Genomic organization, chromosomal localization, and independent
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Shar; Sh0284; cyclin_c, .

Shar; sh00385; cyclin; 1.

PROSITE; PS00292; CYCLINS; 1.

Cyclin; Cell cycle; Cell division; Multigene family.

Cyclin; Cell division; Multigene family.

Cyclin; Cell 
                                                                                                                                                                                                                                                        Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                to the EMBL/GenBank/DDBJ databases
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(Rel. 25, Last sequence update)
(Rel. 40, Last annotation update)
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1; Mismatches
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InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92347850; PubMed=1386335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M88080; AAA51928.1; JOINED.
EMBL; M88081; AAA51928.1; JOINED.
BERL; M88082; AAA51928.1; JOINED.
PIR; A42822; A42822.
PIR; S26580; S26580.
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                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-240 FROM N.A.
Oncogene 8:1049-1054(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:1583; CCND2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (START) TRANSITION
                                                                                                             Submitted (MAR-1993)
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                                                                                                                                                                                                     TISSUE=Bone marrow;
Strausberg R.;
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;
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16-OCT-2001 (
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P30280;
                                                                                                                                                                                                                                                                                                                                                                                                                                Look A.T.;
                                                                                        Miyajima
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CGD2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
-!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
A SERINE/THREONINE KINASE HOLOENZWE COMPLEX.
IMPARTS SUBSTREATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91235305; PubMed-1827757;
Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.;
Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.;
Colony-stimulating factor 1 regulates novel cyclins during the G1
phase of the cell cycle.";
Cell 65:701-713(1991).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                          Marks P.A.; "Cloning of a D-type cyclin from murine erythroleukemia cells."; Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
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                                                                                                                                                                          MEDLINE-92196134; Pubmed-1372445;
Kiyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 32; DB 1; Length 289; 60.0%; Pred. No. 29;
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SEQUENCE 289 Aa; 32897 MW; 58F322771DDIDA3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 36, Created) . (Rel. 36, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M83749; AAA37519.1; -.
EMBL; M86182; AAA37503.1; -.
PIR; B40035; B40035.
PIR; A41984; A41984.
MGD; MGI: 88314; Ccnd2.
InterPro; IPR004366; Cyclin.
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Pfam; PF02984; cyclin, 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
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                                                                               embryogenesis.";
Biochim. Biophys. Acta 1264:257-260(1995).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
(START) TRANSITION.
                                                                                                                                                           -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNI: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBGTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                    farden A., Salomon D., Geiger B.;
"Zebrafish cyclin D1 is differentially expressed during early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 32; DB 1; Length 291; 60.0%; Pred. No. 29; 1. Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00134; cyclin; 1. Pfam; PF02984; cyclin; 1. SMART; SM00385; CYCLIN; 1. PROSITE; PS00292; CYCLINS; 1. Cyclin; Cell cycle; Cell division. SEQUENCE 291 AA; 33067 MW; FAS274CBLB46D5EF CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2001 (Rel. 40, Last annotation update)
G1/S-specific cyclin D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR004366; Cyclin.
Interpro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X87581; CAA60885.1; -
ZFIN; ZDB-GENE-980526-176; cycdl.
                   MEDLINE-96138542; PubMed-8547308;
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Matches 6; Conservative
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P50755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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CGD1_XENLA
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Li H., Grenet J., Kidd V.J.;
"Structure and gene expression of avian cyclin D2.";
Gene 167:341-342(1995).
-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (START) TRANSITION.
-!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                  Score 32; DB 1; Length 291; Pred. No. 29;
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                                                                                                                                                                                                                     Indels
                                                       Pfam; PF02984; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00392; CYCLIN; 1.
PROSTIE; PS00292; CYCLIN; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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InterPro; IPR004367; Cyclin.
Pfam; PF00134; cyclin, 1.
Pfam; PF02984; cyclin, 1.
PROSTIE; PS00292; CYCLIN; 1.
        EMBL; X89475; CAA61664.1; -.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
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                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                CGD2_CHICK
P49706;
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-!- SUBDUTT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBDUIT IMPARTS SUBSTRAITS FREITELTY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                          early development.";
Biol. Cell 88:99-111(1996).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.5%; Score 32; DB 1; Length 291; 60.0%; Pred. No. 29; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                               SEQUENCE FROM N.A.
Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 291 AA; 32959 MW; 9A290F04F1531E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2001 (Rel. 40, Last annotation update)
61/S-specific cyclin D2.
CCND2.
              291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X89476; CAA61665.1; -. EMBL; X83503; CAA58493.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G1/S-specific cyclin D1.
              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGD1_CHICK
P55169;
             CGD2_XENLA
P53782:
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CGD2_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGD1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                     Li H., Lahti J.M., Kidd V.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
(START) TRANSITION. INTERACTS WITH THE CDK4 AND CDK6 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                              KINASES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%; Score 32; DB 1; Length 292; 60.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin; Cell cycle; Cell division; Multigene family. SEQUENCE 292 AA; 33263 MW; 7B543029DB45A67D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
Pfam; PF00134; cyclin, 1.
Pfam: PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00292; CYCLINS; 1.
                                                                                                                                                                                                                                                                                                                                                             EMBL; U40844; AAA83271.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
                                                       SEQUENCE FROM N.A.
Gallus.
NCBI_TaxID=9031;
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Search completed: June 10, 2003, 13:40:16 Job time : 5.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:30:25; Search time 25.7857 Seconds (without alignments) 87.898 Million cell updates/sec Run on:

US-09-909-164-5 52 1 EEVVPXGMSYS 11 Perfect score: Sequence:

ritle:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:* Database :

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:* sp_fungi:*
sp_human:*
sp_invertebrate:* 5: sp_nnemmal:*
7: sp_nhc:*
8: sp_organelle:*
9: sp_bhage:* sp_bacteriap:* sp_plant:* sp_rodent:* sp_virus:* 10: 11: 12:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

			Description	Q98fxl rhizobium l	Q8rq86 fusobacteri	074056 cenarchaeum	Q9ury8 schizosacch	Q8r126 mus musculu	Q8vd18 mus musculu	Q40129 lycopersico	Q9xvk4 caenorhabdi	043733 homo sapien	Q9bha5 plasmodium	Q9bh83 plasmodium	Q01487 rattus norv	Q9pdm6 xylella fas	Q14122 homo sapien	Q12479 saccharomyc	Q971s2 sulfolobus
SUMMARIES			a	Q98FX1	Q8RG86	074056	Q9URY8	Q8R126	Q8VD18	040129	Q9XVK4	043733	Q9BHA5	09вн83	001487	09PDM6	014122	Q12479	097152
			DB	16	16	7	ĸ	11	11	10	5	4	Ŋ	Ŋ	11	16	4	٣	17
	٠		Match Length DB	387	1063	3472	840	471	484	225	425	556	583	583	670	749	1902	156	219
	æ	Query	Match	73.1	73.1	73.1	71.2	69.2	69.2	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	65.4	65.4
			Score	38	38	38	37	36	36	35	35	35	35	35	35	35	35	34	34
		Result	No.	Н	7	3	4	5	9	7	80	6	10	11	12	13	14	15	16

028342 archaeoglob Q96mul homo sapien 092md rhizobium n Q98mb5 rhizobium n Q98mb5 rhizobium n Q98mt0 reaplasma O9urr4 pentcillium Q8xt0 ralstonia s Q96914 homo sapien 028330 archaeoglob Q8vua8 lactococcus Q94ma8 lactococcus Q94ma8 lactococcus Q94ma9 archaeoglob Q8vua8 lactococcus Q94mb5 soil-borne Q94mb5 soil-borne Q94mb5 soil-borne Q94mb5 soil-borne Q94mb5 soil-borne Q94mb5 soil-borne Q96mb5 mus musculu Q8xx0 mus musculu Q8xx0 mus musculu Q9xx0 mus musculu Q9xx0 mus musculu Q9xx0 mus musculu Q9xx1 sulfolobus Q9xx3 sulfolobus Q9xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	094819 09m3t4 05748 090b4 04284 032330 098xf1 098xf1 098xf1 098xf1
028342 098MD1 098MD1 098MD2 098MD2 098MR4 098MR4 098MR4 098MR4 098MR8 098MB3 098MB3 099009 099009 099009 099009 099009 099009 099009 090009	0998L9 0903T4 097A81 097CD0 047284 047284 032330 095XF1 091EM1 091EM1 091EX1
	7510 71301
1100334205252525252525252525252525252525252525	156 174 190 190 200 234 236 243 243 279
$\begin{array}{c} \alpha$	dadadadadada
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11112222222222222222222222222222222222	666 667 668 668 668 668 668 668 668 668

098FX1. 01-0CT-2001 (TrEMBLrel. 18, Created) 01-0CT-2001 (TrEMBLrel. 18, Last sequence update) 01-0CT-2001 (TrEMBLrel. 18, Last annotation update) Hippurate hydrolase. MLR3583. 387 AA PRT; PRELIMINARY; **Q98FX1** RESULT 1 Q98FX1 OF DI

us-09-909-164-5.rspt

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Query Match
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Q8R126
ID Q8R13
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                                                                                                                                                                        Kaneko T., Nakamura Y., Sator S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Sugimoto M., Complete genome structure of the nitrogen-fixing symbiotic bacterium DNA Res. 7:331-338(2000).
EMBL: Ap033002; BAB5045.1; -
InterPro; IPR002933; Peptidase_M20.
Pfam; PF01546; Peptidase_M20.
Pydrolase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 25586;
MEDLINE-1886394; PubMed=11889109;
Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R., Genome sequence and analysis of the oral bacterium Fuscbacterium nucleatum strain ATCC 25866.";
J. Bacteriol. 184:2005-2018(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 9.8; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            41180 MW; 131BFF8E64306829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1063 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusobacterium nucleatum (subsp. nucleatum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O74056;
01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                      SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; Pubmed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 6; Conservative
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367 DEAIPHGMSY 376
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195 EIVPNGLNYS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMSY 10
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                                                               NCBI_TaxID=381;
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Q8RG86;
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                                                                                                                                                                                                                                                                                                   "Genoric analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
J. Bacteriol. 180:5003-5009(1998).
-!- STMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
EMBL; AF083072; AAC62699.1; -..
InterPro; IPR000515; BPD_transp.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40.
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; Aliz2779, CAB6015.1; -.

InterPro; IPR002645; SanAs.

InterPro; IPR001902; Sulfate_transp.

Pfam; PF01140; STAS; 1.

Pfam; PF00116; Sulfate_transp; 1.

TIGRFAMS; TIGR00815; Sullp; 1.

SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CRC64;
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                                                                                                                                                                                                                                                         Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 3472;
Pred. No. 1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 3; Length 840;
Pred. No. 37;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WD repeat.
W; 37F80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPAC860.05C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Probable sulfate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00320; WD40; 2.

PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.

Hypothetical protein; Repeat; WD repeat.

SEQUENCE 3472 AA; 367058 WW; 37F80707030F9355 C
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                      Archaea; Crenarchaeota; Cenarchaeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                       STRAIN=B;
MEDLINE=98422450; PubMed=9748430;
                       01-JUN-2002 (TrEMBLrel. 21, Last
Hypothetical 367.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.18;
54.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.28;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 54.5%
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2294 EDVIPRGISFS 2304
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                              Cenarchaeum symbiosum.
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                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                NCBI_TaxID=46770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4896;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                  Query Match
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Q9XVK4;
                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                              CHAIN
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043733
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
14-pothetical 25.2 kDa protein precursor.
15-copersicon esculentum (Tomato).
15-copersicon esculentum (Tomato).
16-copersicon esculentum (Tomato).
16-copersicon esculentum (Tomato).
16-copersicon esculentum (Tomato).
17-copersicon esculentum (Tomato).
18-copersicon esculentum (To
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 11; Length 484;
                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1; --
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ECO17637; AAH17637.1; --
MGD; MGI:2138595; AW536441.
                                                                                                                                                                                                                                                                                                                SEQUENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
Q8R126;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 54.5 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 AA
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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Best Local Similarity 60.0-
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239 EVIPAGASYN 248
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226 EVIPAGASYN 235
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TISSUE=SALIVARY GLAND;
                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q8VD18
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Q40129
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Rhabditidae; Peloderinae; Caenorhabditis.
STRAIN=VP36; TISSUE-PISTIL;

X MEDLINE-95375233; PubMed=7647301;

MIlligan S.B., Gasser C.S.;

Milligan S.B., Gasser C.S.;

Mature and regulation of pistil-expressed genes in tomato.";

Plant Mol. Biol. 28:691-711(1995).

R PRBL, U95052; AAA80497.1; -.

R InterPro; IPR002160; Kunitz_legume.

R ProDom; PD000491; Kunitz_legume; 1.

R ProDom; P000452; STI; 1.

R PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.

M Hypothetical protein; Signal.
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Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 425;
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                  21 225 UNKNOWN.
225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
R10012.10 protein.
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043733;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281109; CAB03241.1; -
InterPro; IPR000719; Euk_pkinase.
Pfam; PF000609; Pkinase; 1.
Probom; PD000001; Euk_pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                        67.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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335 EQIVPGGLQY 344
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EMBL; AY007374; AAK14818.1; -.
EMBL; AY007373; AAK14817.1; -.
InterPro; IPR002123; AQYltransferase.
Pfam; PF01553; AQYltransferase; 1.
SEQUENCE 583 AA; 66918 MW; 4DF83D7530527474 CRC64;

DR DR SO

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                                                   Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ben Mamoun C., Gluzman I.Y., Goldberg D.E.,;
"Plasmodium falciparum choline transporter (PfSCT1) gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AY007372; AAR14816.1;
EMBL, AX007375; AAG17947.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ben Mamoun C., Gluzman I.Y., Goldberg D.E.; "Plasmodium falciparum choline transporter (PfSCT1) gene."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         Score 35; DB 4; Length 556;
Pred. No. 64;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%; Score 35; DB 5; Length 583; 55.6%; Pred. No. 67; 1.1ve 3; Mismatches 1; Indels
                                                                                                                   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 298050; CAB10847.1; ...
                                                                                                                                                                           SEQUENCE 556 AA; 59059 MW; ECB00E4033FB2528 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SEQUENCE 583 AA; 66917 MW; 2B2BFAE3E395E049 CRC64;
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 AA
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           DNA binding protein (Fragment).
DJ451B15.2.
                                                                                                                                                                                                         67.3%;
                                                                                                                                                                                                                                      6; Conservative
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244 VVPAGLTYS 252
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227 IIPVGLSYS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum.
                                                                                                                                                                                                                                                              3 VVPXGMSYS 11
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                                      Homo sapiens (Human).
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Best Local Similarity
                                                                                                         SEQUENCE FROM N.A.
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                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                           09BHA5
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                                                                                                                                                                                                                                                                                                                                   RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEX CLASS I ENHANCES. BYOMCHEL AND COMPLEX COMPLEX COMPLEX CLASS I ENHANCES. 19:141-147(1991).

- I FUNCTION: BINDS TO THE ALPHAL-ANTITRYPSIN PROMOTER, TO THE KAPPA I FUNCTION: BINDS TO THE ALPHAL-ANTITRYPSIN PROMOTER, TO THE KAPPA COMPLEX CLASS I ENHANCER; IT PLAYS A ROLE AS TRANSCRIPTIONAL REGULATOR. CONCERNING THE ALPHAL-ANTITRYPSIN EXPRESSION IT MAY ACT AS A NEGATIVE REGULATOR BY INTERFERING AT THE ALPHAL-ANTITRYPSIN PROMOTOR WITH ANOTHER NUCLEAR PROTEIN, CALLED LF-B.

- I SUBCELLULAR LOCATION: NUCLEAR PROTEIN, CALLED LF-B.

- I SUBCELLULAR LOCATION: MUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSCRIPTIONAL ACTIVATION.

1- STATIARRITY: HIGHLY SIMILAR TO AT-BP1 AND TO THE PRDII-BF1 FACTOR.

EMBL; X54250; CAA38151.1; -.

HSSP; P15822; 1BB0.

InterPro; IPR000822; Znf_C2H2.

Ffam; PF00096; zf-C2H2; 2.

SMART; SM00355; Znr_C2H2; 2.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.

PROSITE; PS0157; ZINC_FINGER_C2H2_2; 2.

Zinc_finger; Nuclear protein; DNA-binding; Transcription regulation; Metal-binding; Multigene family.
                                   Gaps
                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NA-binding protein AT-BP2 (ALPHAl-antitrypsin promoter binding protein 2) (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY; TISSUE-THYROID;
MEDLINE-91187610; PubMed-1901405;
Mitchelmore C., Traboni C., Cortese R.;
"Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-antitrypsin promoter and to the major histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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 DB 5; Length 583;
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C(2)H(2) CLASS.
CDD2324152590C17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 11;
Pred. No. 78;
                                                                                                                                                                                 670 AA.
67.3%; Score 35; DB 55.6%; Pred. No. 67; Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC-FINGERS.
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66.78;
             Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                 PRELIMINARY;
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160
74
104
                                                                                   227 IIPVGLSYS 235
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                                                               3 VVPXGMSYS 11
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82
670 AA;
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Matches 6; Conserv
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Query Match
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DOMAIN
ZN_FING
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Q01487;
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RESULT 13

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                       SEQUENCE
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                    Matches
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BRANK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          749 AA; 83344 MW; 4DCD10F480EE0257 CRC64;
                                         -OCT-2000 (TrEMBLrel. 15, Created)
-OCT-2000 (TrEMBLrel. 15, Last sequence update)
-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last annotat
DNA-binding protein (Mbp-1) (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00521; DNA_topoisoIV; 1.
ProDom; PD000742; DNA_topoisoIV; 1.
SMART; SM00434; TOP4c; 1.
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                                                                                                                                                                                                                                   MEDLINE=20365717; PubMed=10910347;
                                                                                          Topoisomerase IV subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 77.8
                PRELIMINARY;
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                                                                                                                          Xylella fastidiosa
                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE 749 AA
                                                                                                                                                                        NCBI_TaxID=2371;
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Q14122;
                09PDM6
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014122
AC 01412
DT 01412
DT 01-NO
DT 01-NO
DT 01-MA
DE DE NOA-B
OS HOMO-OC EUKAR
09PDM6
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Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
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                                                           Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-
hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Blosci. Biotechnol. Blochem. 58:391-395(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "CYC2 encodes a factor involved in mitochondrial import of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 4; Length 1902;
Pred. No. 2.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          1902 AA; 207457 MW; 35BBF0D961E6ED20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 AA.
                                                                                                                                                                                                                                                           InterPro; IPR000822; Inf_C2H2.
Pfam; PF00096; If-C2H2; 3.
SMART; SM000355; Inf_C2H3; 2.
PROSITE; PS50157; INC_FINGER_C2H2_1; 2.
PROSITE; PS50157; INC_FINGER_C2H2_2; 2.
DNA-Dinding; Metal-binding; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
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Mol. Cell. Biol. 13:6442-6451(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94019318; PubMed=8413243;
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MEDLINE=94169519; PubMed=7764548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1590 VVPAGLTYS 1598
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                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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STRAIN=JCM 10545 / 7;
SUBMINED 11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijina K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-9604943; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 34; DB 17; Length 219; 66.7%; Pred. No. 38;
                                                                                 65.4%; Score 34; DB 3; Length 156; 66.7%; Pred. No. 27; 1ve 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodail strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000985; BAB66548.1;
InterPro; IPR004788; RpiA.
InterPro; IPR004788; RpiA.
Isomerase; Hypothetical protein; Complete proteome.
SEQUENCE 219 AA; 24541 MW; A4E9A3F2C4006D90 CRC64;
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EMBL; Z74920; CAA99201.1; -.
EMBL; X87331; CAA60762.1; -.
SGD; S0005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cell division inhibitor (MIND-2).
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01-DEC-2001 (TREMBLrel. 19, Last seque
01-MAR-2002 (TrEMBLrel. 20, Last annot
Putative ribose 5-phosphate isomerase.
                                                                                                                                                                                                                                                               PRT;
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                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 66.7 les 6; Conservative
                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                 2 EVVPXGMSY 10
                                                                                                                                                                               50 EVMPLGMDY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                           Sulfolobus tokodaii.
                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=111955;
                                                                                   Query Match
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Q971S2
                                                                                                                 Matches
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loffus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gooayne J.D., Weidman J.F., McDonald L., Utterback T., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96MUI;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ31891 fis, clone NT2RP7003304, weakly similar to YceA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        'The complete genome sequence of the hyperthermophilic, sulphate-
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                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 34; DB 17; Length 252; 75.0%; Pred. No. 44;
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66.7%; Pred. No. 52;
live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR056453; BAB7188.1; -.
InterPro; IPRO1763; Rhodanese-like.
Pfam: PF00581; Rhodanese; 1.
SEQUENCE 290 AA; 32972 MW; 41FB7FB0217C1421 CRC64;
                                                                                                                                                                                                                                                                               InterPro; IPR000707; ATPase_ParA.
Pfam; PF00991; ParA; 1.
Hypothetical protein; Cell division; Complete proteome.
SEQUENCE 252 AA; 27130 MW; A401DC1F93EBC538 CRC64;
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                                                                                                                                                                                                           reducing archaeon Archaeoglobus fulgidus.";
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01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                         Nature 390:364-370(1997).
EMBL; AE000970; AAB89318.1; -.
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Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                         Venter J.C.;
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Q92MD6
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445 EELVPVGKAY 454
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Q9URR4;
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Boistard P., Becker A., Kahn D., Kiss E., Lelaure V., Masuy D.,

Godile T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

Pohl T., Portetelle D., Puenler A., Purnelle B., Ramsperger U.,

Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

Sinchizoblum mellioti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:987-9882(2001).

EMBL: AL591791: CAC47269.1;

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Rembl: AF591791: CaC47269.1;

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Proc. Natl. Acad. Sci. U.S.A. 98:987-9882(2001).

Rembl: AF591791: CaC47269.1;

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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                             Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Pred. No. 70;
3; Mismatches 2; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Putative HIPPURATE hydrolase protein (EC 3.5.1.32). HIPOl OR R02690 OR SWC00682.
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Last annotation update)
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Pred. No. 1e+02;
2; Mismatches 2;
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PROSITE; PS50160; DNA_LIGASE_A3; 1.
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MEDLINE=21082930; PubMed=11214968;
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EMBL; AP003006; BAB51927.1; -.
InterPro; IPR000977; DNA_ligase.
Pfam; PF01068; DNA_ligase: 1.
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Best Local Similarity 50.00,
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DEAIPHGISY 376
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01-JUN-2002
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Schuurs T.A., Newbert R.W., Turner G., Konings W.N., Driessen A.J.M.;
"Sulfate Transport in Penicillium chrysogenum: Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
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                                                                                                                                                                                                                                                               Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 34; DB 16; Length 544; 70.0%; Pred. No. 1e+02; 2; Indels Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete sequence of the mucosal pathogen Ureaplasma ureallylicum.";
Nature 407:757-762(2000).
EMBL; AE002133; AAF30768.1; -.
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PROSITE; PS01130; SULFATE_TRANSP; UNKNOWN_1.
SEQUENCE 842 AA; 91865 MW; 839A55486E733D15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 544 AA; 61291 MW; CF8756202A389C00 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                               Last sequence update)
Last annotation update)
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Pred. No. 1.6e+02;
2; Mismatches 1;
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J. Bacteriol. 181:7228-7234(1999).
EMBL; AF163974; AAF14539.1; -.
InterPro; IPR0012645; STAS.
Pfam; PF01740; STAS; 1.
Pfam; PF00116; Sulfate_transp.
                                                                                                                                                                                   Putative ABC substrate-binding protein-iron. ABCSBP-5 OR UU359.
544 AA
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                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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66.78;
                                                                                                                                                                                                                                                                                                                                          Mycoplasmataceae; Ureaplasma
NCBI_TaxID=134821;
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PRELIMINARY;
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01-JUN-2002 (TrEMBLrel
Sulfate permease SutB.
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Best Local Similarity
Matches 6; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 7; Conserv
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60.08;

Best_Local Similarity 60.0 Matches 6; Conservative

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Gaps

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2; Indels

us-09-909-164-5.rspt

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Score 33;
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AAK33100.1; JOINED.
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                                                                                                                 EMBL; AY029487; AAK33100.1; JOINED
                                                                                                                           AAK33100.1; JOINED AAK33100.1; JOINED
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                                                                                                                                                                                                                                                                  AAK33100.1; JOINED
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STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed-11930014;
                                   PubMed=11353404;
                                                                                                                                                             JOINED
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                                                                                                                                                                                                                                                                                                                InterPro; IPR001757; ATPase_E1-E2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15734 MW;
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72.7%;
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                                                                                                                                                              AAK33100.1;
Genet. 28:19-20(2001).
                                                                                                                                                                                                 AAK33100.1
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8; Conserv
                    SEQUENCE FROM N.A.
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                                   MEDLINE=21313119;
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AY029496;
AY029497;
AY029498;
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                                                                                                                                                                                                                                                                                                    EMBL; AY029503;
                                                                                                                                        AY029489;
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Matches
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative aminophospholipid translocase (Aminophospholipid-transporting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S., Oshimura M.;
A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome.";
                                                                                                                                                                                                                                                            MEDLINE-21681879; PubMed=11823852; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlan M., Blllault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Weissenbach J., Buoucher C.A., Whalen M., Wincker P., Levy M., Genome sequence of the plant pathogen Relstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                            Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.4%; Score 34; DB 16; Length 1075.0%; Pred. No. 2.18+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSS0156; SSD; 1.
Plasmid; Complete proteome.
SEQUENCE 1049 AA; 111769 MW; CB59674B670089CE CRC64;
                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable multidrug efflux system transmembrane protein.
MEXD OR RSD0312 OR RSD0457.
Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                        PRT; 1049 AA
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                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL646078; CAD17463.1; -
InterPro; IPR001036; Acrflvin_res.
InterPro; IPR004764; HAE1.
InterPro; IPR000731; HMGCR/patch_5TM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21225279; PubMed=11326269;
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
TIGREAMS; TIGRO0915; 2A0602; 1.
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Best Local Similarity 75.0،
مات مات 6
                                                                                         PRELIMINARY;
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                      111 VVPQGMAYA 119
         3 VVPXGMSYS 11
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                                                                                                                                                                                  Plasmid megaplasmid
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     STRAIN-GMI1000;
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ATP10C.
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Q96914;
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Q8XT05
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Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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EMBL; AE010372; AAM02027.1; --
Herzing L.B.K., Kim S.J., Cook E.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATP10C maps
adjacent to UBE3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505(2001).
EMBL; AB001358; BAB47392.1; -.
EMBL; AX029504; AAK33100.1; -.
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Pred. No. 3+02;
0; Mismatches 3; Indels
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PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 1499 AA; 167687 MW; D4996A4D0635A68D CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR001454; Hignase/hydrlase.
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AY029502; AAK33100.1; JOINED.
AY029503; AAK33100.1; JOINED.
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0; 0; Gaps 3; Indels Best Local Similarity 60.0%; Pred. No. 40; Matches 6; Conservative 1; Mismatches

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Search completed: June 10, 2003, 13:46:26 Job time: 29.7857 secs

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/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1984.DBT:*
/SIDS2/gcgdata/geneseqy-embl/AA1986.DBT:*
/SIDS2/gcgdata/geneseqp-embl/AA1986.DBT:*
/SIDS2/gcgdata/geneseqy-embl/AA1987.DBT:*
/SIDS2/gcgdata/geneseqy-embl/AA1987.DBT:*
/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1989.DBT:*
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/SIDS2/gogdata/geneseg/genesegp-embl/AA1998.DAT:
/SIDS2/gogdata/geneseg/genesegp-embl/AA1999.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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52
1 EEVVPXGMSYS 11
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Match
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ALIGNMENTS

RESULT 1 ABB80521 ID ABB80521 standard; peptide; 11 AA.

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L carbonyl forming keto-amide linkage with 7 "
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Pred. No. 0.0011;
0; Mismatches 0;
                                                         'note= "N-terminal acetyl"
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                                                                                                                       "D-form residue"
                               Location/Qualifiers
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                                                                                  "Norvalyl
residue 7
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-Ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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/note= "C-terminal amide"
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                      19-JUL-2001; 2001WO-US23169.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                 /note= "C-terminal amide"
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es 11; Conserv
Misc-difference 8
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                                                                                                                                                                                                                                                                                     hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory
                                                                                                                                             activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.2%; Score 50; DB 23; Length 11; 100.0%; Pred. No. 0.0011; ive 0; Mismatches 0; Indels
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                                                         Lim-wilby M, Levy OE, Brunck TK;
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                                                                                                                                                                                                                              Claim 17; Page 65; 69pp; English.
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Matches 11; Conservative
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               (CORV-) CORVAS INT INC
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44
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                                                                                                                                                                                                                  DB 23; Length 11;
0.0011;
hes 0; Indels
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Claim 17; Page 65; 69pp; English.
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Matches 11; Conservative
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                                                                                                                                                                                     11 AA;
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ABB80565

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
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Pred. No.
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                                                   ABB80566 standard; peptide; 11 AA
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100.0%; Pre
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lty useful for treating disorders associated with hepatitis C
protease
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                                   Length 11;
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Pred. No.
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                    96.2%; Suc-
100.0%; Pre
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                                                               Conservative
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Matches 11; Conservative
                                                                                          1 EEVVPXGMSYS 11
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                         Query Match
Best Local Similarity
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11 AA;
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31-JAN-2002

Novel pep activity

Seguence Query Match

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Gaps

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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                /note= "Alpha-propynyl-glycinyl-carbonyl residue forming a keto-amide linkage with residue 7"
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                                                                  "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatitis C virus (HCV) professe inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
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                                                                                                                                                       'note= "N-terminal acetyl"
                                                                                                                                                                                                                                          "C-terminal amide"
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                                                                                                                       Location/Qualifiers
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus protease
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Lim-wilby M, Levy OE,
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                                                                                                                                                                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HVV) protease inhibitory activity. The peptides of the invention are alpha-ketocamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                     Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                             ABB80528 standard; peptide; 11 AA.
                                                                                                                                                                         Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                         88.5%;
90.9%;
                     19-JUL-2001; 2001WO-US23169
                                          21-JUL-2000; 2000US-220101P.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                    Lim-wilby M, Levy OE,
                                                                (CORV-) CORVAS INT INC
                                                                                                         WPI; 2002-361643/39
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                                                                                                                                                                                                                                                                                     11 AA;
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31-JAN-2002
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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0.0075;
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Pred. No. 0.00
0; Mismatches
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11
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Brunck TK;
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                                                                                                                            Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                        88.5%;
90.9%;
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Best Local Similarity
Matches 10; Conserv
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                                                                                                virus protease
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Synthetic
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                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
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                                                                                                                                                                      Length 11;
                                                                                                                                                                                             1; Indels
                                                                                                                                                                      DB 23;
                                                                                                                                                           Score 46; DB 23;
Pred. No. 0.0075;
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                       Claim 17; Page 64; 69pp; English.
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90.9%;
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ses 10; Conservative
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  virus protease
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                                                                                                                                             Sequence
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                               Gaps
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                                                                                                                   Length 11;
                                                                                                                                              1; Indels
                                                                                                                Score 46; DB 23;
Pred. No. 0.0075;
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                                                                                                                                                                                                                                                                         17
                                                                                                                  88.5%;
                                                                                                                                                                                                                                                                    ABB80562 standard; peptide;
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                                                                                                                                                                       1 EEVVPXGMSYS
                                                                                                                              Similarity
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                                                                                      11 AA;
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                                                                                                             Query Match
Best Local Simi.
Matches 10;
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EEVVPXGMSYS 11

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                                                                                                                                                                                                                                                                                            /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                        Gaps
                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3
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                                     Length 11;
                                                      1; Indels
                                   Score 46; DB 23;
Pred. No. 0.0075;
); Mismatches 1
                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
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                                                                                                                                     ABB80523 standard; peptide; 11 AA.
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                                    88.5%;
90.9%;
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                                                                       1 EEVVPXGMSYS 11
                                                                                 FEVVPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORV-) CORVAS INT INC
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                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                   11 AA;
                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus protease
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                                                                                                                                                                                                                                        Synthetic.
                   Sequence
                                     Query Match
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                                                                                                                   RESULT 17
SXC
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/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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Pred. No. 0.012;
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90.9%;
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EEVVPXGMHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC
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Best Local Similarity
Matches 10; Conserv
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                                                                                     RESULT 18
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ID ABB8
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Indels

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86.5%; Score 45; DB 23, 90.9%; Pred. No. 0.012; Live 0; Mismatches

Conservative

Best_Local Similarity Matches 10; Conserv

Query Match

DB 23; Length 11;

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carbonyl forming keto-amide linkage with
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                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-Ketcoamide peptide analoques. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Pred. No. 0.012;
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                                                     /note= "N-terminal acetyl"
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                                                                                                                  "D-form residue"
                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                TK;
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                                                                             "Norvalyl
residue 7
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90.9%;
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es 10; Conserv
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  Synthetic
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                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #15.
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0.012;
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Pred. No.
                                                                                                                                                      Location/Qualifiers
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90.9%;
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           ABB80535;
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virus protease
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                                                                                                                                                                                                                       hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha'stchoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                       pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                             peptide compound having hepatitis C virus protease inhibitory Ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                              sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #20
                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                Score 45; DB 23; Length 11;
Pred. No. 0.012;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-terminal acetyl"
                        /note= "C-terminal amide"
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       /note= "D-form residue"
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                                                                                                                             Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                          ABB80540 standard; peptide; 11 AA.
                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                86.5%;
90.9%;
                                                                           19-JUL-2001; 2001WO-US23169.
                                                                                           21-JUL-2000; 2000US-220101P.
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                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                           (CORV-) CORVAS INT INC
                                                                                                                                            WPI; 2002-361643/39
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Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 9
                                                                                                                                                                                                                                                                                11 AA;
                                         WO200208251-A2
                                                                                                                                                                            virus protease
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                 Modified-site
                                                                                                                            Lim-wilby M,
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                                                          31-JAN-2002
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                                                                                                                                                             Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38
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                                                                                                                                                                                Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 65; 69pp; English.
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19-JUL-2001; 2001WO-US23169.
                                                          21-JUL-2000; 2000US-220101P.
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                                                                                                                     (CORV-) CORVAS INT INC
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Query Match
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Matches 10
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                                                                                                    hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                            "Norvalyl carbonyl forming keto-amide linkage with residue 7\,\mathrm{m}
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                            The sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40
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                                                                                                                                                                                  Score 45; DB 23; Length 11; Pred. No. 0.012;
                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                   0; Mismatches
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         Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunck TK;
                                                                          Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                 86.5%;
90.9%;
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                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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         Levy OE,
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                         WPI; 2002-361643/39
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                                                                                                                                                                 11 AA;
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                                                            virus protease
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       Lim-wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Novel peptide compound having hepatitis {\tt C} virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
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Pred. No. 0.012;
0; Mismatches 1;
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                                                                                                         Claim 17; Page 65; 69pp; English.
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90.9%;
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Search completed: June 10, 2003, 13:39:06 Job time: 32.3571 secs

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OM protein - protein search, using sw model

June 10, 2003, 13:31:45; Search time 9.64286 Seconds (without alignments) 33.564 Million cell updates/sec Run on:

US-09-909-164-6 52 1 EEVVPXGMSYS 11 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:* Issued_Patents_AA:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		ø			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ΩI	Description
7	34	65.4	947	4	US-09-228-986-73	Sequence 73, Appl
7	33	63.5	45	N	US-08-637-759B-236	236,
æ	33	63.5	45	ო	-355A-	
4	33	63.5	45	4	US-09-201-945-236	236,
5	33	63.5	65	9	5177197-51	. 5177
9	33	63.5	410	9	5177197-1	Patent No. 5177197
7	33	63.5	П	9	5177197-30	Patent No. 5177197
æ	32	61.5		4	7-952-6	
თ	32	61.5		4	US-09-521-650-66	99
10	32	61.5		4	US-09-168-888-66	99
11	32	61.5		7	US-08-580-988A-23	23,
12	32	61.5	152	7	US-08-460-694-4	4, A
13	32	61.5	152	ო	US-08-460-744-4	4
14	32	61.5	-	٣	US-07-667-711B-4	4
15	32	61.5	7		US-08-193-977-7	7,
16	32	61.5		7	US-08-464-517-21	21,
17	32	61.5		7	US-08-246-361A-21	21,
18	32	61.5		٣	US-08-463-772-21	21,
19	32			S	PCT-US93-05000-21	21,
20	32	61.5		N	US-08-464-517-22	22,
21	32			N	US-08-246-361A-22	22,
22	32			m	US-08-463-772-22	
23	32			ស	PCT-US93-05000-22	Sequence 22, Appl
24	32			7	US-08-464-517-6	Sequence 6, Appli
25	32	٠		m	US-08-463-772-6	Sequence 6, Appli
26	32		289	~	US-08-246-361A-4	4
27	32	61.5	289	Ŋ	PCT-US93-05000-4	Sequence 4, Appli

Sequence 6, Appli Sequence 23, Appl Sequence 24, Appli Sequence 20, Appli Sequence 20, Appl	equence 52, equence 4, equence 4, equence 18, equence 2,
200000000000000000000000000000000000000	US-08-444-818- US-08-844-086- US-09-018-211- PCT-US94-04174- US-08-834-776A
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32 32 32 32 32 32 32 32 32 32	57. 0 57. 0 57.
627 E E E E E E E E E E E E E E E E E E E	. 71 72 73 74 75

## ALIGNMENTS

US-09-228-986-73

US-09-228-986-73

Sequence 73. Application US/09228986

Patent No. 6359198

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

CURRENT FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 130

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 73

LENGTH: 947

; TYPE: PRT ; ORGANISM: Pinus radiata US-09-228-986-73

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RESULT 4
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                                                 Gaps
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Query Match 65.4%; Score 34; DB 4; Length 947; Best Local Similarity 66.7%; Pred. No. 1e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%; Score 33; DB 2; Length 45; 60.0%; Pred. No. 5.1; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: LBM PC COMPOLIDATE
COMPUTER: TEAD PC COMPOLIDATE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY 1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION 135
ATTORNEY/AGBWT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: RPMS 101
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
FURNEY/AGBWT SERVICES:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   US-08-637-759B-236

Sequence 236, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TILLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patea L. Pabst
STREET: 1200 one Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 236, Application US/08871355A
Patent No. 6015669
GNERAL INFORMATION:
GNERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 45 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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686 VMPSGISYS 694
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                                                                                  3 VVPXGMSYS 11
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Best Local Similarity
'' '' 6; Conserva'
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                        COMPUTER PORDS 3430

COMPUTER FELDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEB PC compatible

COMPUTER: TEB PC compatible

CORPRATIOS SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,355A

FILING DATE: 09-JUN-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: PCT/GB95/02875

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: RPMS 101 CON

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ 1D NO: 236:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 236, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTON: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/201,945
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APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 45 amino acids
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Best Local Similarity
6; Conserva
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                                                                                                       COUNTRY: USA
ZIP: 30309-3450
                                                             CITY: Atlanta
STATE: Georgia
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STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KANZAKI, TETSUTO:OLOFSSON, ANDERS; MOREN, ANITA;
WERNSTEDT, CHRISTER:HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
LENA; HELDIN, CARL-HENRIK
TILLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENA; HELDIN, CARL-HENRIK

HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/487,343

FILING DATE: 27-FEB-1990
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45.5%; Pred. No. 63;
tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                            Score 33; DB 4; Length 45;
Pred. No. 5.1;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%; Score 33; DB 6; Length 65;
45.5%; Pred. No. 7.8;
tive 3; Mismatches 3; Indels
                                                                           RPMS 101
         ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/CDOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
INFORMATION FOR SEQ ID NO: 236: SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                              63.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                linear
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Best Local Similarity
Matches 5; Conserv
CLASSIFICATION:
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5177197-51
                                                                                                                                                                                                                                                                                                    us-09-201-945-236
                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Patent No.
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Gaps

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Conservative

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APPLICANT: Decwe, John A.
APPLICANT: Decwe, John A.
APPLICANT: Fang, Wu
TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for W
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
CURRENT APPLICATION NUMBER: US/09/357,952
CURRENT APPLICATION NUMBER: US 60/093,642
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-UUL-1998
NUMBER OF SEO ID NOS: 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                      PEPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
WERNSTEDT, CHRISTER,HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
ELDA;HELDIN, CARL-HENRIN;
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING;
HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 6; Length 1394;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66, Application US/09521650; Patent No. 6335429 GENERAL INFORMATION:
APPLICANT: Weber, Eckard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66, Application US/09357952 Patent No. 6248904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                       :|: | || |:
399 KEICPGGMGYT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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399 KEICPGGMGYT 409
EEVVPXGMSYS 11
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                              5177197-30
;Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                              ; SEQ ID NO:30:
; LENGTH: 1394
5177197-30
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Tumor Necrosis Factor
Receptor-I-Associated Protein Kinase And Methods
For Its Use
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Patent No. 5888655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 77071
COMPUTER READBLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Francis of Interior Invention: For Interior Invention: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/580,988A
                                                                                                                                                                          Sequence 23, Application US/08580988A Patent No. 5856161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          January 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
DESCRIPTION: protein
                      1 EEVVPXGMSY 10
                                               1 DDIVPCSMSY 10
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    Houston
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                               RESULT 11
US-08-580-988A-23
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APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John F.W.
APPLICANT: Drewe, John F.W.
THIS DEWENTON: Drewe, John R.W.
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
FILE REFERENCE: 1735.0290002
CURRENT APPLICATION NUMBER: US/09/521,650
CURRENT APPLICATION NUMBER: US/09/521,650
CURRENT APPLICATION NUMBER: 09/168,888
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.0290002
CURRENT APPLICATION NUMBER: US 60/061,582
EARLIER PAPLICATION NUMBER: US 60/061,582
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER APPLICATION NUMBER: US 09/033,661
SARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SEQ ID NO 66
SEQ ID NO 66
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US-09-168-888-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 1.5;
3; Mismatches 2; Indels
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Pred. No. 1.5;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%;
50.0%;
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50.0%;
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Best Local Similarity 50.0%
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Best Local Similarity 50.0
Matches 5; Conservative
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APPLICANT: ARNOLD, Andrew
APPLICANT: ARNOLD, Andrew
TILLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 2; Length 152;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08460744 Patent No. 6107541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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60.0%;
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202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 152 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0%
                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-5;
TELEPHONE: 202-5;
TELEPHONE: 202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-460-694-4
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20 EEVFPLAMNY 29
           STREET: 1100
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                                                                           COUNTRY:
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                                                                                                                           Score 32; DB 3; Length 152;
Pred. No. 33;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ARNOLD, ANDREW TITLE OF INVENTION: Pradl Cyclin and Its cDNA NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSE: STERRE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVE., NW, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/667,711B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
                                                                                                                           61.5%; Score 32;
60.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/07667711B Patent No. 6110700 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08193977; Patent No. 5625031
GENERAL INFORMATION:
APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PEPTIDE INH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
             TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 371-260
TELEFAX: (202) 371-2640
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: not relevant; MOLECULE TYPE: peptide US-07-667-711B-4
LENGTH: 152 amino acids
                                                                                                           Ouery Match
Best Local Similarity 60.0-
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Matches 6; Conservative
                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-460-744-4
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MEDIUM TYPE: Floppy
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20 EEVFPLAMNY 29
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20 EEVFPLAMNY 29
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                     RESULT 14
US-07-667-711B-4
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TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
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APPLICANT: BEAGH, David H.
TILLE OF INFORMATION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 state Street
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 173; 38;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/08/193,977
FILING DATE: 08-FEB-1994
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0016
TELEFOMMUNICATION INFORMATION:
TELEFOMMUNICATION INFORMATION:
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
TVDER: AMINO acids
TVDER: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB Pred. No. 38; 1; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                     CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILLING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILLING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08464517
Patent No. 5869640
                                     NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%;
60.0%;
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Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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CLASSIFICATION: 435
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PF
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STATE: MA
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US-08-464-517-21
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Gaps
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APPLICANT: BEACH, David H.
TITLE OF INFORMATION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 2; Length 189;
Pred. No. 42;
1; Mismatches 3; Indels
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SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                  NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-246-361A-21
; Sequence 21, Application US/08246361A
; Patent No. 5998582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 21
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.5
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 EEVFPLAMNY 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Bost
STATE: MA
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Sequence 22, Application US/08464517
Sequence 22, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                 APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
UNDBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 189; 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                         Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION: DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32;
Pred. No. 4
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 616-861-9000 INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 189 amino acids TYPE: AMINO ACID
                                                                                                          STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%;
60.0%;
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; MOLECULE TYPE: protein
PCT-US93-05000-21
                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| | |:|
74 EEVFPLAMNY 83
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 GENERAL INFORMATION:
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                                                                                            ADDRESSEE:
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                                                                                                                                                                  COUNTRY:
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APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 32; DB 3; Length 189; 60.0%; Pred. No. 42;
                                                                       Score 32; DB 2; Length 189;
Pred. No. 42;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 10 DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAX-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAX-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIIT(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 21, Application PC/TUS9305000
                                                                                                                                                                                                                                                                                                                                                                                CESSEE: LAHIVE & COCKFIELD
ET: 60 State Street
: Boston
                                                                                                                                                                                                                                                                                 Sequence 21, Application US/08463772 Patent No. 6066501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
                                                                           61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.00
                                                                         Query Match 61.5
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
TOPOLOGY: linear
MOLECULE TYPE: peptide
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74 EEVFPLAMNY 83
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PCT-US93-05000-21
                                      US-08-246-361A-21
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Gaps

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US-08-246-361A-22
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Patent No. 5998582
BENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 2; Length 236;
Pred, No. 54;
1; Mismatches 3; Indels
FILING DATE: 16-OCT-1992

APPLICATION NUMBER: US 07/888,178
FILING DATE: 26 MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C.
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRICA PAPLICATION DATA:
APPLICATION NUMBER: US/053,308
FILING DATE: 16-OCT-1992
PRICA PAPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
PRICA PAPLICATION NUMBER: US/07/888,178
FILING DATE: 16-MAY-1992
PRICA PAPLICATION NUMBER: US/07/701,514
FILING DATE: 16-MAY-1991
ATTONEY FACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFENDE/CDOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
INPORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.5
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| | |:|
20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: E
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APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-IYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: BOSTON
                                                                                                                             Score 32; DB 2; Length 236;
Pred. No. 54;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 3; Length 236;
Pred. No. 54;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             RESULT 22
US-08-463-772-22
Sequence 22, Application US/08463772
Patent No. 6066501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                             61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%;
60.0%;
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 amino acids
                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-463-772-22
                                                                                                                                                                                                       1 EEVVPXGMSY 10
                                                                                                                                                                                                                            20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSY 10
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RY: USA
02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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STATE: MA
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RESULT 25
US-08-463-772-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                      APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.5%; Score 32; DB 5; Length 236; 60.0%; Pred. No. 54; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTONNEY,AGENT INFORMATION:
NAME: Granahan, Particia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                    Sequence 22, Application PC/TUS9305000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08464517
Patent No. 5869640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BEACH, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 236 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-05000-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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ZIP: 02109
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PCT-US93-05000-22
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Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 2; Length 280;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0C-1992
APPLICATION NUMBER: US 07/88,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTHEW P. VINCENT
NAME: MALTHEW P. VINCENT
RESISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MII-004C TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Matthew P. Vincent REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-517-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSY 10
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model - protein search, OM protein June 10, 2003, 13:46:50 ; Search time 15 Seconds (without alignments) 75.710 Million cell updates/sec Run on:

1 EEVVPXGMSYS 11 US-09-909-164-6 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

392085 seqs, 103240269 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

100% Post-processing: Minimum Match 08 Maximum Match 100

Listing first 75 summaries

Published_Applications_AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### Sequence 2, Appli Sequence 4, Appli Sequence 54, Appl Sequence 1061, Appl Sequence 4, Appli Sequence 4, Appli Sequence 73, Appl Sequence 108, Appl Sequence 108, Appl Sequence 184, Appl Sequence 184, Appl Sequence 108, Appl Sequence 4, Appl Sequence 4, Appli Sequence 66, Sequence 53, Sequence 108 Sequence 26, Description US-10-114-766-43 US-09-924-340-108 US-09-92-600A-108 US-09-92-600A-108 US-10-000-489-108 US-10-000-986-108 US-09-847-387-66 US-09-947-387-66 US-09-947-387-66 US-09-947-387-66 US-09-947-387-66 US-10-024-066-2 US-09-919-497-54 US-09-925-300-1061 US-09-923-304-4 US-10-027-801-4 US-10-101-464A-73 US-10-027-806-4 SUMMARIES Length DB Match Query 63 63 63 63 61 61 Score Result

Sequence 2, Appli Sequence 10384, A Sequence 878, App Sequence 124, App Sequence 1124, App Sequence 1124, App Sequence 124, App Sequence 1124, App Sequence 1134, App Sequence 1349, App Sequence 2, Appli Sequence 2, Appli Sequence 4454, App Sequence 10439, Appli Sequence 4454, App Sequence 10439, Appli Sequence 10439, Appli Sequence 10439, Appli Sequence 10439, Appli Sequence 136, Appli Sequence 1359, Appli Sequence 144, App Se	equence 35 equence 35 equence 44 equence 44
925-731 -815-242 -925-731 -915-242 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847 -946-847	US-09-997-428-35 US-09-997-666-35 US-10-173-700-44 US-10-174-572-44
2011 2011 2011 2011 2011 2011 2011 2011	2222
001111 0011111111111111111111111111111	
	00000
	722 733 75

## ALIGNMENTS

US-210-027-806-4
Sequence 4, Application US/10027806
Sequence 10-02020160476A1
Sequence 10-02020160476A1
Sequence 10-02020160476A1
Sequence 10-02020160476A1
Sequence 10-02020160476A1
Sequence 10-02020160476A1
TILE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILLE REFRENCE: DCORP.0023 US/10/027,806
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21 RESULT 1

Appl

Sequence 4, Appli

US-10-101-921-4

Gaps

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1; Indels

Length 3472;

Score 38; DB 9; 1 Pred. No. 1.2e+02; 4; Mismatches 1;

Query Match 73.1%; Best Local Similarity 54.5%; Matches 6; Conservative

|:|:| |:|:| 2294 EDVIPRGISFS 2304

g

1 EEVVPXGMSYS 11

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Sequence 4, Application US/10034623

Sequence 4, Application US/10034623

Sequence 4, No. US20020199365A1

SEDERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFWWARE: FastSEG for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10027801

Sequence 4, Application US/10027801

Sequence 4, Application No. US20030054364A1

GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa
ITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A

CURRENT APPLICATION NUMBER: US/10/027,801

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 3472
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020 PRIOR FILING DATE: 1999-09-29 NUMBER OF SEQ ID NOS: 123 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 3472
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                                                                                                                                                                                                                                              Query Match 73.1%; Score 38; DB 9; Length 3472; Best Local Similarity 54.5%; Pred. No. 1.2e+02; Matches 6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.1%; Score 38; DB 9; Length 3472; 54.5%; Pred. No. 1.2e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                          ; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Cenarchaeum symbiosum US-10-027-801-4
                                                                                                                                                                                                                                                                                                                                                                                   |:|:| |:|:|
2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:|:| |:|:|
2294 EDVIPRGISFS 2304
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Matches 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3472
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Sequence 73, Application US/10101464A

Publication No. US20030046728A1

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Higgins, Colleen
TILE REFERENCE: 11000.1020c2
TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
TITLE OF INVENTION: Compositions Isolated from plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
TITLE OF INVENTION: USO20c2
CURRENT FILING DATE: 2002-03-18
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR PELICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SEQ ID NO 73
LENGTH: 947
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Sequence 43, Application US/10214766

Publication No. US2030084473A1

GENERAL INFORMATION:
APPLICANT: Gocal, Greg

TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS

FILE REFERENCE: CA1138

CURRENT APPLICATION NUMBER: US/10/214,766

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 53

SSCHWARE: Patentin version 3.2
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Best Local Similarity 66.,
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Pinus radiata
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686 VMPSGISYS 694
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US-10-101-464A-73
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LENGIH: 426
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1 EEVVPXGMSY 10

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Gaps

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Indels

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Mismatches

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6; Conservative
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    Matches
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US4.DIV
                                                                                                                                                                                                                    APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.052.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
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60.0%; Pred. No. 1.4e+02;
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60.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 3;
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PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PAPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PELING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PELING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/992,600A CURRENT FILING DATE: 2001-11-13
                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-05
PRIOR PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 108
LENGTH: 478
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PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108, Application US/09992600A Publication No. US20030027161A1 GENERAL INFORMATION: Stephane APPLICANT: Benjanin, Stephane APPLICANT: Tanaka, Hiroaki
                                                                                                                                           ; Sequence 108, Application US/09924340; Publication No. US20030027248A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 60.0
Matches 6; Conservative
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SOFTWARE: JPatent
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            223 EFVIPAGQSY 232
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Best Local Similarity
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Gaps
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APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%; Score 33; DB 9; Length 478; 60.0%; Pred. No. 1.4e+02; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <ur>
Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-746-783-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMONICATION NUMBER: 46,931
TELECOMONICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPROX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 184:
                                                                                                                                                                                                                                                                                                                             Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 108, Application US/10000489; Publication No. US20030092011A1; GENERAL INFORMATION:
                                                                                                                                                                             Sequence 184, Application US/09746783 publication No. US20030044935Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                McCoy, John M.
Lavallie, Edward R.
Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
1;
                                                                                                                                                                                                                                              APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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STATE: MA
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                                                                              239 EVAPAGASYN 248
                                       2 EVVPXGMSYS 11
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Best Local Similarity
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US-09-820-843A-26
Sequence 26, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT APPLICATION UNMBER: US/09/820,843A
CURRENT APPLICATION DATE: 2001-03-30
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

MAME/KEY: misc_feature

CTHER INFORMATION: iron(III) ABC transporter, permease protein

NAME/KEY: misc_feature

CTHER INFORMATION: gi|9654609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.5%; Score 33; DB 9; Length 653; Best Local Similarity 66.7%; Pred. No. 1.9e+02; Matches 6; Conservative 2; Mismatches 1; Indels
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PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 10
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ORGANISM: Artificial Sequence
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                        LENGTH: 653
TYPE: PRT
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| Publication No. US20030096247A1
| GENERAL INFORMATION:
| APPLICANT: Benjanh, Stephane
| APPLICANT: Tanaka, Hiroaki
| TITLE OF INVENTION: HUMAN CINAK
| TITLE OF INVENTION: HUMAN CINAK
| FILE REFERENCE: 91.US9.DIV
| CURRENT APPLICATION NUMBER: US/10/000,986
| CURRENT APPLICATION NUMBER: US/0/000,986
| CURRENT APPLICATION NUMBER: US/0/000,986
| PRIOR FILING DATE: 2001-08-06
| PRIOR PLING DATE: 2001-08-06
| PRIOR FILING DATE: 2001-09-06
| PRIOR FILING DATE: 2001-07-13
| PRIOR FILING DATE: 2001-07-13
| PRIOR FILING DATE: 2001-06-29
| PRIOR FILING DATE: 2001-06-29
| PRIOR FILING DATE: 2001-06-15
| PRIOR FILING DATE: 2011-06-15
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Pred. No. 1.4e+02;
1; Mismatches 3; Indels
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60.0%; Pred. No. 1.40+02;
tive 1; Mismatches 3; Indels
             CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-15
SOFTWARE: JPatent
SEQ ID NOS: 112
SOFTWARE: JPatent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%;
60.0%;
FILE REFERENCE: 91.US6.DIV
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Best Local Similarity 60.0
Matches 6; Conservative
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SOFTWARE: JPatent
SEQ ID NO 108
LENGTH: 478
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US-10-000-489-108
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; ORGANISM: Homo sapiens
US-10-000-986-108
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Best Local Similarity
The 6; Conserva
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Gaps

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Sequence 66, Application US/09947387

Sequence 66, Application US/09947387

Patent No. US20020150885A1

GENERAL INFORMATION:

APPLICANT: Reana, John F.W.

APPLICANT: Reana, John F.W.

APPLICANT: Zhang, Han-Zhong

TITLE OF INVENTION: No. US20020150885A1e1 Fluorogenic or Fluorescent Reporter Mol

TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

TITLE OF INVENTION: Use Thereof

CURRENT APPLICATION NUMBER: US/09/947,387

CURRENT FILIS DATE: 2001-09-07

DETAILS OF THE OF 
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; OTHER INFORMATION: Peptide
02-09-947-387-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
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Pred. No. 3.5;
3; Mismatches 2; Indels
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us-09-909-164-6.rapb

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GENERAL INFORMATION:

APPLICANT: Field, Loren J.

APPLICANT: Field, Loren J.

APPLICANT: Field, Kishore Babu S.

TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

FILE REFERENCE: 7037-450

CURRENT APPLICATION NUMBER: 104/10/24,066

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/139,942

PRIOR PILING DATE: 2000-06-19

PRIOR PILING DATE: 2000-06-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE PATENTIN VOICE: 201

SEQ ID NO 2

LENGTH: 289
       US-09-778-927A-53

i Sequence 53, Application US/09778927A

j Patent No. US20020068342A1

g GENERAL INFORMATION:
TITLE OF INVENTION: WOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

FILE REFERENCE: 2786-0160P

CURRENT APPLICATION NUMBER: US/09/778,927A

CURRENT FILING DATE: 2001-02-08

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 81

SOFTWARE PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)..(254 ); OTHER INFORMATION: Xaa = any amino acid, unknown, or other US-09-778-927A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/10024066
; Patent No. US20020166134A1
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Best Local Similarity 60.00
Local 6; Conservative
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Matches 6; Conservative
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US-10-024-066-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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LENGTH: 254
TYPE: PRT
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US-10-024-066-2
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RESULT 13
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RESULT 15 US-10-024-066-4

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                                                              APPLICANT: Field, LOTEN J.
APPLICANT: Field, LOTEN J.
APPLICANT: Field, LOTEN J.
APPLICANT: Field, LOTEN J.
APPLICANT: PAGUMATHI, Kishore Babu S.
TITLE OF INVENTION: CANDIOMYCCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
FILE REFERENCE: 7037-450
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/139,942
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFFWARE: PATENTIN VET: 2.1
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Patent No. US20020106662A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTON: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

CURRENT FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn version 3.0

SEQ ID NO 54

LENGTH: 289

TYPE: PRT
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Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels
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Sequence 1061, Application US/09925300

Patent No. US20020151681A1

GENERAL INFORMATION:
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08
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Pred. No. 1.3e+02;
1; Mismatches 3;
Sequence 4, Application US/10024066 Patent No. US20020166134Al GENERAL INFORMATION:
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60.0%;
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US-09-919-497-54
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US-09-919-497-54
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Length 691;

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Query Match 61.5%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                    TYPE: PRT
CORGANISM: Homo sapiens
US-10-101-921-4
                      LENGIH: 691
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                                                                                                                                                                                                                                                      ; LOCATION: (277)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-300-1061
                                                                                                                                                                                                             OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICAMY: KATZ, RUTH
APPLICAMY: VIANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
FILE REFERENCE: UFSC:5580S
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT PILING DATE: 2011-08-06
NUMBER OF SEQ ID NOS: 11
SED ID NOS: 11
SED ID NOS: 12
SED ID NOS: 17
TYPE: PRT
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Pred. No. 1.3e+02;
2; Mismatches 2; Indels
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Sequence 4, Application US/10101921
GENERAL INFORMATION:
APPLICANT: Nezu, Jun-Ichi
APPLICANT: TSuli, Akira
APPLICANT: TSuli, Akira
TITLE OF INVENTION: TRANSPORTER GENES OATP-B, C, D, AND E
FILE REFERENCE: 06501-104031
CURRENT APPLICATION NUMBER: 2021-06-28
PRIOR PILING DATE: 2002-06-28
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 1999-09-21
PRIOR FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VET. 2.0
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Patent No. US20020081612A1
GENERAL INFORMATION:
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60.0%;
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Best Local Similarity 50.0-
Best Local 5; Conservative
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48 QEVLPPGLKY 57
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Matches 6; Conserv
                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (243)
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                                                                          SEQ ID NO 1061
LENGTH: 295
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US-10-101-921-4
                                                                                                                     TYPE: PRT
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61.5%; Score 32; DB 10; Length 691;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels
Score 32; DB 9; Length by., Pred. No. 3.2e+02;
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yau, H. Howard
TITLE OF INVEWITON: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09925731

Patent No. US20020090622A1

GENERAL INFORMATION:
APPLICANT: ADEDKUN, ANTHONI MONISOLA
APPLICANT: AMBROSE, HELEN JEAN
APPLICANT: DUDLEY, ADAM JESTON
TITLE OF INVENTION: CHEMICAL COMPOUNDS
FILE REFERENCE: DJB/009901/0282795
CURRENT APPLICATION UNDHER: US/09/925,731
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/226,909
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10384, Application US/09815242
Patent No. US20020061569A1
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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APPLICANT: Haselbeck, Robert
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.1
LENGTH: 691
                                                                                                                                                                   188 IVPLGLSY 195
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ORGANISM: Homo sapiens
                                                                                                                       3 VVPXGMSY 10
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188 IVPLGLSY 195
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US-09-815-242-10384
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LOCATION:
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APPLICANT: Sutherland, Lindfield
APPLICANT: Watts, Colin K.
TITLE OF INVENTION: No. US20020192160Alel Human Tumour Suppressor Gene
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Pred. No. 6.7e+02;
4; Mismatches 2; Indels (
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FESTSEQ for Windows Version 4.0
SSO ID NO 10384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/151,736
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 09/403,402
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1998-10-27/AU98/00280
PRIOR FILING DATE: 1998-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 2799
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Publication No. US20030054375A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10151736; Publication No. US20020192160A1
                                                                                                                                                                                                                                                                               61.5%;
45.5%;
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Matches 6; Conservative
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US-10-151-736-4
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hes 5; Conserva
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LENGIH: 53
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-092-154-878
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Sequence 878, Application US/09764847

Patent No. US20020132767A1

GENERAL INFORMATION:

APPLICANT: ROSSEN et al.

TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC009

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 2003

SOSTWARE: PatentIn Ver. 2.0
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Pred. No. 33;
1; Mismatches 2; Indels
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APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BAUDITZ, PETER
APPLICANT: BAUDITZ, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REPERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/09/948,080
CURRENT FILING DATE: 2001-09-06
PRIOR FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTERO for Windows Version 3.0
                                                                                                             Length 53
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                                                                                                           Score 31; DB 9
Pred. No. 33;
1; Mismatches
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; Patent No. US20020102702A1
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APPLICANT: VAN DER OSTEN, CLAUS
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Best Local Similarity 66...
6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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LENGTH: 53
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LENGTH: 59
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QQ δ

1 EEVVPXGMSYS 11 |::| |:|| 38 EKHIPGGLEYS 48

Search completed: June 10, 2003, 14:35:40 Job time: 15.0714 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

June 10, 2003, 13:31:15; Search time 11.2143 Seconds (without alignments) 94.297 Million cell updates/sec Run on:

US-09-909-164-6 52 1 EEVVPXGMSYS 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_73:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	hypothetical 367K	probable sulfate p	sulfate permease	V1 protein - tobac	DNA segregation AT	hypothetical prote	hypothetical prote	Ω	topoisomerase IV s	DNA-binding protei	hypothetical prote	cell division inhi	probable ABC subst	hypothetical prote	50S ribosomal prot	hypothetical prote	hypothetical prote			beta-ketoacyl-ACP	hypothetical prote	3-phosphoshikimate	cdc37 protein - fi	iron(III) ABC tran	bacteriocin BCN5 -	ATP-dependent DNA	conserved hypothet	transforming growt	DNA-directed RNA p
SUMMAKIES	ΩI	T31308	T39116	T40413	A42452	B97355	S57810	T24111	S22293	H82691	A34203	S54619	H69491	C82900	I40758	E90544	D69493	C81374	T34536	S75817	T47670	F72281	D82163	T43653	D82352	A30481	AF3286	D87046	A35626	G82336
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оR	Query Match	73.1	71.2	71.2	69.2	69.2	67.3	67.3	67.3	67.3	67.3	65.4	65.4	65.4	63.5	•	63.5		•		63.5		•	٠. س	•	63.5	-	63.5	63.5	63.5
	Score	38	37	37	36	36	35	35	35	35	35	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33.	33	33	33
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04644046	20H00840460H00	555 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

## ALIGNMENTS

hypothetical 367K protein - Cenarchaeum symbiosum C; Species: Canarchaeum Species: C; Species: Canarchaeum C; Species: Canarchaeum C; Species: Canarchaeum C; Species: Canarchaeum, C; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V. J. Bacteriol. 180, 5003-5009, 1998
A; Title: Genomic analysis reveals chromosomal variation in natural populations of the A; Reference number: 220994; MUID: 98422450; PMID: 9748430
A; Reference number: 220994; MUID: 98422450; PMID: 9748430
A; Reference number: Area Species: Cenarchaeum C; Species: Cenarc

RESULT 1 T31308

A,Molecule type: DNA A,Residues: 1-3472 <SCH> A,Cross-references: EMBL:AF083072; NID:g3599393; PID:g3599394; PIDN:AAC62699.1 C,Superfamily: Cenarchaeum symbiosum hypothetical 367K protein

Score 38; DB 2; Length 3472; Pred. No. 59; 4; Mismatches 1; Indels

ö Gaps ö Query Match 73.1%; Best Local Similarity 54.5%; Matches 6; Conservative

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A; Cross-references: GB: M81103; NID: q335283; PIDN: AAA47947.1; PID: q335284
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60.0%;
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60.0%;
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54.5%;
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Best Local Similarity 60.00
Best Local 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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32 DEVVPNGKTYA 42
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C;Species: tobacco yellow dwarf virus
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
A;Reference number: A42452; MUID:92188538; PMID:1546458
A;Accession: A42452
                                                                                                                            probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: T39116
B;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, November 1999
A;Recence number: Z21829
A;Recence number: Z1829
A;Accession: T39116
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Status: 1-840 <-HUN>
A;Coss-references: EMBL:AL132779; PIDN:CAB60015.1; GSPDB:GN00066; SPDB:SPAC869.05c
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: O3-bec-1999 #sequence_revision 03-bec-1999 #text_change 03-bec-1999
C;Accession: T40413
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Submitted to the EMBL Data Library, August 1998
A;Reference number: 221926
A;Accession: T40413
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-877 <LXN>
A;Cross-references: EMBL:AL031261; PIDN:CAA20298 1; GSPDB:GN00067; SPDB:SPBC3H7.02
C;Genetics: Carrell SPDA: Cosmid C3H7
C;Genetics: Carrell SPDA: Cosmid C3H7
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Pred. No. 22;
1; Mismatches 1; Indels
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Pred. No. 21;
1; Mismatches 1
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.2%;
Best Local Similarity 77.8%;
Matches 7; Conservative
1:|:| |:|:|
2294 EDVIPRGISFS 2304
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Best Local Similarity 77.8
Matches 7; Conservative
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|35 VVPQGMSYA 143
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A; Residues: 1-102 <MOR>
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                                                                                           RESULT 2
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Cipates Clostridium acetobutylicum Cipates Clostridium Clostridium Cipates Clostridium Cipates Clostridium acetobutylicum Arcession Comparimental Source: Clostridium acetobutylicum Arcession Comparimental Source: Clostridium acetobutylicum Arcessa
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B97355
DNA segregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appothetical protein precursor (clone TPP11) - tomato
Cyspecies: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Accession: S57810
R;Milligan; S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato.
A;Reference number: S57808; MUID:95375233; PMID:7647301
A;Reference number: S57808, MUID:95375233; PMID:7647301
A;Reference number: S57808
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-225 <MIL>
A;Residues: 1-225 <MIL>
A;Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:9924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
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hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R;Percy, C.
                                                                   Gaps
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Pred. No. 13;
3; Mismatches 2; Indels
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Score 36; DB 2;
Pred. No. 3.5;
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Pred. No. 63;
2; Mismatches
                                                               3; Mismatches
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chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martin A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sa,Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, T. Wallada, A.C.R.; da Silva, V.; Saveleire, M.A.; da Silva, V.; Saveleire, M.S.; Valva Jr., W.A.; da Silva, V. Yallada, A.S.; Verfore, A.B.; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: XF1353
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomer.
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Mol. Cell. Biol. 10, 1406-1414, 1990
A;Title: A large protein containing zinc finger domains binds to related sequence e
A;Reference number: A34779; MUID:90205817; PMID:2108316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 801-1072, Nv, 1074-1168, Kr, 1170-1225, Vv, 1227-1434, Nv, 1436-1607, 'I', 16
A; Cross-references: GB:M32019
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiFan, C.M.; Maniatis, T.
Genes Dev. 4, 29-42, 1990
A;Title: A DNA-binding protein containing two widely separated zinc finger motifs
A;Reference number: A34203; MUID:90169514; PMID:2106471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein 02612; hypothetical protein YOL303.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names: major histocompatibility complex enhancer-binding protein
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C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; S66879
R;Ge Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
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A;Residues: 1-156 CDEH>
A;Cross-references: EMBL:X87331; NID:91041652; PIDN:CAA60762.1; PID:9829123
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C;Accession: A34203; A34779
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A; Residues: 1-2717 <FAN>
A; Residues: 1-2717 <FAN>
A; Cross references: EMBL:X51435; NID:938017; PIDN:CAA35798.1; PID:938018
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66.7%; Pred. No. 1.9e+02;
iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 2; Length 749;
Pred. No. 48;
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77.8%;
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Best Local Similarity 6b...
6. Conservative
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Matches 7; Conservative
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2405 VVPAGLTYS 2413
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C.Species: Vylella fastidiosa
C.Species: Nylella fastidiosa
C.Species: Vylella fastidiosa
C.Species: Vilella fastidiosa
C.Spec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zinc finger protein AT-BP2 - rat (fragment)

c;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999

C;Accession: 22293; 178656

R;Mitchelmore, C;Traboni, C; Cortese, R.

Nucleic Acids Res. 19, 141-147, 1991

Nucleic Acids Res. 19, 141-147, 1991

A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: I58280; MUID:91187610; PMID:1901405

A;Reference number: I58280; MUID:91187610; PMID:1901405

A;Residues: 1-670 cMIT>

A;Residues: 1-670 cMIT>

A;Residues: 1-670 cMIT>

A;Residues: I-670 cMIT>

A;Note: the authors did not translate the codon for residue 1

C;Superfamily: HIV-EP2 chhancer-binding protein

C;Keywords: DNA binding; transcription regulation; zinc finger
                  submitted to the EMBL Data Library, October 1996
A;Reference number: 219842
A;Recesion: T24111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WILD>
A;Residues: 1-425 <WILD>
A;Cross-references: EMBL:Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A;Experimental source: clone R10D12
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.3%; Score 35; DB 2; Length 425; 50.0%; Pred. No. 26; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:R10D12.10
A;Map position: 5
A;Introns: 23/3; 56/3; 113/3; 257/2
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Best Local Similarity 50.0
Matches 5; Conservative
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Matches 6; Conservative
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Gaps

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hypothetical protein 1 - Campylobacter jejuni (fragment)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140798; S47317
R;Hani, E.K.; Chan, V.L.
A;Hani, E.K.; Chan, V.L.
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine amic
A;Reference number: 140758; MUID:95247673; PMID:7730270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Mycoplasma pulmonis
C; Date: 24 *May-2001 #sequence_revision 24 *May-2001 #text_change 03 *Aug-2001
C; Date: 24 *May-2001 #sequence_revision 24 *May-2001 #text_change 03 *Aug-2001
C; Accession: E90544
R; Chambaud, I:; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A; Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein AF1949 - Archaeoglobus fulgidus

Lispeciaes Archaeoglobus fulgidus

Cispeciaes Archaeoglobus fulgidus

Cibate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000

CiAccession: D69493

R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do. F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

Alauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes
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A;Experimental source: strain UAB CTIP
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50S ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: Z36940; NID: 9535805; PIDN: CAA85392.1; PID: 9535806
                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 2; Length 94; Pred. No. 13; 2; Mismatches 2; Indels
                                     Indels
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A;Genetic code: SGC3
C;Superfamily: Escherichia coli ribosomal protein L20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: 140758
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-94 <RES>
                                     Mismatches
                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%;
55.6%;
                             7; Conservative
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Best Local Similarity 55.6
Matches. 5; Conservative
                                                                                                                                                                                         135 EEVVPHYLSY 144
                                                                                                         1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 DIFPSGMSY 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGMSYS 11
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A;Molecule type: DNA
A;Residues: 1-116 <KUR>
                                 Matches
                                                                                                                                                                                                                                                                                                                    RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
C;Accession: H66491
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
F;Fletschmann, R.D.; Quackehush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: PrelIminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-252 <RIE>
A;Cross-references: GB:AE000970; GB:AE000782; NID:92689293; PIDN:AAB89318.1; PID:926486C
C;Superfamily: cell division inhibitor minD
                                                                                                                                                                                                          A;Cross-references: EMBL:274920; NID:91420109; PIDN:CAA99201.1; PID:91420111; MIPS:YOR01
A;Experimental source: strain $288C
C;Genetics:
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A;Residues: 1-544 <GLA>
A;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; FIDN:AAF30768.1; GSPDB:GN001
A;Experimental source: serovar 3; blovar 1
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65.4%; Score 34; DB 2; Length 156;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.4%; Score 34; DB 2; Length 252; 75.0%; Pred. No. 24; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 544;
55;
submitted to the Protein Sequence Database, July 1996
A.Reference number: $66877
A.Rocession: $66879
A.Molecule type: DNA
A.Residues: 1-156 < DEW>
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 15R
C; Superfamily: hypothetical protein YOR013w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.4%;
70.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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81 EVIPAGMS 88
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Best Local Similarity
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A; Genetic code: SGC3
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C,Accession: $75817
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Ya DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gross_references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18276.1; PID:d1°A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, R submitted to the Protein Sequence Database, February 2000
A;Reference number: 224471
A;Accession: T47670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: F72281
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; )
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-ketoacyl-ACP reductase-like protein - Arabidopsis thaliana
N;Alternate names: protein T26112.190
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
                                                                                                                                                                                     C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                               hypothetical protein slr1275 - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic_acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-284 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 33; DB 2; Length 284;
55.6%; Pred. No. 44;
tive 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75817
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A; Cross-references: EMBL:AL132954
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Matches 5; Conservative
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Matches 5; Conservative
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208 VIPAGVSYT 216
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C;Spacies: Campylobacter jejuni
C;Spate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: C81374
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C,W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;ittle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyfe A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Recession: C81374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <PAR>
A;Cross references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73246.1; PID:g696842
A;Cross references: GB:AL130076; GB:AL111168
                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-165 <KLE>
A;Cross-references: GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89307.1; PID:g264859
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF1949
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69493
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                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C,Species: Homo sapiens (man)
C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Accession: T34556
R. Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, October 1999
A. Reference number: 221540
A. Recession: T34536
A. Status: preliminary
A. Molecule type: mRNA
A. Residues: 1-259 <POU>
A. Cross-references: EMBL: AL122063
A. Experimental source: adult testis; clone DKFZp434C031
C. Genetics: C. Contractions of the contraction of the contract
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                                                                                                                                                                                                                                                                                                                                                                                      63.5%; Score 33; DB 2; Length 165; 60.0%; Pred. No. 25; tive 1; Mismatches 3; Indels
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Matches 6; Conservative
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Matches 6; Conservative
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185 DIFPSGMSY 193
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60 EESIPDGASY 69
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Matches 5; Conserv
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iron(III) ABC transporter, permease protein VC0203 [imported] - Vibrio cholerae (st
C;Species: Vibrio cholerae
C;Date: IB-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: D82352
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Nature, 406, 477-483, 2000
A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Cross-references: GB:AE004110; GB:AE003852; NID:g9654600; PIDN:AAF93379.1; GSPDB:CA)Experimental source: serogroup 01; strain N16961; biotype El Tor
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C; Species: Clostridium perfringens plasmid piP404
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Nov-1999
C; Accession: A30481; S.03779
B; Garnier, T.; Cole, S.T.
J. Bacteriol. 168, 1189-1196, 1986
A; Title: Characterization of a bacteriocinogenic plasmid from Clostridium perfringen
A; Reference number: J70354; MUID:87057020; PMID:2877971
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A;Resldues: 1-890 <GAR>
A;Cross-references: GB:M32882; GB:J03309; NID:g150738; PIDN:AAA98249.1; PID:g150739
                                                 A:Cross-references: EMBL:AL049769; PIDN:CAB42371.2; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid c9B6
R:Westwood, P.K.; Preston, N.C.; Fantes, P.A.
Submitted to the EMBL Data Library, March 1999
A:Description: Schizosaccharomyces pombe cdc37 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 2; Length 466;
Pred. No. 76;
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bacteriocin BCN5 - Clostridium perfringens plasmid pIP404
                                                                                                                                                                                                        A; Accession: T43654
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-466 < WE2>
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66.7%; Pred. No. 1.1e+02
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Best Local Similarity 66.
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A; Introns: 8/2; 17/2; 21/1
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Best Local Similarity
Local 5; Conserve
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                              A; Residues: 1-466 <WOO>
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A; Molecule type: DNA
A; Residues: 1-653 <HEI>
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A;Gene: bcn
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                                                                                                  A, Residues: 1-368 <ARN>
A, Cross-references: GB:AE001778; GB:AE000512; NID:g4981757; PIDN:AAD36291.1; PID:g498176
A, Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 1
C;Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAF94882.1; GSPDB:GN001
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cdc37 protein - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 2.1-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C; Accession: T43653; T40791; T43654
R; Westwood, P.K.; Preston, N.C.; Fantes, P.A.
submitted to the EMBL Data Library, March 1999
A; Reference number: 222602
A; Reference number: 222602
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-466 cWES>
A; Residues: 1-467 cWES>
A; Rooss-references: EWBL:AJ132376; PIDN:CAB38757.1
R; Wood, V.; Rajandream, M.A.; Barrell, W. 1999
A; Reference number: 221875
A; Rocession: T40791
A; Reference Lype: DNA
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                                                                                                                                                                                                                                                                                               Score 33; DB 2; Length 368;
Pred. No. 59;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.5%; Score 33; DB 2; Length 426; 60.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                          A;Gene: TM1216
C;Superfamily: NADH dehydrogenase (ubiquinone) 49K protein
A; Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                               63.5%;
55.6%;
                                                                                                                                                                                                                                                                                                             Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 IVPKGMAYA 302
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                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-426 <HEI>
                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                            A; Molecule type: DNA
                                A; Accession: F72281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: VC1732
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
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Gaps

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A;Genome: plasmid
C;Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5
C;Keywords: bacteriocin
Query Match 63.5%; Score 33; DB 2; Length 890;
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Query Match 63.5%; Score 33; DB 2; Length 890; Best Local Similarity 66.7%; Pred. No. 1.5e+02; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps

; 0

> Qy 2 EVVPXGMSY 10 | | | | | | | | | Db 170 EVVPGGFTY 178

Search completed: June 10, 2003, 13:49:09 Job time: 11.2143 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 10, 2003, 13:25:04 ; Search time 4.5 Seconds (without alignments) 101.387 Million cell updates/sec

US-09-909-164-6 52 1 EEVVPXGMSYS 11 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ption	fusobacteri	schizosacch	tobacco vel		homo sapien		homo sabien	mvcoplasma	campylobact	vibrio chol	Schizosacch	homo sapien		homo sanian		homo canion			π	mis misculu		Xenonis lae	dallus dall	xencons lae	qallus qall	homo sapien		mus musculu	rattus norv	haemophilus	homo sapien		
		Description	08rq86	074377	P31619	004351	P15822	P23622	060312	098qv0	P45489	Q9krb0	094740	O9nzm5	P08696	P22064	09kv29	014766	000418	004827	P30279	P30280	090459	P50755	P49706	P53782	P55169	P30281	P24385	P25322	P39948	P44677		9v616	P52384
																	,																		
SOMMAKIES	;	ID	CARB_FUSNN	SULH_SCHPO		Y1A9_CLOAB	ZEP1_HUMAN	CY14_NEUCR	A10C_HUMAN	RL20_MYCPU	Y990_CAMJE	AROA_VIBCH	CC37_SCHPO	GSR2_HUMAN	BCN5_CLOPE	LTBS_HUMAN	RPOC_VIBCH	LTBL_HUMAN	LTB1_RAT	CGD2_RAT	CGD2_HUMAN	CGD2_MOUSE	CGD1_BRARE	CGD1_XENLA	CGD2_CHICK	CGD2_XENLA	CGD1_CHICK	- 1	CGD1_HUMAN	CGD1_MOUSE	CGD1_RAT	FOLB_HAEIN	ENP3_HUMAN	DAT6_HUMAN	PRTP_HSV6U
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		Length	1058	118	102	1498	2717	788	1499	116	253	426	466	478	890	1394	1401	1595	1712	288	289	289	291	291	291	291	292	292	295	295	295	427	529	169	726
æ		Match	73.1	;,	•	٠				63.5														61.5			∹,	٠	•	•	٠	٠	61.5	∹,	61.5
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P32784 saccharomyc Q62571 rattus norv P28931 tomato aspe P16916 escherichia P16918 escherichia P16917 escherichia P16917 escherichia P169771 homo profestatichia P169771 h		059042 methanococc 09zle3 helicobacte P56006 helicobacte P28233 rattus norv P87033 ustilago ma P26391 salmonella
	1 REVI 1 COBH 1 PURO 1 PURO 1 PURO 1 Y939 1 Y939 1 ADDG 1 ADDG 1 PLSB 1 PLSB 1 RPOC. 1 TEVA. 1 TEVA. 1 ATPE. 1 PURO 1 TEVA. 1 TEVA. 1 TEVA. 1 TEVA. 1 TEVA. 1 TEVA. 1 TEVA.	
61.5 61.5 61.5 61.5 61.5 61.5 61.5	29.6 124 31 59.6 128 31 59.6 228 31 59.6 228 31 59.6 228 31 59.6 228 31 59.6 228 31 59.6 228 31 59.6 276 31 59.6 483 31 59.6 483 31 59.6 483 31 59.6 1407 31 59.6 1407 32 57.7 121 33 57.7 121 34 57.7 223	57.7 0 57.7 0 57.7 0 57.7 0 57.7
3.85 3.37 3.39 4.0	44444444444444444444444444444444444444	

# ALIGNMENTS

							Carbamoy1-phosphate synthase large chain (EC 6 3 5 5) (Carbamow1-	T Compared to the contract of									Kapatral V., Anderson I., Ivanova N., Reznik G., Los T. Lubidie A	Bhattacharyya A., Bartman A., Gardner W. Grechkin G., 1, 1	Man E Hernal A	Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn P.	/ : W = 100 to 200 to 2	"Genome sequence and analysis of the oral hacterium Euscharterium	TOTAL THE ENDORGOET THE		-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O - 2 ADP +	
		1058 AA.			date)	podate	in / EC	}		, mil.							Reznik	J. Gre	301+6	i d		al hac	1		mine +	
		10			e upo	ton	cha			c]eat	HI I							ber v	0	Pusc	2	e or	}		yluta	
		PRT;		e F	adneuc	notat	large	chain		ab. nu	pacter					39109:	nova	Gard	Chag	LS T	rbeek	of t	; ;	002).	+ L-C	
		STANDARD;		15-JUN-2002 (Rel. 41, Created)	(Rel. 41, Last se	(Rel. 41, Last a	sosphate synthase	phosphate synthetase ammonia chain).	22.	Fusobacterium nucleatum (subsp. nucleatum)	Bacteria; Fusobacteria; Fusobacterium	6856;		M N.A.	25586;	MEDLINE=21886394; PubMed=11889109:	Anderson I., Ive	a A., Bartman A.,	Chu L., Kogan Y.,	Souza M., Waluna	Fonstein M., Kyrpides N., Overbeek R :	ence and analysis	nucleatum strain ATCC 25586.";	. 184:2005-2018(2	C ACTIVITY: 2 ATF	
RESULT 1	CARB_FUSNN	CARB_FUSNN	לפספה,	7007-NOC-CT	15-JUN-2002	15-JUN-2002	Carbamoyl-ph	phosphate sy	CARB OR FN0422.	Fusobacteriu	Bacteria; Fu	NCBI_TaxID=76856;	[1]	SEQUENCE FROM N.A.	STRAIN=ATCC 25586;	MEDLINE=2188	Kapatral V.,	Bhattacharyy	Vasieva O.,	Larsen N., D	Fonstein M.,	"Genome sedu	nucleatum st	J. Bacteriol	-!- CATALYTI	
RESU	CARE	QI	) E	- E	<u>.</u>	DŢ	DE	DE	U	SO	႘	X _O	RN	RP	2	RX	RA	RA	КA	RA	RA	RŢ	RT	RL	y S	

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3 WPXGMSYS 11
 STRAIN=972;
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
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 phosphate + L-glutamate + carbamoyl phosphate.
--- COFACTOR: Binds three manganese ions (By similarity).
--- PATHWAY: Arginine biosynthesis.
--- PATHWAY: Pyrimidine biosynthesis, first step.
--- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                      OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS008667; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                    TIP-binding; Manganese; Complete proteome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.1%; Score 38; DB 1; Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                            -1- SIMILARITY: BELONGS TO THE CARB FAMILY
                                                                                                                                                                                                          EMBL; AE010554; AAL94625.1; ALT_INIT.
                                                                                                                                                                                                                    InterPro; IPR005483; CPase_L.
InterPro; IPR005489; CPase_L_D2.
InterPro; IPR005480; CPase_L_D3.
InterPro; IPR005481; CPase_L_D3.
InterPro; IPR004362; MGS_like.
Pfam; PF00289; CPSase_L_Chain; 2.
Pfam; PF02786; CPSase_L_D3; 2.
Pfam; PF02787; CPSase_L_D3; 1.
Pfam; PF02187; MGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1058 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                     similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULH_SCHPO 074377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPBC3H7.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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NP_BIND
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            MEDLINE-2184401; PUDMEGG-11809480;

RA WOOD V. GWIlliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA WOOD V., GWIlliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C. M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C. M.,

RA GOLLINS M., Connor R., Cronni A., Davis P., Feltwell T., Fraser A.,

RA Gottles S., Goble A., Hamilan N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Taylor K., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tavey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckeart G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckeart G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckeart G., Aert R., Robben J., Grymonprez B.,

RA Gable D., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Goffeau A., Caddeu E., Jimenez S., Ganchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado. L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado. L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado. L., Jimenez J., Sanchez M., del Rey F.,

RA Daga R.R., Cruzado. L., Jimenez J., Sanchez M., del Rey F.,

RA Daga R.R., Cruzado. L., Jimenez J., Sanchez M., del Rey F.,

RA Daga R.R., Revuelta J.L., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RI The genome sequence of Schizosaccharomyces pombe.";

RI The genome sequence of Schizosaccharomyces pombe.";

RI THRIFATTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
--- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
--- SIMILARITY: CONTAINS 1 STAS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EWBL; AL031261; CAA20298.1; -
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PP00916; Sulfate_transp; 1.
Pfam; PF01740; STAS; 1.
PROSITE; PS01130; SLC26A; 1.
PROSITE; PS50801; STAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. POTENTIAL.
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MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96373 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.28;
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TRANSMEM 133 153
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543
594
877 AA;
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RESULT 5
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MEDLINE-21359325; PubMed=11466286;
Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng O.,
Gibson R., Lee H.M., Dubols J., Qlu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92108538; PubMed-1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonous plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein.
102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                  Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBL_TaxID=31599;
                                                                                                                                                                   Last sequence update)
Last annotation update)
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16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Hypothetical protein CAC3709.
                                                                                                       102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A42452; A42452.
InterPro; IPR002621; Gemini_mov.
Pfam; PF01708; Gemini_mov; 1.
Hypothetical protein.
                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-OCT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.2%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVVPSGINYS 16
148 VVPQGMSYA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                 Y11K_TYDVA
P31619;
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Q04351;
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                                                                                 Y11K_TYDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y1A9_CLOAB
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                                                             RESULT 3
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16-0CT-2001 (Rel. 40, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-EP1) (Major histocompatibility complex binding protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                                                                                                                                                                                       to frameshifts
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Biochemistry 29:9324-9334(1990).
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                                                                                                          Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: BELONGS TO THE FTSK/SPOIIE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "High-resolution solution structure of the double Cys2His2 zinc
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Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 1498;
Pred. No. 23;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                              -1- CAUTION: Ref.2 sequence differs from that shown due in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              675 682 ATP (POTENTIAL).
1498 AA; 168968 MW; FF42037A335A9649 CRC64;
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Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Complete proteome.
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                                         VKM B-1787;
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InterPro; IPR002543; FtsK_SpoIIIE.
Pfam; PF01580; FtsK_SpoIIIE; 2.
Hypothetical protein; ATP-biding; CC
NP_BIND 675 682 ATP (PO)
SEQUENCE OF 1-108 FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B
MEDLINE-93273706; Pubmed=8501044;
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STRUCTURE BY NMR OF 2113-2142.
WEDLTINE-91064333; PubMed-2248949;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE007866; AAK81629.1; -.
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60.0%;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1276 EQKIPMGMSY 1285
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P15822;
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         BIOCHEMISTRY 31:3907-3917(1992).

-I FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
NUMBROUS VIRAL PROMOTERS SUCH AS THOSE OF SY40, CWY, OR HIVI.
IN ADDITION, RELAFED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
MHC, INTERLEUGIN-2 RECEPPOR, AND INTERFERON-BETA GENES. IT MAY ACT
IN T-CELL ACTIVATION.
                                                                                                                             -!- SUBCELLULAR LOCATION: Nuclear.
-!- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
-!- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED AND RECOGNIET THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER IN-BETWEEN.
-!- SIMILARITY: STRONG, TO HIVEP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Transcription regulation; Zinc_finger; Metal-binding; DNA-binding;
Nuclear protein; Repeat; 3D-structure.
DOMAIN 406 456 ZINC_FINGERS.
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Pred. No. 70;
2; Mismatches 1; Indels
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finger from the human enhancer binding protein MBP-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000822; Znf_C2H2.
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PRINTS; PR00048; ZINCFINGER.
SMART; SM00355; ZnF_C2H2; 4.
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66.78;
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MIM; 194540; -
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2405 VVPAGLTYS 2413
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PDB; 42NF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.
-i- MISCELLANEOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.
-i- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                     MEDLINE=94188926; PubMed=8140616; Sandal N.N., Marcker K.A.; Sandal N.N., Marcker K.A.; "Similarities between a soybean nodulin, Neurospora crassa sulphate permease II and a putative human tumour suppressor."; Trends Blochem. Sci. 19:19-19(1994).
                                                                                                          SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
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                             Score 34; DB 1; Length 788;
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15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M59167; AAA33615.1; ALT_SEQ.
                                                                                                                                                                                               Biochemistry 30:1780-1787(1991).
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060312; 096914;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87864 MW;
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66.7%;
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6; Conservative
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213
291
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             Sulfate permease II
                                                                                                                                                                                                                         PROBABLE REVISIONS.
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SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
Nomura N., Ohara O.;
Nomura N., Ohara O.;
Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 5:13-99(1998)
L. CATALYITC ACTIVITY: ATP + H(2)O = ADP + phosphate.
IL CATALYITC ACTIVITY: ATP + H(2)O = ADP + phosphate.
TISSUE SPECIFICITY: Wide expression, with highest levels in
Kidney, followed by lung, brain, prostate, testis, ovary, and
small intestine.
C. INGERSE: Defects in ATP10C may be a cause of Angelman syndrome
(AS), also known as 'happy puppet syndrome'.
C. SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
APPASES). SUBSPANILY IV.
                                                                                                                                                                                                                             "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-21225279; PubMed-11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(Aminophospholipid-transporting ArPase VC (EC 3.6.3.1) (ATPVC)
ATP10C OR ATPVC OR KIAA0566.
                                                                                                                                                                                                                                                                                                                       Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.; "The human aminophospholipid-transporting ArPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression."; Am. J. Hum. Genet. 68:1501-1505(2001).
                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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JOINED.
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MEDLINE-21313119; Pubmed-11353404;
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MEDLINE=98290545; PubMed=9628581;
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                                                                                         PRINTS, PRO0119; CATATPASE.
PROSITE: PS00154; ATPASE_E1_E2; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C., Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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Pred. No. 62;
); Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> R (IN REF. 3).
D4996A4D0635A68D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                 POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (PÒTENTIAL).
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                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
RPLT OR MYPU_2610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                    InterPro; IPR001757; ArPase_E1-E2.
InterPro; IPR001454; Hlgnase/hydrlase.
Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21267165; PubMed-11353084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 47
388 38
1499 AA;
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ses 8; Conserv
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1250
1268
1268
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1193
1200
1223
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                  105830; -
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Q98QV0;
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DOMAIN
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Matches
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DOR NO DO
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EMBL; 236940; CAA85392.1; -. Hypothetical protein; Complete proteome. SEQUENCE 253 AA; 29783 MW; F96D3FF3265FBA6A CRC64;

SOW

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                 This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-WCTC 11168;
WEDLINE-20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouall M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Expression and characterization of Campylobacter jejuni
Denzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 116; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                          Prodom; PD002389; Ribosomal L20; 1.
TIGRRAMs; TIGR01032; rplT_bact; 1.
PROSITE; PS000937; RIBOSOMAL_L20; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
SEQUENCE 116 AA; 13565 MW; C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P45489; Q9PNVO;
01-NOV-1995 (Rel. 32, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein Cj0990c.
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                     IPR001081; Ribosomal_L20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 177:2396-2402(1995).
                                                                                                                                                                                                         InterPro; IPR001081; Ribosomal_L2
Pfam; PF00453; Ribosomal_L20; 1.
PRINTS; PR00062; RIBOSOMALL20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 43431 / TGH 9011;
MEDLINE-95247673; PubMed-7730270;
Hani E.K., Chan V.L.;
                                                                                                                                                                    EMBL; AL445563; CAC13434.1; -. MypuList; MYPU_2610; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL139076; CAB73246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 160-253 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 63.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 VRPLGMSYS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=197;
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Y990_CAMJE
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-EI TOT N16961 / Serotype 01;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vanathevan J., Bass S., Oin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:477-483(2000).
-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids blosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001986; EPSP_syntase.
Pfam; PF00275; EPSP_syntase; 1.
ProDom; P0001867; EPSP_syntase; 1.
PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
Aromatic amino acid biosynthesis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                   63.5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 426;
                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNIT: Monomer (By similarity),
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                              426 AA.
                                      Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 27;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 33; 60.0%; Pred. No. 3
                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE004251; AAF94882.1; -.
Ouery Match
Best Local Similarity 55.0.
5; Conservative
                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 60.0
Matches 6; Conservative
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223 EFVIPAGOSY 232
                                                                                                                               185 DIFPSGMSY 193
                                                                                            2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sixth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIGR; VC1732;
                                                                                                                                                                                                                      AROA_VIBCH
Q9KRB0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae."
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                                                                                                                                                                                                         AROA_VIBCH
                                                                                                                                                                                    RESULT 10
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RX MEDLINE=21848401; PubMed=11859360;
RA WOOd V., GW11land R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA WOOD V., GW11land R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Rajandream M.A., Lyne M., Lyne R., Stewart A., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Muckle E.J., Hunt S., Jagels K., RA, Holroyd S., Mones L., Jones M., Leather S., McDonald S., McLean J., RA, Monosy P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E., R. Autherford K., Rutter S., Saunders D., Quall M.A., Rabbinowitsch E., R. Raylor K., Taylor R.S., Taylor R.S., Taylor R.S., Taylor R.S., Taylor R., Taylor R., Walsh S.V., Warren T., Whitehead S., Ratljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Hu. R. Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Hu. R. Auchs M., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Bozzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Galibert E., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Galibert E., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Adalbert E., Lowe T., Moreno S., Amrastrong J., Forsburg S.L., Adander E., Draeno S., Allada V.A., Garzon A., Thode G., Doninguez A., Revuelta J.L., Moreno S., Amrastrong J., Forsburg S.L., Romannes Squence of Schizosaccharomyces pombe. "

RA Shakovskii G.V., Ussery D., Barrell B.G., Nurse P.; Ribester R., Revueltr B., Revuelter B., Revuelt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity (By similarity).
-1- SUBUNIT: Forms a complex with Hsp90. Interacts with a number of
                                                                                                                           15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
HSP90 co-chaperone Cdc37 (HSp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDC37 OR SPAC9B6.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Westwood P.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ132377; CAB38758.1; -.
EMBL; AJ123376; CAB38757.1; -.
EMBL; AL049769; CAB42371.2; -.
Chaperone; Call division; Cell cycle.
SEQUENCE 466 AA; 52554 MW; 647238B34CABB3C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinases (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: BELONGS TO THE CDC37 FAMILY.
                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                     466 AA.
                                                                                                     (Rel. 41, Created)
                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBL_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                     15-JUN-2002
                                                CC37_SCHPO
094740;
                  CC37_SCHPO
RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus I regulatory proteins ICP22 and ICP0 is modified in a cell-type specific manner and is recruited to the nucleus after infection.";
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 199-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Subhitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBGNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
-!- SUBCELLULAR LOCATION: Nuclear.
                                        ö
                                                                                                                                                                                                               GSR2_HUMAN STANDARD; PRT; 478 AA.
09NZM5; Q9NRP1; Q9NF4; Q9UF12; Q9BTC6; Q9HAX6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
61joma tumor suppressor candidate region gene 2 protein (p60).
63.5%; Score 33; DB 1; Length 466; 50.0%; Pred. No. 30;
                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION. MEDLINE=99214318; PubMed=10196275;
                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF182076; AAF62873.1; -. EMBL; BC004229; AAH04229.1; -. EMBL; BC006311; AAH06311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 218-477 FROM N.A.
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                                      Conservative
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                                                                                                    : :| |||||
98 DSAIPGGMSY 107
                                                                           1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
            Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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  Query Match
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KGPNPAPGHRIAA (IN REF. 3).
SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWPGCLFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WAGPVGPMPRG (IN REF. 5).
EGNILRDRFKSFORRNMIEPRERAKFKRYKVKLVEKRAFR
                                                                                                                                                                                                                                                                                                                    RRKEQLWEKLAKOGELPREVRRAQARLLINPSATRAKPGPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEGNILRDRFKSFORRNMIEPRERAKFKRKYKVKLVEKRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REIQ -> VLTVSCRGAPCPVMTPSLLPVPPRGYGRHHGCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIQL -> RGQHSFETGSRAFRGGI (IN REF. 3).
7F18923E348CB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; Plasmid 19:134-150(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CPN50; MEDLINE=87057020; PubMed=2877971; Garnier T., Cole S.T.; "Characterization of a bacteriocinogenic plasmid from Clostridium perfringens and molecular genetic analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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GGS -> HEG (IN REF. 2; AAH04229).
G -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                  (IN REF. 3).
A -> S (IN REF. 2; AAH04229).
D -> H (IN REF. 3).
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Last annotation update)
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J. Bacteriol. 168:1189-1196(1986).
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01-JAN-1988 (Rel. 06, Last sequ
01-OCT-1994 (Rel. 30, Last anno
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, BC010095, AAH10095.1;
AF296124; AAG30413.1;
AL359335; CAB94786.1;
AL359336; CAB94786.1;
AL122063; CAB94787.1;
                                                                                                                                                                                                  protein; Polymorphism
                                                                                                                       SWISS-2DPAGE; Q9NZM5; HUMAN.
Genew; HGNC:4333; GLTSCR2.
MIM; 605691; -.
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60.0%;
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Best Local Similarity 60.0.
Best Conservative
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P08696;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETAL FROM PLATELETS IS COMPOSED OF THE TGF BETAL MOLECULE NONCOVEMENTLY ASSOCIATED WITH A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETAL PRECURSOR AND A THIRD COMPONENT DENOTED TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BETA1-BP. TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.
-!- ALTERNATIVE PRODICTS: 2 isoforms; a short form (shown here) and a long form (AC Q14766); are produced by alternative splicing.
-!- PTM: CONTAINS HYDOXYLATED ASPARAGINE RESIDUES.
-!- PTM: The N-terminus is blocked.
-!- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kanzaki T., Olofsson A., Moren A., Wernstedt C., Hellman U.,
Miyazono K., Claesson-Welsh L., Heldlan C.-H.;
"TGF-beta 1 binding protein: a component of the large latent complex
of TGF-beta 1 with multiple repeat sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 15 precursor (Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 1; Length 890;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                890 AA; 96699 MW; F4E5E8971C31C6C6 CRC64;
vivo and in vitro.";
Mol. Microbiol. 2:607-614(1988).
-i- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-i- INDUCTION: BY UV IRRADIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fibroblast, and Platelet;
MEDLINE=90275601; PubMed=2350783;
                                                                                                                                                                                                                                                                                       EMBL; M32882; AAA98249.1; -.
PIR; A30481; A30481.
InterPro; IPR003646; SH3_bac.
AMRT; SM00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid.
DOMAIN 815 869 HYDR
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66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 EVVPGGFTY 178
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Best Local Similarity
'-hag 6; Conserve
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P22064;
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LTBS_HUMAN
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DR InterPro; 1PR000152; Asx_hydroxyl.

DR InterPro; 1PR000561; EGF-like.

DR InterPro; 1PR000561; EGF-like.

DR InterPro; 1PR0002212; Fibril-assoc.

DR Pfan; Pr00008; EGF; 15.

DR Pfan; Pr00008; EGF, 13.

DR SMART; SM00179; EGF_CA; 13.

DR SMART; SM00019; EGF_Like; 4.

DR PROSITE; PS00010; ASX_HYDROXXL; 13.

DR PROSITE; PS01186; EGF_2; 11.

DR PROSITE; PS01186; EGF_2; 11.

DR PROSITE; PS01187; EGF_CA; 15.

R PROSITE; PS01187; EGF_CA; 15.

R Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal;

T SIGNAL

SIGNAL
                                                                                                                                                                                                                                                                   EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
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EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                        LATENT TRANSFORMING GROWTH FACTOR BETA
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       EMBL; M34057; AAA61160.1;
PIR; A35626; A35626.
                   HSSP, P00750; 1TPG
GlycoSuiteDB; P22064; -.
Genew; HGNC:6714; LTBP1.
MIM; 150390; -.
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Pleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES (By similarity).

-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotations beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).
17-JUN-2002 (Rel. 41, Last polymerase beta' chain update)
18-JUN-2002 (Rel. 41, Last polymerase beta' chain update)
18-JUN-2002 (Rel. 41, Last polymerase)
18-JUN-2002 (Rel. 41, Last polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. . . ) (POTENTIAL).
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N.LINKED (GLCNAC. .) (POTENT N.LINKED 
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       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-90275601; PubMed-2350783;

MEDLINE-90275601; PubMed-2350783;

MEDLINE-90275601; PubMed-2350783;

MAYAZONO A., Olofsson A., Moren A., Wernstedt C., Hellman U.,

MIYAZONO K., Claesson-Welsh L., Heldin C.-H.;

"TGF-beta 1 binding protein: a component of the large latent complex of TGF-beta 1 with multiple repeat sequences.";

Cell 61:1051-1061(1990).

COMPOSED OF THE TGF-BETA1 MOLECULE NONCOVALENTLY ASSOCIATED WITH A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETA1 PRECURSOR AND A THIRD COMPONENT DENOTED TGF-BETA1-BP. TGF-BETA1 BD DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A SHIDD DIRECTLY TO ACTIVE TGF-BETA1.
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"Efficient association of an amino-terminally extended form of human latent transforming growth factor-beta binding protein with the extracellular matrix.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1L precursor
(Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN (By similarity).
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human),
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 33; DB 1; Length 1401; 50.0%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1401 AA; 155021 MW; DFDB0F2B5514504F CRC64;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
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nes 5; Conservative
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581 QIVPKGLPYS 590
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Q14766;
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                                                                                                                                                                                                                                                                                                                             InterPro: IPR000152; Asx_hydroxyl.

R InterPro: IPR00251; EGF-like.

R InterPro: IPR00212; Fibril-assoc.

R InterPro: IPR00212; Fibril-assoc.

R Ffam; PF00008; EGF; 15.

R Ffam; PF00181; EGF; 15.

R PROSTIE; PS001010, ASX HYDROXYL; 13.

R PROSTIE; PS01186; EGF_2; 11.

R PROSTIE; PS01186; EGF_2; 11.

R ROSTIE; PS01187; EGF_CA; 15.

R Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal; W Growth factor binding; Repeat; PS01180; EGF_CA; 15.

R Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal; W Growth factor binding; Popervial.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
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EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
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EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL)
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EGF-LIKE 1, CALCIUM-BINDING (POFENTIAL)
TISSUE SPECIFICITY: The long isoform is found in fibroblasts. PTM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES (BY SIMILARITY). SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
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EGF-LIKE 15.

EGF-LIKE 16.

CELL ATTACHMENT SITE (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.
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SIMILARITY: CONTAINS 18 EGF-LIKE DOMAINS
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     LTB1_RAT STANDARD; PRT; 1712 AA.
000918;
001-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1 precursor
(Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-1) (Transforming growth factor beta-1 binding protein, large subunit).
LTBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=91062373; PubMed=2247454;
Tsuji T., Okada F., Yamaguchi K., Nakamura T.;
"Molecular cloning of the large subunit of transforming growth factor type beta masking protein and expression of the mRNA in various rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIOC. Natl. Acad. Sci. U.S.A. 87:8835-8839(1990).
-1- SUBDATT: THE LARGE LATENT COMPLEX OF TGF-BETAL FROM PLATELETS IS
COMPOSED OF THE TGF-BETAL MOLECULE NONCOVALENTLY ASSOCIATED WITH
A MASKING PROTEIN CONSISTING OF A DISULFIDE-BONDED COMPLEX OF A
DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETAL PRECURSOR AND
A THIRD COMPONENT DENOTED TGF-BETAL-BP (OR MP LARGE SUBUNIT).
TGF-BETAL-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETAL).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
BY SIMILARITY.
BY SIM
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Pred. No. 1.1e+02;
3; Mismatches 3; Indels
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45.5%;
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Best Local Similarity 45.5
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                                                                                                                                                                                                                                                                                                                                               EMBL; MS5411; AAA42235.1; -

R PIR; A38261; A38261.

R HSSP; Pi6109; IPS8

InterPro; IPR000152; As_hydroxyl.

InterPro; IPR001521; Fibril-assoc.

R InterPro; IPR002212; Fibril-assoc.

R InterPro; IPR00179; EGC_CA;

R Pfam; PF00008; EGF_16.

R SMART; SM000179; EGC_CA; 13.

R SMART; SM00019; EGF_11ke; 5.

R ROSITE; PS001001; AS_LHYDROXYL; 13.

R ROSITE; PS01186; EGF_2: 10.

R ROSITE; PS01187; EGF_2: 10.

R Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal.
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EGF-LIKE 2.

INTERNAL REPEAT 1.

EGF-LIKE 3.

INTERNAL REPEAT 2.

EGF-LIKE 4.

EGF-LIKE 4.

EGF-LIKE 5.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 1.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE
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LATENT TRANSFORMING GROWTH FACTOR BETA
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                                                       SECUENCE FROM N.A.
MEDLINE=95011623; PubMed=7926809;
Hosokawa Y., Onga T., Nakashima K.;
"Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S transition by prolactin in rat Nb2 cells.";
Gene 147.249-252(1994).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
(START) TRANSITION.
                                                                                                                                                                                   -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell cycle; Cell division; Multigene family; Proto-oncogene.
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MEDLINE=93205384; PubMed=8455931;
Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;
"Cyclins Di and D2 are differentially expressed in human B-lymphoid cell lines.";
                                                                                                                                                                                                              IMPARIS SUBSTRATE SPECIFICITY TO THE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92347851, PubMed-1386336, Xiong Y., Menninger J., Beach D., Ward D.C., Molecular cloning and chromosomal mapping of CCND genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 29;
1; Mismatches 3; Indels
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C -> V (IN REF. 2).
T -> A (IN REF. 2).
', 4B522BF4E9835FC1 CRC64;
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InterPro; IPR004367; Cyclin_Cterm.
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32826 MW;
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60.0%;
                             Oncogene 8:1661-1666(1993).
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Genomics 13:575-584(1992).
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288 AA;
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              cyclin D2.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-93275661; PubMed-8502486;
Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
Francke U., Jolicoeur P.;
"The Vin-1 gene, identified by provirus insertional mutagenesis,
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Pred. No. 1.1e+02;
3; Mismatches 3; Indels
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01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CCND2 OR VIN-1.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
-:- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
A SERINE/THREONINE KINASE HOLOENZYME COMPLEX.
IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-:- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Actinopterygil; Neopterygil; Teleostel; Ostariophys1; Cypriniformes;
CCprinidae; Danio.
NCBL_TaxID=7955;
                 CCND2 OR CYL-2.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                   Marks P.A.; "Cloning of a D-type cyclin from murine erythroleukemia cells."; Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
                                                                                                                                                                                                                                                                                                                                                                              Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.;
"Colony-stimulating factor 1 regulates novel cyclins during the phase of the cell cycle.";
Cell 65:701-713(1991).
                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-92196134; PubMed-1372445;
Kiyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 32; DB 1; Length 289; 60.0%; Pred. No. 29;
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EMBL; M86182; AAA37503.1; -.

PIR; A40035; B40035.

PIR; A41984; A41994.

MGD; MGI:88314; Ccnd2.

MGD; MGI:88314; Ccnd2.

R InterPro; IPR004366; Cyclin.

R InterPro; IPR004366; Cyclin.

Pfam; PF00134; cyclin. 1.

Pfam; PF002984; cyclin. 2.

R SAART; SM00385; CYCLIN; 1.

R PROSITE; PS00292; CYCLINS; 1.

R PROSITE; PS00292; CYCLINS; 1.

R Cyclin; Cell cycle; Cell division; Multigene family.

SEQUENCE 289 AA; 32897 WW; 58F322771DDIDA3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91235305; PubMed=1827757;
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31/S-specific cyclin D2.
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Q90459;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use. by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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-:- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
-:- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
A SERIME/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-:- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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PROSITE: PS00292; CYCLINS; 1.
CYCLIN; Cell division; Multigene family.
CYCLIN; Cell division; Multigene family.
CONFLICT 166 167 KL -> NV (IN REF. 5).
CONFLICT 224 224 T -> H (IN REF. 5).
                                                                                                   Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                    expression of human cyclin D genes.";
Genomics 13:565-574(1992).
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InterPro; IPR004367; Cyclin_Cterm.
Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 1.
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MEDLINE=92347850; PubMed=1386335;
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                                                                                                                                                                                                                                                                       SEQUENCE OF 1-240 FROM N.A.
  Oncogene 8:1049-1054(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:1583; CCND2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSY 10
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01-APR-1993 (Rel. 25,
01-APR-1993 (Rel. 25,
16-OCT-2001 (Rel. 40,
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Best Local Similarity
                                                                                                                                                                           FISSUE=Bone marrow;
                                                   SEQUENCE FROM N.A.
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                     Strausberg R.;
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CGD2_MOUSE
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EMBL;
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291 AA.

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                                                                      embryogenesis.";
Biochim. Biophys. Acta 1264:257-260(1995).
-I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                -!- SUBUNT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cockerill M.J., Hunt T.,
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
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-!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.

-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                     Yarden A., Salomon D., Geiger B.;
"Zebrafish cyclin Dl is differentially expressed during early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%; Score 32; DB 1; Length 291; 60.0%; Pred. No. 29; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SMO0385; CYCLIN; 1.
PROSITE; PSO0292; CYCLINS; 1.
CYCLIN; Cell CyCle; Cell division.
SEQUENCE 291 AA; 33067 MW; FA5274CB1B46D5EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
G1/S specific cyclin D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X87581; CAA60885.1; -ZFIN; ZDB-GENE-980526-176; cycdl.
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
SEQUENCE FROM N.A. MEDLINE-96138542; PubMed-8547308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
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P50755;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=96144302; PubMed=8566807; Li H., Grenet J., Kidd V.J.; "Structure and gene expression of avian cyclin D2."; Gene 167:341-342(1995).
-- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (START) TRANSITION.
-!- SUBDUIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZINE COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRANTE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN B SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                       3; Indels
                                                           Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE: PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle; Cell division; Multigene family.
E 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
GJ/S-specific cyclin D2.
CCND2.
                                                                                                                                                                                                                    1; Mismatches
        EMBL, X89475; CAA61664.1; -.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
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InterPro; IPR004367; Cyclin_Cterm.
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Pfam; PF02984; cyclin, 2.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
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                                                                                                                                                             Query Match
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
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hes 6; Conservative
                                                                                                                                                                                                                                                   1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                     73 EEVFPLAMNY 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 EEVFPLAMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                    CGD2_CHICK
P49706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                    RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                        early development.";
Biol. Cell 88:99-111(1996).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                           "Xenopus cyclin D2: cloning and expression in oocytes and during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00385; ČYCLIN; 1.
PROSTIE; PS00292; CYCLINS; 1.
CYCIII; Cell Cell division; Multigene family.
SEQUENCE 291 Aa; 32959 MW; 9A290F04F1531E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                01-ocT-1996 (Rel. 34, Created)
01-ocT-1996 (Rel. 34, Last sequence update)
10-ocT-2001 (Rel. 40, Last annotation update)
G1/S-specific cyclin D2.
                                 291 AA
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InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-97380591; Pubmed-9237366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
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Best Local Similarity bu...
6; Conservative
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                                 STANDARD;
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                                                                                                                                                                                                  Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                          Taieb F., Jessus C.;
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P55169;
                                CGD2_XENLA
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                 CGD2_XENLA
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RESULT 24
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                                                                     Li H., Lahti J.M., Kidd V.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
(START) TRANSITION. INTERACTS WITH THE CDK4 AND CDK6 PROTEIN
KINASES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 292 AA; 33263 MW; 7B543029DB45A67D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin.
Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin; 1.
SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00292; CYCLINS; 1.
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Matches 6; Conservative
                                                       SEQUENCE FROM N.A.
              NCBI_TaxID=9031;
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Search completed: June 10, 2003, 13:40:17

Job time : 5.5 secs

1 EEVVPXGMSY 10 ||| | |:| 75 EEVFPLAMNY 84

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June 10, 2003, 13:30:25; Search time 25.7857 Seconds (without alignments) 87.898 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                        671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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52
1 EEVVPXGMSYS 11
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2: sp_barchea:*
3: sp_lungi:*
4: sp_human:*
5: sp_nmammal:*
7: sp_mmmal:*
7: sp_mmmal:*
10: sp_plant:*
11: sp_rodent:*
11: sp_vertebrate:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_arvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
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17: sp_archeap:*
18: sp_arc

Database :.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q98fxl rhizobium l	Q8rg86 fusobacteri	O74056 cenarchaeum	Q9ury8 schizosacch	Q8r126 mus musculu	Q8vd18 mus musculu	Q40129 lycopersico	Q9xvk4 caenorhabdi	043733 homo sapien	Q9bha5 plasmodium	.Q9bh83 plasmodium	Q01487 rattus norv	Q9pdm6 xylella fas	Q14122 homo sapien	Q12479 saccharomyc	Q971s2 sulfolobus
SUMMARIES		ΩI	Q98FX1	Q8RG86	074056	Q9URY8	Q8R126	Q8VD18	040129	Q9XVK4	043733	Q9BHA5	09вн83	001487	O9PDM6	014122	012479	097152
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		Query Match Length DB	387	1063	3472	840	471	484	225	425	556	583	583	670	749	1902	156	219
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		Score	38	38	38	37	36	36	35	35	35	35	35	35	35	35	34	34
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028342 Q96MU1 Q92MD6 Q92MD6 Q912MC4 Q917705 Q96 Q14 Q97704 Q97704 Q97704	08VUA8 08VUA8 08RUA8 090404 090409 090909 090909 090909 0909090 0909091 0909091 0909091 0909091 0909091 0909091 0909081 0900839 0900833 0900833 0900833 0900833 0900833 0900833 0900833 0900834 099081 099081	ALTGNMENT
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.000000000000000000000000000000000000	
<u> </u>	228 339 331 331 332 333 333 333 333 333	

ALIGNMENTS

		PRT; 387 AA.		Created)	Last sequence update)	Last annotation update)		
		٠.		18,	18,	18,		
		PRELIMINARY;		(TrEMBLrel.	(TrEMBLrel.	(TrEMBLrel.	drolase.	
RESULT 1	'X1	Q98FX1	Q98FX1;	01-OCT-2001	01-OCT-2001 (TrEMBLrel. 18, Last seq	01-OCT-2001 (TrEMBLrel.	Hippurate hydrolase	MLR3583.
RESU	Q98FX	Ω	AC	DŢ	DŢ	DI	DE	S

us-09-909-164-6.rspt

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"Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
J. Bacteriol. 180:5003-5009(1998).
-!- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
EMBL; AF083072; AAC62699.1;
                                                                                                                                                      Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y., Swanson R.V.;
                                                                                                                                                                                                                                                InterPro; IPR000515; BPD_transp.
InterPro; IPR010680; WD40.
InterPro; IPR010680; WD40.
InterPro; IPR010680; WD40.
SMART; SM00320; WD40; 4.
PROSITE; PS004002; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
Hypothetical protein; Repeat; WD repeat.
SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
          01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 367.1 kDa protein.
                                                                      Archaea; Crenarchaeota; Cenarchaeum.
                                                                                                                                       MEDLINE-98422450; PubMed-9748430;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.50,
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                                                       Cenarchaeum symbiosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
                                                                                                           SEQUENCE FROM N.A.
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                                                                                NCBI_TaxID=46770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=972H-;
             01-NOV-1998
01-JUN-2002
                                                                                                                             STRAIN=B;
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Q9URY8;
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                                                                                                           Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokwa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symblotic bacterium
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SirAnt—AllC. 20300;

MEDLINE-21886394; PubMed-11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Wallnas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).
EMBL; AEO10554; AAL94625.1; -.
Ligase; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
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Pred. No. 9.8;
2; Mismatches 2; Indels
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Pred. No. 29;
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                                                                                                                                                                                                        DNA FRES. 7:331-338(2000).

EMBL; AP003002; BAB50445.1; -

InterPro; IPR002933; Peptidase_M20.

Pfam; PF011645; Peptidase_M20; I.

Hydrolase; Complete proteome.

SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1063 AA.
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NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O74056;
01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                 MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                               73.18;
60.08;
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60.08;
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Best Local Similarity 60 o
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                                                                                                                                                                                                                                                                                                                                                                                           367 DEAIPHGMSY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMSY 10
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195 EIVPNGLNYS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGMSYS 11
                                                                                                                                                                                                Mesorhizobium lot1."
                                                                     SEQUENCE FROM N.A. STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8RG86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8RG86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          074056
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
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Gaps

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1; Indels

Length 3472;

73.1%; Score 38; DB 1; 54.5%; Pred. No. 1e+02;

4; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                            JULY AVES S., McDougall R.C., Rajandream M.A., Barrell B.G.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132779, CAB60015.1; -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PP01740; STAS.1.
Pfam; PP01740; STAS.1.
Pfam; PF00916; Sulfate_transp.
TIGRFAMS; TIGR00815; SulP; 1.
SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 3; Length 840;
Pred. No. 37;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                       v.-MAY-2000 (TrEMBLrel. 13, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Probable sulfate permease.
SPAC869.05C.
                                                                                                                              840 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 AA.
                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.28;
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nes 7; Conservative
|:|:| |:|:|
2294 EDVIPRGISFS 2304
                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VVPXGMSYS 11
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QBR126
ID QBR126
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R10D12.10
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9XVK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   043733
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                                                                                                                                                                                                                         SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eŭkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 11; Length 471;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017637; AAH17637.1; -.
MGD; MGI:2138595; AW35644!
SEQUENCE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1; -
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.2 kDa protein precursor.
Lycopersicon esculentum (Tomato).
                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 484 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 54.5 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                69.2%;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 60.0 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 EVIPAGASYN 235
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TISSUE=SALIVARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                     TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Q40129
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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SEQUENCE FROM N.A.
STRAIN-VF36; TISSUE-PISTIL;
MILLIGN S.B., Gasser C.S.;
Milligan S.B., Gasser C.S.;
Milligan S.B., Gasser C.S.;
Malutre and regulation of pistil-expressed genes in tomato.";
Plant Mol. Biol. 28 F691-711(1995).
EMBL; U20592; AAA80497.1; -.
Interpro; IPRO02160; Kunitz_legume.
Pfam; PF00197; Kunitz_legume; 1.
Probom; PD000891; Kunitz_legume; 1.
                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 10; Length 225; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                               CHAIN 21 225 UNKNOWN.
SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 AA.
                                                                                                                                                                                                                 SMART; SM00452; STI; 1.
PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z81109; CAB03241.1; -. InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   043733;
01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                67.38;
                                                                                                                                                                                                                                                                                                                                                                                    54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Transferase. SEQUENCE 425 AA; 49410
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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32 DEVVPNGKTYA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                     Hypothetical protein;
SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R10D12.10 protein.
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Matches
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                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                    Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                 67.3%; Score 35; DB 4; Length 556;
66.7%; Pred. No. 64;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ben Mamoun C., Gluzman I.Y., Goldberg D.E.; February C., Gluzman I.Y., Goldberg D.E.; February falciparum choline transporter (PfSCTI) gene."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 3; Mismatches 1; Indels
                                                                             Tubby B.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                            EMBL; Z98050; CAB10847.1; -.
NON_TER
SEQUENCE 556 AA; 59059 MW; ECB00E4033FB2528 CRC64;
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
                                                                                                                                                                                                                                                            Last sequence update) Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BH83;
01-JUN-2001 (TrEMBLrel. 17; Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 AA.
                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
        DNA binding protein (Fragment).
                                                                                                                                                   6; Conservative
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244 VVPAGLTYS 252
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                                                                                                                                                                   3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
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                                                                                                                                                                                                                                                                           Choline transporter
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                                                                    SEQUENCE FROM N.A.
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                                                    NCBI_TaxID=9606;
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               DJ451B15.2
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Q9BHA5
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Q9BH83
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Mucleic Acids Res. 19:141-147(1991).

C. Complex class I enhancer.";

Nucleic Acids Res. 19:141-147(1991).

C. COMPLEX CLASS I ENHANCER. NUD TO THE MAJOR HISTOCOMPATIBILITY

C. COMPLEX CLASS I ENHANCER; IT PLAYS A ROLE AS TRANSCRIPTIONAL

REGULATOR. CONCERNING THE ALPHAI-ANTITRYPSIN PROPORTININAL

AS A NEGATIVE REGULATOR BY THE PROPIED LF-B.

C. PROMOTOR WITH ANOTHER NUCLEAR PROTEIN, CALLED LF-B.

PROMOTOR WITH ANOTHER NUCLEAR.

C. SHULARITY: HIGHLY SIMILAR TO AT-BPI AND TO THE PRDII-BFI FACTOR.

TRANSCRIPTIONAL ACTIVATION.

C. SHULARITY: HIGHLY SIMILAR TO AT-BPI AND TO THE PRDII-BFI FACTOR.

DR RASSP, P15822; DAF.

C. SHULARITY: HIGHLY SIMILAR TO AT-BPI AND TO THE PRDII-BFI FACTOR.

BREND: X54250; CAA38151.1;

C. SHULARITY: MICHER C2H2;

DR ROSSITE; PS00038; ZINC_FINGER_C2H2.1;

PROSITE; PS00038; ZINC_FINGER_C2H2.2;

PROSITE; PS00038; ZINC_FINGER_C3H2.2;

PROSITE; PS00038; ZINC_FINGER_C3H2
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                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
DNA-binding protein AT-BP2 (ALPHAl-antitrypsin promoter binding protein 2) (Fragment).
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Pred. No. 78;
2; Mismatches 1; Indels
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EMBL; AY007374; AAK14818.1; -.
EMBL; AX007373; AAK14817.1; -.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SEQUENCE 583 AA; 66918 MW; 4DF83D7530527474 CRC64;
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C(2)H(2) CLASS.
C(2)H(2) CLASS.
CDD2324152590C17 CRC64;
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                                                                                                                                                                                                                                                    Pred. No. 67;
3; Mismatches
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                                                                                                                                                                              Query Match
Best Local Similarity 55...
5; Conservative
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82
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670 AA;
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Matches 6; Conserv
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ZN_FING
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Q01487
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RESULT 15
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RA Simpson A.J.G., Relnach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,

RA Alvarenga R., Alves L.D., Bordin S., Bove J.M., Eitones M.R.S.,

RA Bueno M.R.P., Camargo A.A., Costa P.E.A., Carraro D.M., Carrar H.,

RA Bueno M.R.P., Camargo A.A., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Fraga J.S., Franca S.C., Franco M.C.R., Frohme M., Furlan L.R.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Krieger J.E., Kuramee E.E., Junqueira M.L., Kemper E.L., Kitajima J.P.,

RA Krieger J.E., Martins E.M.L., Martins E.M.F., Matsukuma A.Y.,

RA Mardues M.Y., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

RA Mardues M.Y., Martins E.A.L., Monteira M.A.,

RA Mardues M.Y., Martins E.A.L., Monteira M.A.,

RA Mardues M.Y., Martins E.A.L., Monteira M.A.,

RA Machado M.A., Mascimento A.L.T.O., Netto L.E.S.,

RA Mond D.H., Nobrega F.G., Munes L.R., Oliveira M.A.,

RA Goliveira M.C., de Oliveira R.C., Palmari M.A., Pesquero J.B.,

RA Goliveira M.C., de Sliva A.M., de Rosa A.J.M.,

RA de Sliveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.J.M.,

RA de Sluveira J.F., Silvestri M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

RA Zago M.A., Zatz M., Medadis J., Setubal J.C.;

RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA Zago M.A., Zatz M., Medadis J., Setubal J.C.;

RA Rago M.A., Zatz M., Weidalis J., Setubal J.C.;

RA Rago M.A., Zatz M., Medadis J., Setubal J.C.;

RA Rago M.A., Zatz M., Medadis J., Setubal J.C.;

RA Rago M.A., Zatz M., Medadis J., Setubal J.C.;

RE BMEL; ARGOROSOF; ARRALG.1; - D.R. BMEL;

RE BMEL; ARGOROSOF; ARRALG.1; - D.R. BMEL;

RE REMER; REMER; Reverse D.R. D.R. Freezing W.D.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DNA-binding protein (Mbp-1) (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35; DB 16; Length 749; 77.8%; Pred. No. 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               749 AA; 83344 MW; 4DCD10F480EE0257 CRC64;
                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Topoisomerase IV subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1902 AA.
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                     749. AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00434; TOP4c; 1.
TIGRFAMS; TIGR01062; parC_Gneg; 1.
                       PRT;
                                                                                                                                                                                                                           MEDLINE=20365717; PubMed=10910347;
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Best Local Similarity 77.00
Best Local 7; Conservative
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                       PRELIMINARY;
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526 EVDPSGMSY 534
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                                                                                                                        xylella fastidiosa
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=2371;
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                                        Q9PDM6;
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            9мад60
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STRAIN=FY1679;
MEDLINE-94019318; PubMed-8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
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Molecular cloning of a gene, DHSI, which complements a drug-
hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 58:391-395(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CYC2 encodes a factor involved in mitochondrial import of yeast cytochrome C.";
                                                                                           MEDLINE-90205817; PubMed=2108316; Sharp P.A.; Baldwin A.S. LeClair K.P., Singh H., Sharp P.A.; Baldwin A.S. LeClair K.P., Singh H., Sharp P.A.; Baldwin A.S. LeClair K.P. Singh H., Sharp p.A.; Sequence elements in the enhancers of the class I major sequence elements in the enhancers of the class I major histocompatibility complex and kappa immunoglobulin genes."; Mol. Cell. Biol. 10:1406-1414(1990).
EMBL, M32019; AAA17534.1; -...
HSSP; P15822; 1BBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Bukaryota: Fungi; Ascomycota; Saccharomycotia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1902;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%; Score 35; DB 4; Length 190. 66.7%; Pred. No. 2.4e+02; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1902 AA; 207457 MW; 35BBF0D961E6ED20 CRC64;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De haan M., Maarse A.C., Grivell L.A., Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ORF YOR013W.
                                                                                                                                                                                                                                                                                                                              Interpro; IPR000622; Inf_C2H2.
Pfam; PF00096; Inf_C2H2; Inferpro; Info0096; Inf_C2H2; Info0096; Inf_C2H2; Info0096; Inf_TRINGER_C2H2_1; Info0097; Inf_TRINGER_C2H2_1; Info0097; Info0096; Info0096; Info0096; Info0096; Info
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding; Metal-binding; Zinc-finger.
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MEDLINE=94169519; PubMed=7764548;
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Best Local Similarity 60...
Local Similarity 60...
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                                            NCBI_TaxID=9606;
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                                                                                                                    Gaps
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Sulfolobus.
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                           65.4%; Score 34; DB 3; Length 156; 66.7%; Pred. No. 27;
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                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000985; BAB66348.1;
EMBL; Z74920; CAA99201.1; -.
EMBL; X87331; CAA60762.1; -.
SGD; S0005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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Probes, Prof. Par. 1.

Isomerase, Hypothetical protein; Complete proteome.

SEQUENCE 219 AA; 24541 MW; A4E9A3F2C4006D90 CRC64;
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Archaeoglobaceae; Archaeoglobus
                                                                                                                                                                                                                                                                                  01-DEC-2001 (TERBILE1. 19, Last sequence update)
01-MAR-2002 (TERBILE1. 20, Last annotation update)
04141ive ribose 5-phosphate isomerase.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last senotation update)
Cell division inhibitor (MIND-2).
                                                                                                                                                                                                                                            219 AA.
                                                                                                          1; Mismatches
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2; Mismatches
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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                                                                                                       6; Conservative
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                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                 2 EVVPXGMSY 10
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PubMed=11572479;
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                                                                       Query Match
Best Local Similarity
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Q971S2
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Matches
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ31891 fis, clone NT2RP7003304, weakly similar to YceA protein
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                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE000970; AABB9318.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo săpiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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66.7%; Pred. No. 52;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR000707; ATPase_ParA.
Pfam: PF00991; ParA; 1.
Hypothetical protein; Cell division; Complete proteome.
SEQUENCE 252 AA; 27130 MW; A401DC1F93E8C538 CRC64;
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InterPro; IPPR01763; Rhodanese-like.
Pfam; PF00581; Rhodanese; 1.
SEQUENCE 290 AA; 32972 MW; 41FB7FB0217C1421 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)

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445 EELVPVGKAY 454
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MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
MEANDA T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochiatki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome Structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium 1011.";
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Analysis of the Chromosome sequence of the legume symbiont Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

InterPro; IPR002933; Peptidase_M20.
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Batieria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative HIPPORATE hydrolase protein (BC 3.5.1.32).
HIPO1 OR R02690 OR SMC00682.
Rhizobium mellioti (Sinorhizobium mellioti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                        65.4%; Score 34; DB 16; Length 387; 50.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                                                                                                                                      Hydrolase; Complete proteome.
SEQUENCE 387 AA; 41074 MW; 342763088907A6E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
PROSITE; PS50160; DNA_LIGASE_A3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 AA
                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                      MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 7:331-338(2000).
EMBL, AP003006; BAB51927.1; -.
InterPro; IPR000977; DNA_ligase.
Pfam; PF01068; DNA_ligase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligase; Complete proteome. SEOUENCE 541 AA; 60645
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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367 DEAIPHGISY 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable DNA ligase.
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                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                   NCBI_TaxID=382;
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Schuurs T.A., Newbert R.W., Turner G., Konings W.N., Driessen A.J.M.;
Sulfate Transport in Penicillium chrysogenum: Cloning and
Characterization of the suta and sutB Genes.";
J. Bacteriol. 181:7228-7234 (1999).
EMBL; AF163974; AAF14539.1;
Enterpro: IPRO02645; STAS.
Interpro: IPRO01902: Sulfate_transp.
Pfam: PF00196: Sulfate_transp; 1.
TIGRFAMS: TIGRO0815; Sulfate_transp; 1.
TIGRFAMS: PF00916: Sulfate_transp; 1.
FROSITE; PS01130; Sulfate_transp; 1.
PROSITE; PS01130; Sulfate_transp; 1.
SEQUENCE 842 AA; 91865 MW; 839AS5486E733D15 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=5076;
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                                                                                                                                                                                                                                                                                                                                                Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                              Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Wycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 16; Length 544;
Pred. No. 1e+02;
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66.7%; Pred. No. 1.6e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 AA; 61291 MW; CF8756202A389C00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                     O9POD2;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
putative ABC substrate-binding protein-iron.
ABCSBP-5 OR UU359.
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                                                                                                                                                                                                                                                                                                                             STRAIN=SEROVAR 3;
MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE002133; AAF30768.1; -.
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Local Similarity 70.0%;
es 7; Conservative .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 407:757-762(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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PRELIMINARY;
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Best Local Similarity
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Gaps

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Nat. Genet. 28:19-20(2001).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative aminophospholipid translocase (Aminophospholipid-transporting
                                                                                                                                                                                                                                                  A Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S., Arlat M., Genin S., Attiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chadler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Sapin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Squier P., Thebault P., Mhalen M., Wincker P., Levy M., Genome sequence of the plant pathogen Ralstonia solanacearum."; Genome sequence of the plant pathogen Ralstonia solanacearum."; RemBi. An646078; CAD17463.1; -.
InterPro: IPR001936; Acritvin_res.
InterPro: IPR004784; HABI.
RinterPro: IPR004731; HMGCR/Patch_5TM.
Pfam: PF00873; ACR_LIAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
Oshimura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                           Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.4%; Score 34; DB 16; Length 1049; 75.0%; Pred. No. 2.1e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            1049 AA; 111769 MW; CB59674B670089CE CRC64;
                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Probable multidrug efflux system transmembrane protein.
MEXD OR RSP0312 OR RS05457
                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                              PRT; 1049 AA.
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                                                                                                                                                                                                                                          MEDLINE-21681879; PubMed=11823852;
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                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00702; ACRIFLAVINRP.
                                                                             PRELIMINARY;
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 3 VVPXGMSYS 11
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317 MPAGMSYS 324
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                                                                                                                                                                Plasmid megaplasmid
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                 NCBI_TaxID=305;
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9
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Q8XT05;
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                                                    RESULT 23
Q8XT05
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Q96914
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EMBL, Acad. Sci. U.S.A. 99:4644-4649(2002).

Complete proteome.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.J., Cook E.H. Jr., Ledbetter D.H.;
Herzing L.B.K. Kim S.J., Cook E.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression.";
adjacent to GE3A and exhibits similar imprinted expression.";
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PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 1499 AA; 167687 MW; D4996A4D0635A68D CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR001064; Crystallin.
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MEDLINE-21927647; PubMed=11930014;
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Matches 8; Conservative
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Length 143;

63.5%; Score 33; DB 17;

0; Gaps 3; Indels Best Local Similarity 60.0%; Pred. No. 40; Matches 6; Conservative 1; Mismatches

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Search completed: June 10, 2003, 13:46:26 Job time : 25.7857 secs

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June 10, 2003, 13:24:45; Search time 31.3571 Seconds (without alignments) 46.744 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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**Lorioz/godata/geneseq/geneseqp-embl/AA1980.DAT:*

SIDSZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:*

SIDSZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:*

SIDSZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:*

SIDSZ/gogdata/geneseq/geneseqp-embl/AA1984.DAT:*

SIDSZ/gogdata/geneseq/geneseqp-embl/AA1984.DAT:*

SIDSZ/gogdata/geneseq/geneseqp-embl/AA1986.DAT:*

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SIDSZ/gogdata/geneseq/geneseqp-embl/AA1986.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

						SUMMARIES	
			æ				
Re	Result		Query				
	No.	Score	Match Length DB	Length	DB	a	Description
· {		54	96.4	11	23	ABB80523	Hepatitis C virus
>	7	54	96.4	11	23	ABB80527	
	8	54	96.4	11	23	ABB80558	Hepatitis C virus
;	4	54	96.4	11	23	ABB80560	Hepatitis C virus
	ا م	49	87.5	11	23	ABB80537	Hepatitis C virus
	9	49	87.5	11	23	ABB80541	Hepatitis C virus
	7	48	85.7	11	23	ABB80546	Hepatitis C virus
	80	48	85.7	11	23	ABB80550	Hepatitis C virus
	6	48	85.7	11	23	ABB80554	Hepatitis C virus
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ALIGNMENTS

RESULT 1

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ABB80523 ID ABB80523 standard; peptide; 11 AA.

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Ouery Match 96.4
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                        Lim-wilby M, Levy OE,
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                                                                                                                                                                                                                                                                                                                                                                                                          11 AA;
                                                                                                 Misc-difference
                                                                                                                                              WO200208251-A2
                                                                                                                                                                                                                                                                                                virus protease
                                                    Modified-site
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Modified-site
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                          Synthetic
        virucide.
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                                                                                                                                                 "Norvaly1 carbonyl forming keto-amide linkage with residue 7" \,
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                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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                                                                                                                                'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                             /note= "D-form residue"
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Pred. No.
                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 64; 69pp; English.
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100.0%; Pre
0;
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                            (first entry)
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                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                               virus protease
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                                                                                                                     Modified-site
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                            08-OCT-2002
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                                                                                          Synthetic
          ABB80523
                                                                           virucide
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/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                               'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
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                                                                                                                                                                                                                                   /note= "D-form residue"
Location/Qualifiers
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19-JUL-2001; 2001WO-US23169.
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residue ?"
/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40
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                                                              /note= "C-terminal amide"
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                                    /note= "Oxymethionine"
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                                                                                                                                                                                              (CORV-) CORVAS INT INC
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es 11; Conserv
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
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Pred. No. 0.00045;
0; Mismatches 0; Indels
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                     /note= "C-terminal amide"
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100.08; PI
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                            (CORV-) CORVAS INT INC
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Modified-site
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Synthetic
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                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21
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                                                                                                                                                                                                           Score 49; DB 23; Length 11;
Pred. No. 0.0043;
0; Mismatches 1; Indels
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                                           Brunck TK;
                                                                                                         Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                    ABB80541 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                "Norvalyl residue 7
                                                                                                                                                                                                           87.5%;
90.9%;
      21-JUL-2000; 2000US-220101P
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                       (CORV-) CORVAS INT INC
                                          Levy OE,
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                                                         WPI; 2002-361643/39
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                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
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                                       Lim-wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 11;
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Pred. No. 0.0043;
); Mismatches 1;
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                                                                                                            65; 69pp; English.
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 87.5
Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              11 AA;
                                                                                                         Claim 17; Page
                                                          virus protease
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virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                 Score 48; DB 23; Length 11;
Pred. No. 0.0067;
0; Mismatches 1; Indels
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90.9%;
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                                                                                                                                                                                                            Local Similarity
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                                                                                                                                 Sequence
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DB 23; Length 11;

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Query Match

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                           Gaps
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Pred. No. 0.0067;
); Mismatches 1; Indels
Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                      /note= "N-terminal acetyl"
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                        Conservative
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                                               1 EEVVPXGMHYS 11
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           Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                            RESULT
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(first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               11 AA;
                                                                                                                                                                                                                                                                                                       virus protease
                                                                                                                                                            WO200208251-A2
                                                                                       Modified-site
                                                                                                       Modified-site
                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                    Lim-wilby M,
08-OCT-2002
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                                                                                                                                                                              31-JAN-2002
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                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                           virucide
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                                                                                                                                                                     "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 2
Pred. No. 0.006
0; Mismatches
                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                               "D-form residue"
                                                                                                                                                                                                         /note= "D-form residue"
11
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                              residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80531 standard; peptide; 11 AA.
                ABB80555 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%;
90.9%;
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                                                     (first entry)
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGSHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AA;
                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                              virus protease
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                                                    08-OCT-2002
                                                                                                                                                                                                                                                                     31-JAN-2002.
                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                   ABB80555;
                                                                                                virucide.
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ABB80531
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                        . carbonyl forming keto-amide linkage with 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #12.
Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                     'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                             11
/note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                     "Norvalyl
                                                                                                                                                                                                                                                                                                                                                                 residue
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90.9%;
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Misc-difference
     WO200208251-A2.
                                                                                                                                                                    virus protease
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                                                                                                         Lim-wilby M,
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                          31-JAN-2002
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                              "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\sf C}
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 23; Length 11;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
           'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                /note= "C-terminal amide"
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                                                            "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                     Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                        Brunck
                                                                                                                                           19-JUL-2001; 2001WO-US23169.
                                                                                                                                                               2000US-220101P.
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                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                               /note=
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                                                                                                                                                                                  (CORV-) CORVAS INT INC
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                                                                                                                                                                                                        Levy OE,
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                                                                                                                                                                                                                                                                                                                                                                                         11 AA;
                                                Misc-difference
                                                                                                                                                                                                                                                                   virus protease
                                                                                                  WO200208251-A2
Modified-site
                    Modified-site
                                                                     Modified-site
                                                                                                                                                                                                     Lim-wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                          peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
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Pred. No. 0.026;
0; Mismatches 1;
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                                                                                                                                                              Brunck TK;
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19-JUL-2001; 2001WO-US23169.
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                                                     21-JUL-2000; 2000US-220101P.
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Matches 10; Conservative
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                                                                                                           (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                 WPI; 2002-361643/39
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virus protease
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                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                        virucide
                                                                                                                               Query Match
                                                                                                                                         Best Local
                                                                                                                                                  Matches
                                                                                                                                                                                                                   RESULT 16
                                                                                                                                                                                                                             ABB8052
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                                                                                                           The sequence represents a peptide compound of the invention having hepatitis ( virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat discorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                     ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis {\sf C}
                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4
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                                                                                                                                                                                                        Score 45; DB 23; Length 11; Pred. No. 0.026;
                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                               ABB80524 standard; peptide; 11 AA.
                  Brunck TK;
                                                                                           Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                          80.4%;
90.9%;
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nes 10; Conservative
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(CORV-) CORVAS INT INC
                  Levy OE,
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                                    WPI; 2002-361643/39.
                                                                                                                                                                                       11 AA;
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                                                                          virus protease
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                                                      peptide
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                  Lim-wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                 activity
                                                                                                                                                                                                                                                                                                                                                                                                    virucide
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                                                                            hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                      The sequence represents a peptide compound of the invention having
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                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 23; Length 11; Pred. No. 0.026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
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Claim 17; Page 64; 69pp; English.
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90.98;
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10; Conserv
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                                                                                                                                                                                                                                                                                                            11 AA;
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RESULT 18.
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a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                   "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                 Gaps
                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
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                                                           Score 45; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                'note= "N-terminal acetyl"
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                                                            80.4%;
90.9%;
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                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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                                         Sequence
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                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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Pred. No. 0.026;
0; Mismatches 1; Indels
Score 45; DB 23; Length 11;
Pred. No. 0.026;
                                            1; Indels
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    Query Match
Best Local Similarity
Matches 10; Conserv
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Matches 10; Conserv
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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Pred. No. 0.026;
0; Mismatches 1; Indels
                                                                                                                                                       /note= "N-terminal acetyl"
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                                                                                                                                      Location/Qualifiers
                  ABB80529 standard; peptide; 11 AA.
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  RESULT 19
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ABB80559
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/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39.
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Pred. No. 0.026;
0; Mismatches 1;
                                                                                                                                                                                                                                                                        'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Oxymethionine"
                                                                                                                                                                                                                      Location/Qualifiers
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90.9%;
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Matches 10; Conservative
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(CORV-) CORVAS INT INC
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Matches 10; Conserv
                                    Misc-difference 8
                                                                           Misc-difference 9
                                                                                                                                                                                                                                                                                                                                                                                                  11 AA;
                                                                                                                                                                                                                                                                                 virus protease
                                                                                                                         WO200208251-A2
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                                                                          /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                    peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42
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Pred. No. 0.026;
); Mismatches 1; Indels
                                                       'note= "N-terminal acetyl"
                                                                                                                                              /note= "C-terminal amide"
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8
                                                                                                                         "Oxymethionine"
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                                    Location/Qualifiers
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                                                                                                                                                                                                                                                               Brunck TK;
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90.9%;
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                                                                                                                          'note=
                                                                                                                                                                                                                                            (CORV-) CORVAS INT INC
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EEVVPXGMDYS
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AA;
                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                        virus protease
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Modified-site
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virucide
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ID ABBE
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                                                     "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Valy1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
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Pred. No. 0.026;
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/note= "N-terminal acetyl"
6
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                                                                                                                                                                                                                             "C-terminal amide"
                                                                                                             "D-form residue"
                                                                                                                                                                                         "D-form residue"
                                                                                                                                                 "Oxymethionine"
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90.9%;
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(CORV-) CORVAS INT INC
                                                                               virus protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Leucyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44
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                                                                                                                                                                                                                                                                               Score 45; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
11
/note= "C-terminal amide"
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                                                                                                             Brunck TK;
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                                                          19-JUL-2001; 2001WO-US23169.
                                                                          21-JUL-2000; 2000US-220101P
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                                                                                          (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                    Query Match
Rest Local Similarity
'-hnc 10; Conserve
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                                                                                                                                                                                                                                                               11 AA;
                       WO200208251-A2
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory
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                                                                                                                                                 useful for treating disorders associated with hepatitis C
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Pred. No. 0.026;
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Lim-wilby M, Levy OE, Brunck TK;
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90.9%;
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                                                         WPI; 2002-361643/39
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Best Local Similarity
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Claim 17; Page 65; 69pp; English.

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XX

CT he sequence represents a peptide compound of the invention having CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have CC invention are alpha ketoamide peptide analogues. The peptides have CC virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A CC is useful for treating disorders associated with hepatitis C virus.

XX

SQ Sequence 11 AA;

Query Match

Best Local Similarity 90.9%; Pred. No. 0.026; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY I EEVVPXGMHYS 11

DD 1 EEVVPXGMSYS 11
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June 10, 2003, 13:31:45; Search time 9.64286 Seconds (without alignments) 33.564 Million cell updates/sec Run on:

US-09-909-164-7 · 56 1 EEVVPXGMHYS 11 ritle:
Perfect score:
Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched: 262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/packfiles1.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Sequence 4794, Ap	Sequence 19, Appl	7		395(	Sequence 23, Appl	3, 2	Sequence 3, Appli	4,	4,	4	7,	21,	21,	Sequence 21, Appl	21,		Sequence 22, Appl	Sequence 22, Appl	Sequence 22, Appl	Sequence 6, Appli	Sequence 6, Appli	4	Sequence 4, Appli		Sequence 23, Appl	Sequence 6, Appli
	ID	US-09-134-001C-4794	US-08-821-119-19	US-08-821-118-2	US-09-724-864-36	US-09-134-001C-3950	US-08-580-988A-23	US-08-879-995A-3	US-09-215-096-3	US-08-460-694-4	US-08-460-744-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	US-08-246-361A-21	US-08-463-772-21	PCT-US93-05000-21	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22	US-08-464-517-6	US-08-463-772-6	US-08-246-361A-4	PCT-US93-05000-4	PCT-US93-05000-6	US-08-464-517-23	US-08-246-361A-6
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æ	Query Match	69.6	60.7	60.7	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
	Score	39	34	34	33	32	32	32	32		32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
	Result No.	1	7	e	4	2	9	7	80	O	10	11	12	13	14	15	16	17	18	. 19	20	21	22	23	24	25	26	27

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32	1	767	η,	18-463-772-23	eduence 23,
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	57.1	295	_	7-12	
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32	57.1	295	~	-08-460-694	Sequence 2, Appli
32	57.1	295	^	5-08-464-517-1	equence 19,
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1 (		100		1-4136-346-00-0	of agreement
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32	57.1	295	~	S-08-246-361A-2	odnence 🗘
32	57.1	295	m	-463-772-	equence 1
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32	57.1	295	m	-492-8	ò
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1 32	57.1	615	~	3-362-240A-1	, '
	57.1	615	വ	1895	equence 17,
	57.1	618	7	US-08-770-761A-3	'n
	57.1	647	7	3-77	Sequence 8, Appli
	57.1	660	۰,	S-08-770-761A-	7
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32	57.1	507	7	S-08-1/0-1814-	- 1
32	57.1	818	~	-08-464-517-7	7, Appl
32	57.1	819	~	61A	7,
32	57.1	819	m	US-08-463-772-7	Sequence 7, Appli
		819	ď	T-11593-05000	7
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	55.4	447	4	S-08-961-083-	18
	55.4	502	4	12-647	Sequence 4, Appli
31	55.4	529	4	S-09-240-639-	4
7 6		622	c	8-08-459-146-	ď
1.0		200	٠,	5-08-459-065	equence 2.
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3.L	4.00	050	4 .	2-13-245-64-5	3 6
31	55.4	667	4	S-09-342-647-	, a,
31	55.4	738	Н	30-010-	ednence 3,
31	55.4	738	Н	-08-530-010-	Sequence 5, Appli
1.0	4	739	-	5-08-530-010-	
3.1	7				

### ALIGNMENTS

Sequence 4794.

Sequence 4794.

Sequence 4794.

Sequence 4794.

Patent No. 6380370:

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCK

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FALING DATE: 1994-08-13

PRIOR FILING DATE: 1997-08-13

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4794

LENGTH: 1037

ORGANISM: Staphylococcus epidermidis

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TITLE OF INVENTION:
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                                                                                                               New York
                                                                                                                                                USA
                                                                                                                                                              10174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-724-864-36
                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-724-864-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 36
LENGTH: 747
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                                                                                                                                                                                                              Sequence 19, Application US/08821119
Patent No. 581104
GENERAL INFORMATION
APPLICANT: Holker, Torben
APPLICANT: Halker, Torben
APPLICANT: Halker, Torben
APPLICANT: Lehmbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58211040 No. 5821104th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                    Score 39; DB 4; Length 1037;
Pred. No. 16;
2; Mismatches 2; Indels
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Pred. No. 82;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: Fast-ESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4107.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambirls, Ellas J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-821-118-2
; Sequence 2, Application US/08821118
; Patent No. 5999889
                                    69.68;
63.68;
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Best Local Similarity 75.0%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
               Query Match
Best Local Similarity 63.00
To Conservative
                                                                                                                      : | | | | : | | | 199 KEVVSNGLHYS 209 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 212-867-013
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                   1 EEVVPXGMHYS 11
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linear
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31 VPKGWHYS 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                STREET: 405 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
US-09-134-001C-4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10174
                                                                                                                                                                                  RESULT 2
US-08-821-119-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59898890 No. 5989889disk of No. 5989889th America, Inc.
STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Fatent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Marison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050u1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT APPLICATION NUMBER: US. No. 6380362 60/171,678
FRIOR PLING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.9%; Score 33; DB 4; Length 747; 71.4%; Pred. No. 1.6e+02; Live 1; Mismatches 1; Indels
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HAVING TRIPEPTIDE AMINOPEPTIDASE
                                                                                                                                                                                                                                               SOFTWARE: FastERG for Windows Version 2.0 CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4107.400-US
                                                                                                                                                                                                                                                                                                                                                                                               ATTONNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
                      ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%;
75.0%;
                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 600 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 75.0v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-821-118-2
                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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Gaps
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                                                                                                                                                                                                                                         Score 32; DB 2; Length 102;
Pred. No. 29;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: DOS
SOFTWARE: FASTEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 35,749
REFERENCE/DOCKET NUMBER: PF-0326 US
                                                                                                                                                                                                                                               57.1%; Score 32; 60.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08879995A
; Patent No. 5985606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 6; Conservative
LENGTH: 102 amino acids
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                   internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                      DESCRIPTION: protein HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                       24 EEVFPLAMNY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank
                       TYPE: amino acid STRANDEDNESS:
                                                            TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: General Street 163590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
IMMEDIATE SOURCE:
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                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
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US-08-879-995A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-879-995A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANTON: WIGHER BORDES BORDES BORDES BELATING TO STAPHYLOCCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICANTON NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICANTON NUMBER: US 60/065,779
PRIOR PELING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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Pred. No. 19;
1; Mismatches 2; Indels
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MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: apple MacIntosh
COPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLIASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423 REFERENCE/DOCKET NUMBER: D5721CIP2
                                                                                                                                ; Sequence 3950, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dr. Benjamin A. Adler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus epidermidis US-09-134-001C-3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 23. Application US/08580988A Patent No. 5856161
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 62.5
Matches 5; Conservative
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          | |:|||
627 PGGLHYS 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas
                                                                                           RESULT 5
US-09-134-001C-3950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-580-988A-23
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1 EEVVPXGMH 9

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57.1%; Score 32; DB 2; Length 152; 60.0%; Pred. No. 44; tive 1; Mismatches 3; Indels
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                                                                                                                                                  MEDIUM TYPE: FLOPM disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FLING DATE: 02-JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCOncathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFRENCE/DOCKET NUMBER: 35,279
REFRENCE/DOCKET NUMBER: 35,279
REFRENCE/DOCKET NUMBER: 35,279
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCOnathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08460744 Patent No. 6107541
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Best Local Similarity 60.0
المحمد 6; Conservative
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                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-694-4
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20 EEVFPLAMNY 29
Washington
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STRANDEDNESS: not
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                                                              COUNTRY:
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                               STATE:
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Sequence 4. Application US/08460694
Fatent NO. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                      US-09-215-096-3
Sequence 3, Application US/09215096
Sequence 3, Application US/09215096
Sequence 3, Application US/09215096
Sequence 3, Application US/09215096
Sequence 3, Application:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Raser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
OSTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATORNEY, AGENT INFORMATION:
NAME: Bilings, Lucy.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
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LENGTH: 126 amino acids
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Best Local Similarity 66.71
Matches 6; Conservative
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TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Diskett
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28 EQVVPGGGH 36
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28 EQVVPGGGH 36
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LIBRARY: General Control of the Control of
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US-09-215-096-3
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                                                                                                                                 RESULT 8
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 44;
                                                                                     Length 152;
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                                                                                                                       3; Indels
                                                                                                                                                                                                                                                         NGS-07-67-711B-4

Sequence 4, Application US/07667711B

Sequence 4, Application US/07667711B

Sequence 4, Application US/07667711B

Patent No. 611070:

APPLICANT: ARNOLD, ANDREW

TITLE OF INVENTION: Pradl Cyclin and Its CDNA

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667 711P
                                                                                 DB 3;
44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                       Mismatches
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                                                                                 Score 32;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-MAR-1991
CLASSIECATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGIGSRATION NUMBER: 35.811
REFRENCE/CDOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08193977 Patent No. 5625031
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEVIN R.
KEVIN G.
not relevant
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Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                   57.1%;
60.0%;
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TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                    Local Similarity 60.0 ies 6; Conservative
                           , MOLECULE TYPE: peptide US-08-460-744-4
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20 EEVFPLAMNY 29
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APPLICANT: WEBSTER, K
APPLICANT: COLEMAN, K
TITLE OF INVENTION: P
TITLE OF INVENTION: P
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                  linear
 STRANDEDNESS:
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                                                                                       Query Match
                                                                                                        Best Loc
Matches
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Patent No. 5869640
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%; Score 32; DB 1; Length 173; 60.0%; Pred. No. 51; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/193,977

FILING DATE: 08 08 FEB. 1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5998-0016

TELEPROCK TOCKET NUMBER: 5998-016

TELEPROMUNICATION INFORMATION:

TELEPRAX: (415) 617-8999

TELEPRAX: (415) 617-8999

TELEPRAX: (415) 617-8999

TELEPRAX: (415) 27-3231

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 173 antho acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAX-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
                                                          STREET: 635 BRYANI SILLING CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: JA1301
ZIP: FORM:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMHY 10
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Query Match
Best Local Similarity 60.uv
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                              1 EEVVPXGMHY 10
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                     74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-463-772-21
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USA
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                                            US-08-246-361A-21
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Sequence 21, Application US/08246361A

Sequence 22, Application US/08246361A

Sequence 22, Sequence 22, Sequence 23, Sequence 24, Sequence 24, Sequence 24, Sequence 25, Sequence 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%; Score 32; DB 2; Length 189; 60.0%; Pred. No. 56; tive 1; Mismatches 3; Indels
FILING DATE: 16-MAY-1991

ATTORNEY/AGENT INFORMATION:
NAME: MATCHEW P. VINCENT
FEGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MI-004C

TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

NEORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: ALIOCHERISS: single
MOLECULE TYPE: peptide
US-08-464-517-21
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PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTONNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFRENCE/CDCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 60.03
Matches 6; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 EEVFPLAMNY 83
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Out: Watch

Sutchase 5, Conservative 1, Mismatches 3; Indels 0, Gaps 0

Watches 6, Conservative 1, Mismatches 3; Indels 0, Gaps 0

1 | ITHINGHER 10 | I Mismatches 1, Indels 0, Gaps 0

THENDERSHIP 10 | I Mismatches 1, Indels 0, Gaps 0

THENDERSHIP 10 | I MISMATCHER 10 | I Mismatches 1, Indels 0, Gaps 0

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amino acid
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ZIP: 02109
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US-08-246-361A-22
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Patent No. 5669640
BAPPLICANT: No. 5669640
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 5; Length 189;
Pred. No. 56;
1; Mismatches 3; Indels
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
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APPLICATION NUMBER: US 07/963,308
FILLING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 21:
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60.0%;
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AMINO ACID
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Best Local Similarity 60...
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-05000-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                      COUNTRY:
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Setent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 32; DB 2; Length 236; 60.0%; Pred. No. 72; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 26-MAY-1992
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMONINICATION INFORMATION:
TELECHNONE: (617) 227-7400
TELECHNONE: (617) 227-7400
TELECAX: (617) 227-7591
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MII-004C
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MITELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 amino acids
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Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide US-08-464-517-22
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                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                         Query Match 57.1%; Score 32; DB 2; Length 236; Best Local Similarity 60.0%; Pred. No. 72; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 3; Length 236;
Pred. No. 72;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/08463772
Patent No. 6066501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.1%;
60.0%;
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LENGTH: 236 amino acids
TYPE: amino acid
                 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-22
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                      1 EEVVPXGMHY 10
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Matches 6; Conserv
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ZIP: 02109
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US-08-463-772-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US93-05000-22
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                               APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREET: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 5; Length 236;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                    COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY, AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IN PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
; Sequence 22, Application PC/TUS9305000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 617-861-6240
616-861-9540
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
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20 EEVFPLAMNY 29
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 60 startor
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                                                                                                                                                                                                                        02173
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US-08-464-517-6
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0; Gaps

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Query Match 57.1%; Score 32; DB 3; Length 280; Best Local Similarity 60.0%; Pred. No. 87; Matches 6; Conservative 1; Mismatches 3; Indels
rrPE: amino acid; TOPOLGY: linear; MOLECULE TYPE: protein US-08-463-772-6
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US-08-246-361A-4
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Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTOR: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 2; Length 280;
Pred. No. 87;
1; Mismatches 3; Indels
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1991
FILING DATE: 26-MAY-1991
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATHEW P. VINCENT
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 6:
                                                          APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTHAW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECHONNICATION INFORMATION:
TELECHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
      APPLICATION NUMBER: US 07/963,308 APPLICATION UMBER: US 07/800 TERING DAMP.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein '
US-08-464-517-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
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APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%; Score 32; DB 2; Length 289; 60.0%; Pred. No. 90; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/246,361A
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEFROM: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                Sequence 4, Application US/08246361A
Patent No. 5998582
                                                                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 289 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-246-361A-4
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75 EEVFPLAMNY 84
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Sequence 4, Application PC/TUS9305000
GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application PC/TUS9305000
Sequence 6, Application PC/TUS9305000
Separation:
APPLICANT: MITOTIX
TITLE OF INVENTION:
D'TYPE OF SEQUENCES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Learington
STREET: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%; Score 32; DB 5; Length 289; 60.0%; Pred. No. 90; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFTCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 26-MAY-1992
ATTORNEY, AGENT INFORMATION:
MAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION:
TELEFAN: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein PCT-US93-05000-4
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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June 10, 2003, 13:46:50; Search time 15 Seconds Run on:

(without alignments) 75.710 Million cell updates/sec

US-09-909-164-7 56 Perfect score:

1 EEVVPXGMHYS 11

Sedneuce:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Searched:

392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Published_Applications_Aai.

1. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

2. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

3. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

4. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

5. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

6. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

7. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

8. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

10. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

11. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

11. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

12. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

13. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

14. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

14. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:* Published_Applications_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Describeron	Sequence 126, App	Sequence 4919, Ap	Sequence 663, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 53, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 54, Appl	Sequence 26, Appl	16, 7	Sequence 15, Appl	-	Sequence 52, Appl	Sequence 14, Appl	Sequence 40832, A	Sequence 119, App	Sequence 171, App
SUMMAKES	Ş	LD	US-10-270-333-126	US-09-738-626-4919	US-09-866-050A-663	US-10-027-806-4	US-10-034-623-4	US-10-027-801-4	US-09-778-927A-53	US-10-024-066-2	US-10-024-066-4	US-09-919-497-54	US-09-820-843A-26	US-09-252-088-16	US-09-252-088-15	US-10-047-542-80	US-09-870-759-52	US-09-948-080-14	US-09-864-761-40832	US-10-001-857-119	US-09-986-480-171
	9	E :	σ	6	6	6	σ	σ	10	6	σ	10	6	6	0	σ	5	10	10	σ	0
	1	Match Length DB	567	622	747	3472	3472	3472	254	289	289	289	653	715	793	662	847	59	73	192	192
	Query	Match	58.9	58.9	58.9	58.9	58.9	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	56.2	56.2	55.4	55.4	55.4	55.4
	ē	Score	33	33	33	33	33	33	32	32	32	32	32	32	32	31.5	31.5	31	31	31	31
	Result	No.	7	7	m	4	ស	9	7	60	6	10	11	12	13	14	15	16	17	18	19

Sequence 13489, A Sequence 13613, A Sequence 10697, A Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 14, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli Sequence 19, Appli Sequence 10, Appli Sequence 13, Appli Sequence 135, Appli Seq	equence 4 equence 4 equence 6 equence 6 equence 6 equence 6
US-09-815-242-13489 US-09-815-242-10697 US-09-815-242-10697 US-09-816-42-10697 US-10-188-405-8 US-10-188-405-8 US-09-943-798-4 US-09-943-798-4 US-09-943-798-4 US-09-943-798-4 US-09-943-798-4 US-09-978-738-62-5315 US-09-769-773-38 US-09-769-773-8 US-09-976-773-8 US-09-976-773-8 US-09-976-773-8 US-09-978-109-4 US-09-984-465A-10 US-09-984-465A-10 US-09-984-465A-10 US-09-984-465A-10 US-09-984-465A-10 US-09-984-465A-10 US-09-984-465A-10 US-09-984-465A-10 US-09-984-465A-10 US-09-984-465A-10 US-09-981-168-8 US-09-981-168-8 US-09-882-797-68 US-09-882-797-68 US-09-882-797-68 US-09-882-797-85 US-09-882-797-85 US-09-982-11-18-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-359 US-09-989-733-334-334-334-334-334-	US-10-175-752-44 US-10-176-757-44 US-10-176-757-44 US-10-176-757-44 US-10-180-552-44 US-10-180-557-44 US-09-990-438-35
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# ALIGNMENTS

Sequence 126, Application US/10270333

Publication No. US20030092124A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS

TITLE OF INVENTION: UNCHER AS INSECTICIDAL TARGETS

FILE REFERENCE: CLO00733CON

CURRENT APPLICATION NUMBER: US/10/270,333

CURRENT FILING DATE: 2002-10-15 RESULT 1 US-10-270-333-126

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LENGTH: 3472
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                        APPLICANT:
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                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MAKAGAWA, SATOSHI
APPLICANT: MAKAGAWA, SATOSHI
APPLICANT: MAKAGAWA, MIKIRO
APPLICANT: ANDO, SEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: UP 09/377484
PRIOR APPLICATION NUMBER: UP 09/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PELICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATEITIN VAY: 3.0
SEQ ID NO 4919
PRIOR APPLICATION NUMBER: 60/168,677
PRIOR FILING DATE: 1999-12-03
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/175,691
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 198
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
LENGTH: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4919, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 663, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            Query Match 58.9
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.v.
6; Conservative
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US-10-270-333-126
                                                                                                                                                                                                                                                                                                                                                                                                                             402 PSGMHY 407
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                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
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APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Stanson, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFRENCE: DCORP.002A
CURRENT APPLICATION NUMBER: U5/10/027,806
CURRENT APPLICATION NUMBER: BALLIER APPLICATION NUMBER: 09/408,020
PRIOR PRIOR PRILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10034623
Publication No. US20020198365A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Swanson, Robert A.
APPLICANT: Schleger, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.1e+03;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                               58.9%; Score 33; DB 9; Length 747; 71.4%; Pred. No. 3.8e+02; Live 1; Mismatches 1; Indels
                                TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods for Their Use FILE REPERENCE: 11000.1011.04 UCURRENT APPLICATION NUMBER: US/09/866,050A CURRENT FILING DATE: 2001-05-24 NUMBER OF SEQ ID NOS: 725 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 663 LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10027806
Patent No. US20020160476A1
                 Murison, James G.
Kumble, Krishanand D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.5.
Best Local 5; Conservative
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Onrust, Rene
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; ORGANISM: Rat
US-09-866-050A-663
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RESULT 8
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Patent No. US20020068342A1
GRNERAL INFORMATION:
APPLICANT: KHOSRAVI.
APPLICANT: KHOSRAVI.
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 1L 134453
                                                                                                                                                                                                                                                                                                                                                                                Sequence 123 Control of Application US/10027801

Publication No. US20030054364a1

GENERAL INFORMATION:

APPLICANT: Swanson, Ronald V.

APPLICANT: Schleper, Christa

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM

FILE REFERENCE: DCORP.002A

FILE REFERENCE: DCORP.002A

CURRENT APPLICATION NUMBER: US/10/027,801

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/408,020

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123

SOFFWARE: FastSEO for Windows Version 3.0
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| LOCATION: (1)..(254)

| COTHEN INFORMATION: Xaa = any amino acid, unknown, or other

US-09-778-927A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.9%; Score 33; DB 9; Length 347
45.5%; Pred. No. 2.1e+03;
Live 4; Mismatches 2; Indels
                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                4; Mismatches
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL135341
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 53
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
                                                                          ; ORGANISM: Cenarchaeum symbiosum US-10-034-623-4
                                                                                                                                                       58.9%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 45.5
Matches 5; Conservative
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2294 EDVIPRGISFS 2304
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2294 EDVIPRGISFS 2304
                                                                                                                                                         Query Match 58.9
Best Local Similarity 45.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-027-801-4
                                                                                                                                                                                                                                                                                                                                                                            US-10-027-801-4
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Sequence 4, Application US/10024066

Sequence 4, Application US/10024066

Patent No. US20020166134A1

GENERAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Field, Loren J.
TITLE OF INVENTION: CARDIOMYCCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 289
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                                                                                                                                                                                                                                         Sequence 2, Application US/10024066

Patent No. US20020166134A1

GENERAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Field, Loren J.
TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/139,942
PRIOR FILING DATE: 2000-06-18
PRIOR FILING DATE: 2000-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                               Gaps
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Score 32; DB 10; Length 254; Pred. No. 1.8e+02; 3; Indels
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60.0%; Pred. No. 2.1e+02;
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                                                 1; Mismatches
       57.1%;
60.0%;
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Best Local Similarity 60.0.
Best Local 6; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 289
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         Query Match 57.18
Best Local Similarity 60.08
Matches 6; Conservative
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                                                                                                1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mus musculus
US-10-024-066-2
                                                                                                                                          74 EEVFPLAMNY
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Best Local Similarity
Matches 6; Conserv
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US-10-024-066-4
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1 EEVVPXGMHY 10

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APPLICANT: LARRICK, JAMES W.
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.004.C1PI
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILLING DATE: 2001-10-26
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                   APPLICANT: CHARLEBOIS, ISAbelle
APPLICANT: HAMEL, Jose
APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Denis
TITLE OF INVENTION. NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER PILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
LEMOTH: 715
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.1%; Score 32; DB 9; Length 715; Best Local Similarity 75.0%; Pred. No. 5.7e+02; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-092-252-088-15

Sequence 15, Application US/09252088

PUBLICATION NO. US20030031682A1

GENERAL INFORMATION

APPLICANT: BRODEUR, Bernard R.

APPLICANT: RIOUX, Climent

APPLICANT: BOYER, Martine

APPLICANT: CHARLEBOIS, Isabelle

APPLICANT: HAMEL, Jose

APPLICANT: MARTIN, Denis

TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS

FILE REFERENCE: 8331-9002

CURRENT APPLICATION NUMBER: US/09/252,088

CURRENT FILING DATE: 1999-02-18

EARLIER APPLICATION NUMBER: US/60/075,425

EARLIER APPLICATION NUMBER: US/60/075,425

SOFTWARE: PARLIER PLING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 80, Application US/10047542
; Patent No. US20020168367A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: group B streptococcus US-09-252-088-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT / ORGANISM: group B streptococcus US-09-252-088-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.07
Post Local 6; Conservative
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LENGTH: 793
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                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Sequence 26, Application US/09820843A
Sequence 26, Application US/09820843A
Sequence 26, Application US/09030303963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVEWTION: USEFUL AS ANTI-INFECTIVES
TITLE OF INVEWTION: USEFUL AS ANTI-INFECTIVES
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT APPLICATION NUMBER: US/09/820,843A
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
TENDENT 65
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                                                                                                                                                                            APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR PILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
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CTHER INFORMATION: iron(III) ABC transporter, permease protein;
NAME/KEY: misc_feature
CTHER INFORMATION: gi|9654609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%; Score 32; DB 10; Length 289; 60.0%; Pred. No. 2.1e+02; tive 1; Mismatches 3; Indels
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US-09-252-088-16
; Sequence 16, Application US/09252088
; Publication No. US20030031682A1
; GENERAL INFORMATION:
; APPLICANT: BRODEUR, Bernard R.
; APPLICANT: RIOUX, Clment
; APPLICANT: BOYER, Martine
                                                                                                               ; Sequence 54, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
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Best Local Similarity 60.00
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Best Local Similarity 75.0v
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  74 EEVFPLAMNY 83
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; ORGANISM: Homo sapiens
US-09-919-497-54
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APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT PAPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 52
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                                                                                                                                                                                                                                       56.2%; Score 31.5; DB 9; Length 662; 43.8%; Pred. No. 6.5e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HALKIER, TORDEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BANDITZ, PETER
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/09/948,080
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US/08/963,851
PRIOR APPLICATION NUMBER: 1997-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN Ver. 2.1
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APPLICANT: VAN DER OSTEN, CLAUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 52, Application US/09870759 Patent No. US20020177551A1 GENERAL INFORMATION:
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US-09-948-080-14
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                                                                                                                                                                                                                                                                  Best Local Similarity 43.83
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                ; ORGANISM: Homo sapiens US-10-047-542-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-948-080-14
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LENGTH: 59
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                                                                                                                    SEQ ID NO 80
LENGTH: 662
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GENERAL INFORMATION:
APPLICANT: Penh, Sharron G.
APPLICANT: Penh, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenshen GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL I.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                      ö
                                                                                             Gaps
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.0
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
           55.4%; Score 31; DB 10; Length 59; 45.5%; Pred. No. 57; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine Vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXPRESSED IN HELA, SIGNAL = 4
EXPRESSED IN LUNG, SIGNAL = 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE DEFENDER ADOMICA X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/00/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PLICATION NUMBER: US/00/36,359
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: MAP TO AL136528.9 INFORMATION: EXPRESSED IN HELA,
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40832, Application US/09864761 Patent No. US20020048763A1
Query Match
Best Local Similarity 45...
Best Local Si Conservative
                                                                                                                                                                            1 EEVVPXGMHYS 11
                                                                                                                                                                                                                       |: :| |: ||
38 EKHIPGGLEYS 48
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-864-761-40832
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LENGTH: 73
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROKATYOTES

FILE REFERENCE: ELITRA, 0.11A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT PILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLICATION NUMBER: 60/25,655

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/253,625
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Pred. No. 2.9e+02;
1; Mismatches 3; Indels
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TITLE OF INVENTION: Identification of Essential Genes in
FILLE OF INVENTION: Prockaryotes
FILLE REFERENCE: ELITRA.011A
CURRENT APPLICATION HOWER: U5/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 260
                                                                                                                                                                                                Sequence 13489, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 13613, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                         Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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Best Local Similarity 60.0%;
Matches 6; Conservative
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; APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                          Wall, Daniel
Trawick, John D.
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                                     2 EVVPXGMHYS 11
                                                                                 52 ENIPEGLNYS 61
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US-09-815-242-13489
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APPLICANT:
APPLICANT:
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Sequence 119, Application US/10001857

Publication No. US20020183500A1

GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sel-Yu
APPLICANT: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEx-0.273

CURRENT APPLICATION NUMBER: US/10/001,857

CURRENT APPLICATION NUMBER: US/12/001,857

CURRENT FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 208

SOUTHWARE: PatentIn version 3.1
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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8

; OTHER INFORMATION: EST_HUMAN HIT: AW027739.1, EVALUE 7.00e-14

US-09-864-761-40832
                                                                                                                        55.4%; Score 31; DB 10; Length 73; 71.4%; Pred. No. 72; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
55.4%; Score 31; DB 9; Length 192
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%; Score 31; DB 9; Length 192; 50.0%; Pred. No. 2.1e+02; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION AND ADDRESS OF THE APPLICATION AND ADDRESS OF TITLE REPERENCE: PSSOOP1
CURRENT APPLICATION NUMBER: US/09/986,480
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: PCT/US00/12788
PRIOR PILING DATE: 2000-05-11
PRIOR PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 456
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 171, Application US/09986480
; Publication No. US20030027999A1
; GENERAL INFORMATION:
                                                                                                                                                                       Conservative
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Matches 5; Conservative
                                                                                           Ouery Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapien US-10-001-857-119
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145 IIPKGMH 151
                                                                                                                                                                                                                                                                60 VVPSGLH 66
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US-09-986-480-171
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; ORGANISM: HOMO
US-09-986-480-171
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LENGTH: 192
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LENGTH: 192
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GENERAL INFORMATION:

APPLICANT: Vogeli, Cabriel

APPLICANT: Vogeli, Cabriel

APPLICANT: Wood, Linds A.

APPLICANT: Wood, Linds A.

APPLICANT: Wood, Linds A.

APPLICANT: Wood, Linds A.

TILE REPRENCE: 4105PHRM311

CURRENT PAPLICATION NUMBER: 05/09/782,974C

CURRENT APPLICATION NUMBER: 06/165,838

PRIOR APPLICATION NUMBER: 06/165,838

PRIOR PELING DATE: 2000-11-16

PRIOR FILING DATE: 2000-11-16

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 1999-11-17

PRIOR FILING DATE: 1999-11-17

PRIOR FILING DATE: 1999-11-19

PRIOR FILING DATE: 1999-11-19

PRIOR FILING DATE: 1999-11-19

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 2000-02-22

PRIOR PELICATION NUMBER: 60/185,54

PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-03-28

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02
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GENERAL INFORMATION:
APPLICANT: Pfizer Ltd. (EP(GB) only)
APPLICANT: Pfizer Inc. (US, JP, EB except GB)
TITLE OF INVENTION: No. US20030022282A1e1 Polypeptide
FILE REFERENCE: PC10959AGPR
CURRENT FILING DATE: 2001-12-18
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2001-10-09
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                                                                                                                                                                                                                                                   Sequence 86, Application US/09782974C Publication No. US20030082534A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin version 3.1
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Best Local Similarity 50.0
Matches 5; Conservative
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                                   1 EEVVPXGMHY 10
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US-09-782-974C-86
                                                                                                                                                                                                         RESULT 23
US-09-782-974C-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 10; Length 260;
Pred. No. 2.9e+02;
1; Mismatches 3; Indels
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APPLICANT: Chisen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE REPERENCE: ELTTRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/201,08
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-110-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-22
PRIOR FILING DATE: 2001-12-22
PRIOR PELING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10697
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10697, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Enterococcus faecalis US-09-815-242-10697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.4%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Karl L. APPLICANT: Zyskind, Judith W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.4
Best Local Similarity 40.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13613
LENGTH: 260
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g δ

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RESULT 25

US-10-270-144-2

Squence 2. Application US/10270144

Publication No. US20030049790A1

GENERAL INFORMATION:
APPLICATE NET. MINGHHI et al.
ITILE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR INTERTION: PROTEINS, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/270,144

CURRENT APPLICATION NUMBER: 60/205,196

PRIOR PILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

SEQ ID NO 2

SEQ ID NO 2

LENGTH: 337

TYPE: PRI

CORGANISM: Human

US-10-270-144-2
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                                                                                                                                                                                                                                                                 Query Match 55.4%; Score 31; DB 9; Length 337; Best Local Similarity 50.0%; Pred. No. 3.8e+02; Matches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.4%; Score 31; DB 9; Length 337; Best Local Similarity 50.0%; Pred. No. 3.8e+02; Matches 5; Conservative 2; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: US 60/296,660
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: GB 0111031.1
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 337
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGMHY 10
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26 DENIPLKMHY 35
                                                                                                                                                                                                  ) ORGANISM: Homo sapiens
US-10-023-775B-2
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Search completed: June 10, 2003, 14:35:41 Job time : 16.0714 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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June 10, 2003, 13:31:15; Search time 11.2143 Seconds (without alignments) 94.297 Million cell updates/sec Run on:

1 EEVVPXGMHYS 11 US-09-909-164-7 Perfect score: Sedneuce: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	ftsH proteinase ac	carbamoy1-phosphat				hypothetical prote	conserved hypothet		GMP synthetase, su	hypothetical prote	T518.1 protein - A	diphthine synthase	hypothetical prote	3-dehydroquinate s	probable DNA ligas	-	hypothetical prote		hypothetical prote	₽		polyamine transpor	conserved hypothet	probable amino aci	cid anti	finger protein (cl	cytochrome-c3 hydr	0	hypothetical prote
ū	A72207	F89892	A42452	AE2001	S69046	S38143	D82618	T02590	H69194	T24111	G86430	G69117	C75538	B75478	T35025	E69086	C83903	S58132	T28717	AF3286	S54619	E83607	G82253	G71542	Н81697	865811	HQDVLB	A69284	T08564
DB	2	7	N	~	7	~	7	~	7	7	7	7	7	7	~	~	N	7	7	7	~	7	7	N	~	~	7	N	7
Length DB	308	1057	102	252	460	743	156	233	311	425	510	264	279	350	355	360	425	426	495	1028	156	367	441	466	466	487	514	534	545
* Query Match	66.1	66.1	64.3	64.3	64.3	64.3	62.5	62.5	62.5	62.5	62.5		60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	58.9	58.9	58.9	58.9	58.9	58.9	58.9	58.9	58.9
Score	37	37	36	36	36	36	35	35	35	35	35	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33
Result No.	1	171	ıe	4	S	9	7	60	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	. 36	27	28	29

DNA mismatch repai macrophage-stimula C14B9.8 protein - L-shaped tail fibe hypothetical 367K tachykinin B precu heme exporter prot hypothetical prote ribosomal protein	ribosomal protein probable TunA prot hypothetical prote cyclin D2 - rat cyclin D2 - rat cyclin D2 - mouse cyclin D2 - mouse cyclin D2 - human cyclin D1 - Africa cyclin D2 - Africa	cyclin D2 control cyclin D3 - when a cyclin D3 - human cyclin D1 - human cyclin D1 - mouse cyclin D1 - rat hypothetical prote hypothetical prote probable periplasm probable periplasm probable periplasm probable periplasm	probable aspartate hypothetical prote hypothetical prote 2-methyl-branched-hypothetical prote probable b2IP tran conserved hypothet beta-glucoside-spe iron(III) ABC tran zlnc finger protei	phage tränsposase hypothetical prote SCT1 protein - yea hypothetical 92.4K probable sulfate p sulfate permease - tegument protein h
		JC62730 B42822 B42822 A58977 A58523 JC2342 T25498 JX0116 A83470		
		2001 2000 2000 2000 2000 2000 2000 2000		
58. 58. 57.	57. 57. 57. 57. 57. 57.	557 557 557 557 557 557 557	77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00	527
<u> </u>	, <b>, , , , , , , , , , , , , , , , , , </b>	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	.,.,.,.,.	
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	0 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	55 60 60 60 60 60 60 60 60 60 60 60 60 60	000 007 127 728 748 748

## ALIGNMENTS

firsh proteinase activity modulator HflK - Thermotoga maritima (strain MSB8) C; Species: Thermotoga maritima (c; Species: Thermotoga maritima (c; Species: In-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C; Accession: A72207 F. R. R. Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; igarrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson

RESULT 1

Nature 399, 323-329, 1999
A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genor A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genor A, Reference number: A72200, MUID:99287316, PMID:10360571
A, Reference number: A72207
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-308 <ARN>
A, Cross-references: GB:AE001819, GB:AE000512; NID:94982396; PIDN:AAD36885.1; PID:G. C;Genetics:

A;Gene: TM1822 C;Superfamily: erythrocyte band 7 integral membrane protein

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                                                                                                                                                                                                                                                                                  carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variation - tobacco yellow dwarf virus (strain Australia)

Variation - tobacco yellow dwarf virus (strain Australia)

C;Species: tobacco yellow dwarf virus

C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-oct-1999

C;Accession: A42452

A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellow A;Reference number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gispecies: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2001
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, §
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: pyrAB
C; Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
                                                                                                                                                                                                                                                                                                                                                    C'Accession: F89892
R'Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; R'Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; G.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A'Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A'Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                        ô
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A;Molecule type: DNA
A;Residues: 1-1057 <KUR>
A;Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
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                                                                                                                                                                                                                                                                                                             C; Species: Staphylococcus aureus
C; Date: 10-May.2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                      Gaps
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A.Residues: 1-102 <MOR>
A.Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE2001
hypothetical protein alr1563 [imported] - Nostoc sp. (strain PCC 7120)
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                                Score 37; DB 2; Length 308;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 102;
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                                                                            1; Mismatches
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Pred. No. 5;
3; Mismatches
                                66.1%;
75.0%;
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60.0%;
Query Match
Best Local Similarity 75.v.
6. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 60.0 les 6; Conservative
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                                                                                                                      3 VVPXGMHY 10
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Matches
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DNA Res. 8, 205-213, 2001
A;Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacteriu A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-460 <HAL>
A;Cross-references: EMBL:U43703; NID:g1244769; PIDN:AAB68221.1; PID:g1244776; MIPS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-743 <VAN>
A; Residues: 1-743 <VAN>
A; Cross-references: EMBL: 228292; NID: 9486536; PIDN: CAA82146.1; PID: 9486537; MIPS: YKR
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S69046
R; Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, submitted to the EMBL Data Library, December 1995
A; Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A; Reference number: S69040
A; Accession: S69046
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                      A;Molecule type: DNA
A;Residues: 1-252 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB77929.1; PID:917135383; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Saccharomyces cerevisiae
C; Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                         Gaps
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C;Superfamily: Saccharomyces cerevisiae transcription modulator WTM1
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                                                                                                                                                                                                                                                                                                   Score 36; DB 2; Length 252;
Pred. No. 13;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein YPL139c - yeast (Saccharomyces cerevisiae)
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64.3%; Score 36; DB 2; Length 460;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 1; Indels
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64.3%; Score 36; DB 2; Length 743;

Best Local Similarity 75.0%; Pred. No. 43;

Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: SGD:S0006060; MIPS:YPL139c
                                                                                                                                                                                                                                                                                                64.3%;
50.0%;
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A;Cross-references: SGD:S0001775
A;Map position: 11R
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMHY 10
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85 IVPLGLHY 92
                                                                                                    A; Status: preliminary
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, S. Mith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Gibson, R.; Jiwani, G., Gibson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: H69194
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: NATH
A; Cross-references: GB:AE000850; GB:AE000666; NID:92621794; PIDN:AAB85215.1; PID:928
A; Experimental source: strain Delta H
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: G86430
C;Accession: G86430
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewa ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, B16-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K
                                                             GMP synthetase, subunit B - Methanobacterium thermoautotrophicum (strain Delta H) C;Species: Methanobacterium thermoautotrophicum C;Species: 05-Dec-1997 *sequence_revision 05-Dec-1997 *text_change 22-Oct-1999
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C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T24111
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A; Reference number: 219842
A; Accession: T24111
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Matches 7; Conservative
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219 EEVVESGLHES 229
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Plant Cell 7, 173-182, 1995
A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene responsi
A;Reference number: 214671; MUID:95276459; PMID:7756828
A;Accession: T02390
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                        conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c) (Species: Xylella fastidiosa (Species: Xylella fastidiosa (Species: Xylella fastidiosa (Species: Yylella fastidiosa (Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #sequence_revision 20-Aug-2000 #sequence (Species: 18-Aug-2000 #sequence (Species: 18-Aug-2000 #sequence of the plant pathogen Xylella fastidiosa (Species: The genome sequence of the plant pathogen Xylella fastidiosa (Species: A) *Reference number: A82515; MUID: 20365717; PMID: 10910347 A) *Note: for a complete list of authors see reference number A59328 below
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C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
C;Accession: T02590
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A; Residues: 1-233 -00MA
A; Cross-references: EMBL:D38126; NID:9790362; PIDN:BAA07324.1; PID:91208498
A; Experimental source: strain BY4; tissue-type leaf
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60.0%; Pred. No. 19;
tive 1; Mismatches
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Matches 5; Conservative
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                                                                         294 VVPCGLHY 301
3 VVPXGMHY 10
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-156 <SIM>
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A,Map position: 1
C,Superfamily: Deinococcus radiodurans hypothetical protein DR0271
                                                             A; Gene: DR0271
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G.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A;Razo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A:Reference number: A69000; MUID:98037514; PMID:9371463
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A; Residues: 1-264 <MTH>
A; Cross-references: GB: AE000940; GB: AE000666; NID: 92623011; PIDN: AAB86340.1; PID: 9262301
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C;Species: Deinococcus radiodurans
C;Decies: Deinococcus radiodurans R1.
S;Decies: Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036996; PMID:10567266
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A Status: preliminary
A Molecule type: DNA
A Status: 1-279 <WHI>
A Status: 1-279 <WHI>
A Cross-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
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A;Residues: 1-510 <STO>
A;Cross-references: GB:AE005172; NID:g4587512; PIDN:AAD25743.1; GSPDB:GN00141
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Pred. No. 45;
2; Mismatches 2; Indels
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C; Superfamily: hexose phosphate transport protein uhpT
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                62.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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Best Local Similarity 62.5.
5, Conservative
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235 VVPAGLHF 242
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                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: MTH1874
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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C:Species: Definococcus radiodurans
C:Decies: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Date: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: B75478
C:Accession: B75478
C:Accession: B75478
R:White, O:Esen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
A.Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: DNA
A,Residues: 1-350 <WHI>
A,Cross-references: GB:AE001932; GB:AE000513; NID:g6458481; PIDN:AAF10353.1; PID:g6
A,Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Streptomyces coefficion
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35025
R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Seeger, S.; Harris, D.; James, Y.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Seeger on the EMBL Data Library, June 1999
A;Reference number: Z21565
A;Residues: T350 <SEE>
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C;Superfamily: 3-dehydroquinate synthase; 3-dehydroquinate synthase homology
                                                                                   Gaps
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Ouery Match 60.7%; Score 34; DB 2; Length 279; Best Local Similarity 75.0%; Pred. No. 38; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                  3-dehydroquinate synthase - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.7%; Score 34; DB 2; Length 350; 60.0%; Pred. No. 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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Best Local Similarity 71.4°
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGMHYS 11
                                                                                                                                                                                    100 VPLGRHYS 107
                                                                                                                          4 VPXGMHYS 11
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                           RESULT 14
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A;Cross-references: EMBL:Z50154; NID:g1052827; PID:g1052828
                                                           60.78;
                                                                                   Similarity 44.4%;
4; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 50.0°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 ENIVPICKHH 227
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                                                                                                                                                                                                              52 DOVIPAGLH 60
                                                                                                                                                                 1 EEVVPXGMH 9
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-495 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: AF3286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: BMEI0275
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                                                                                                              Matches
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                                                cell division protein - Methanobacterium thermoautotrophicum (strain Delta H)
C; Species: Methanobacterium thermoautotrophicum
C; Species: Methanobacterium thermoautotrophicum
C; Species: Methanobacterium thermoautotrophicum
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C; Accession: E69086
R; Smith, D. R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A; Recession: E69086
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Status: 1-360 ATHEN
A; Cross-references: GB: AE000923; GB: AE000666; NID: G2622766; PIDN: AAB86115.1; PID: G262277
A; Status: MH1642
C; Superfamily: cell division protein MJ0174
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submitted to the EMBL Data Library, July 1995
A;Description: S1S1p, an endoplasmic reticulum component, is involved in the protein tra
A;Reference number: S58132
A;Accession: S58132
A;Accession: S58134
A;Accession: preliminary
A;Accession: preliminary
A;Accession: DNA
A;Residues: 1-426 <BOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein BH2027 [imported] - Bacillus halodurans (strain C-125)
C; Species: Bacillus halodurans
C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C; Accession: C83903
R; Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MuID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05746.1; GSPDB:GNOC
A;Experimental source: strain C-125
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C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Sep-1997
C;Accession: S58132
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Pred. No. 50;
4; Mismatches 2; Indels
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60.0%; Pred. No.
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Best Local Similarity 45.5%;
Matches 5; Conservative 4
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Best Local Similarity 60.0
Matches 6; Conservative
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A;Gene: BH2027
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Ribelvechin, V.C.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ival, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella me. A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-dependent DNA helicase BMEI0275 [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF022972; PIDN:AAC48234.1; GSPDB:GN00023; CESP:Fl0D2.3 A;Experimental source: strain Bristol N2; clone Fl0D2
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A;Residues: 1-1028 (40R>
A;Crost-references: GB:AbG008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AF3286
                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.7%; Score 34; DB 2; Length 495; 50.0%; Pred. No. 70; tive 2; Mismatches 3; Indels
Score 34; DB 2; Length 426;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%; Score 34; DB 2; Length 102
54.5%; Pred. No. 1.5e+02;
iive 2; Mismatches 3; Indels
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 5
A;Introns: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Graves, T.; Wohldmann, P.; Gillam, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F10D2.
A;Reference number: Z20515
                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F10D2.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                    4; Mismatches
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A;Cross-references: GB:AE004182; GB:AE003852; NID:99655461; PIDN:AAF94166.1; GSPDB: A;Experimental source: serogroup 01; strain N16961; biotype El Tor C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable amino acid transporter - Chlamydia trachomatis (serotype D, strain UW3/Cx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Date: 13-Sep-1998 #text_change 19-May-2000
C; Accession: G71542
A; Tetle: Genome sequence_revision 13-Sep-1998 #text_change 19-May-2000
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch Science 282, 754-759, 1998
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia A; Mcfession: G71542
A; Reference number: A71570; MUID: 99000809; PMID: 9784136
A; Accession: G71542
A; Status: precliminary
A; Molecule type: DAR
A; Molecule type: DAR
A; Molecule type: DAR
A; Csatus: Drefininary
A; Csatus: Dr
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A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR3 A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-466 <TET>
A;Cross-references: GB:AE002317; GB:AE002160; NID:97190522; PIDN:AAF39334.1; PID:971
                                   1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Fitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Accession: G82233
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1
C;Superfamily: conserved integral membrane protein HP0758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2;
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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C;Superfamily: L-lysine transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.9%;
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Best Local Similarity 62.5%;
Matches 5; Conservative
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les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-441 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: VC1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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A; Residues: 1-156 <DEW>
A; Cross-references: EMBL:274920; NID:91420109; PIDN:CAA99201.1; PID:91420111; MIPS:YOR01
A; Experimental source: strain $288C
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A: Molecule type: DNA
A: Experimental source: Strain PAOI
A: Experimental source: Strain PAOI
A: Genetics:
A: Genetics:
C: Superfamily: Escherichia coli spermidine/mutrasoine-biadine
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C; Accession: E88607 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000  
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83607
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C:Species: Pseudomonas aeruginosa
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hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein 02612; hypothetical protein YOL303.3
C.Species: Saccharomyces cerevisiae
C.Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C.Accession: S54619; S66879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: EMBL:X87331; NID:91041652; PIDN:CAA60762.1; PID:9829123 R;de Haan, M.; Grivell, L.A.; Maarse, A.C. submitted to the Protein Sequence Database, July 1996
A.Reference number: S66877
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Best Local Similarity 44.4%; Pred. No. 81;
Matches 4; Conservative 3; Mismatches.
                                                                                                                                                                                                                                                 R;de Haan, M.; Maarse, A.C.; Grivell, L.A. submitted to the EMBL Data Library, May 1995 A;Reference number: S54617 A;Accession: S54619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 15R
C;Superfamily: hypothetical protein YOR013w
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A; Residues: 1-156 <DEH>
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us-09-909-164-7.rpr

0; 0; Gaps Query Match 58.9%; Score 33; DB 2; Length 466; Best Local Similarity 62.5%; Pred. No. 1e+02; Matches 5; Conservative 2; Mismatches 1; Indels

4 VPXGMHYS 11 :| ||:|| 453 IPFGMYYS 460

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Search completed: June 10, 2003, 13:49:11 Job time: 13.2143 secs

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Run on: June 10, 2003, 13:25:04; Search time 4.5 Seconds

(without alignments)
101.387 Million cell updates/sec

Title: US-09-909-164-7 Perfect score: 56

Sequence: 1 EEVVPXGMHYS 11

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	O8rq86 fusobacteri						_	-	099158 yarrowia li	desultovi		-			-			-		xenopu		P53782 xenopus lae		homo		_				2784	7	kv29 vibri	P15822 homo sapien
ID	CARB FUSNN	CARB STAAM	CARB STAAW	Y11K_TYDVA	UME1_YEAST	YK47_YEAST	IDI1_MESAU	GAAB_METTH	SLS1_YARLI	PHSL_DESBA	MUTL_BACSU	KPBA_CAEEL	VLTF_BPT5	TKNK_BOVIN	RR2_CHLVU	CGD2_RAT	CGD2_HUMAN	CGD2_MOUSE	CGD1_BRARE	CGD1_XENLA	CGD2_CHICK	CGD2_XENLA	CGD1_CHICK	CGD3_HUMAN	CGD1_HUMAN	CGD1_MOUSE	CGD1_RAT	HYPE_AZOVI	T2BA_BACAR	SCT1_YEAST	SULH_SCHPO	RPOC_VIBCH	ZEP1_HUMAN
Length DB	1058 1	1057 1	1057 1					308 1	426 1	513 1	627 1	1188 1	1396 1	126 1	267 1	288 1	289 .1	289 1	291 1	291 1	291 1	291 1	292 1	292 1							877 1		2717 1
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Score	000	37	37	36	36	36	35	35	34	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
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## ALIGNMENTS

CARB_FUSNN

ID CARB_FUSNN

CARB_FUSNN

STANDARD; PRT; 1058 AA.

AC GRG&G

ORG&G

I5-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

CARB OR FN0422.

GN

CARB OR FN0422.

RA NCBI_TAXID=76856;

RA MEDLINE-1886394; PubMed=11889109;

RA MEDLINE-1886394; PubMed=11889109;

RA MEDLINE-2886394; PubMed=11889109;

RA DASIGNO O., Chu L., Kogan Y., Cardag O., Goltsman E., Bernal A., Pasten N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Posten M., Kyrpides N., Overbeek R.; Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.;

Genome sequence and analysis of the oral bacterium Fusobacterium R. Tencheaum strain ATCC 25586."

RA MEDLINE-2002.

C -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O - 2 ADP +

STRAIN=Mu50 / ATCC 700699, and N315;

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                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        ö
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Manganese; Complete proteome.

DOMAIN 402 546 OLIGOMERIZATION DOMAIN.

DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARB_STARAM STANDARD: PRT; 1057 AA.
099UR5;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)
CARB OR PYRAB OR SAVI203 OR SAID46.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria: Firmitoutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0098; CPGASE.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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Pred. No. 10;
   Phosphate + L-glutamate + carbamoyl phosphate.
COFACTOR: Binds three manganese lons (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLOSTERIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 10;
3; Mismatches
                                                                                                                                                                                                                                                           EMBL; AE010554; AAL94625.1; ALT_INIT.
InterPro; IPR005483; CPase_L.
InterPro; IPR005489; CPase_L.D2.
InterPro; IPR005480; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR005481; CPase_L.N.
Fam; PF00289; CPase_L.Chain; 2.
Pfam; PF00289; CPase_L.Chain; 2.
Pfam; PF02786; CPase_L.D3; 1.
Pfam; PF02787; CPSase_L.D3; 1.
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60.0%;
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1058
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NP_BIND
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
   MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Maramurol H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
"Mhole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                -I- PATHWAY: Arginine blosynthesis.
-I- PATHWAY: Arginine blosynthesis; first step.
-I- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                               Lancet 357:1225-1240(2001).
-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O - 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.
-!- COFACTOR: Binds three manganese ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFam; PFUZI42,
PRINTS; PR00098; CPSASE.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyriandine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.

401 CARBOXPHOESHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
OLIGOMERIZATION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117171 MW; E3E179EF0591F0F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          similarity).
-!- SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005483; CPase_L.
InterPro; IPR005479; CPase_L.D2.
InterPro; IPR005480; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR00481; CPase_L.N.
InterPro; IPR00489; CPase_L.CAIIN.
Pfam; PF00289; CPSase_L.Chain; 2.
Pfam; PF02786; CPSase_L.D3; 2.
Pfam; PF02787; CPSase_L.D3; 1.
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EMBL; AP003132; BAB42298.1; -.
HSSP; P00968; 1CSO.
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190 EIVSNGLHYS 199
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302 35
284 28
298 29
300 30
820 82
832 83
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METAL
METAL
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RESULT

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NCBI_TaxID=31599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- PATHWAY: Arginine biosynthesis.
-i- PATHWAY: Pyrimidine biosynthesis; first step.
-i- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Lancet 359:1819-1827(2002).
--- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP phosphate + L-glutamate + carbamoyl phosphate.
---- COFACTOR: Binds three manganese ions (By similarity).
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Tawama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
APP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                              15-JUN-2002 (Rel. 41, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
phosphate synthetes enthe synthese large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR PYRAB OR MW1086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arginine blosynthesis; Pyrimidine blosynthesis; Ligase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 1; Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D8E3B09F9BC6F152 CRC64;
                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALLOSTERIC DOMAIN.
                     PRT; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 16;
                                                                                                                                                                                     Staphylococcus aureus (strain MW2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP004825; BAB94951.1; -.
                                                             15-JUN-2002 (Rel. 41, Created)
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                         STANDARD;
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1057
546
1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Manganese.
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300
820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                         NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                                                                                                           acquired MRSA.
                       CARB_STAAW
P58940:
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NP_BIND
METAL
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        CARB_STAAW
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102 AA.

PRT;

STANDARD;

Y11K_TYDVA P31619;

A D

Y11K_TYDVA

g δ

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STRAIN=S288C / AB972;
STRAIN=9731371; PubMed=9169875;
Bussey H., Storms K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis R.W., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., Dietrich F.S., Delius H., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebhing U., Heumann K., Hibbert H., Hillier I., Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                       Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; "The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungl: Ascomycota: Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.3%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 2.3; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein.
102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                    Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMEI_YEAST STANDARD; PRT; 460 AA. 003010; P87330; 01-NOV-1997 (Rel. 35, Created) 11-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meiosis negative regulator UME1.
UME1 OR WTM3 OR YPL139C OR LPI7C.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92188538; PubMed=1546458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A42452, A42452. InterPro; IPROJ05621; Gemini_mov. Pfam; PF01708; Gemini_mov; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 OVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petel F.Y., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Schramm S., Schramm S., Schramm S., Schramm S., Schram S., Sturoder M., Sdicu A.M., Tettelin H., Urestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                     -1- FUNCTION: TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION AND SILENCING. NEGATIVE REGULATOR OF MEIOSIS.
-1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
-1- SIMILARITY: STRONG, TO YEAST WIM1 AND WTW2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kba protein in CCPI-MET1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.3%; Score 36; DB 1; Length 460; 62.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pram; PF00400; WD40; 3.
SNART; SM00320; WD40; 3.
PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
PROSITE; PS500294; WD_REPEATS_2; FALSE_NEG.
PROSITE; PS50294; WD_REPEATS_REGION; FALSE_NEG.
Transcription regulation; Malosis; Repeat; WD_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 743 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WD 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 AA; 51022 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U10280; AAB40937.1; -.
EMBL; U43703; AAB68221.1; -.
TRANSFAC; T04309; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD; S0006060; UME1.
InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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316
379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YK47_YEAST
P36148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isopentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase 1) (Isopentenyl pyrophosphate isomerase 1) (IPP11).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
-1- PATHWAY: ISOPRENOID BIOSYNTHETIC PATHWAY WHOSE END PRODUCTS
INCLUDE DOLICHOLS, VITAMINS A, D, E, AND K, STEROID HORMONES,
CAROTEROIDS BLLE ACIDS AND CHOLESTEROI.
-1- SUBCELLULAR LOCATION: PERCAXISOMAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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InterPro; IPR002667; IPP_isomerase.
InterPro; IPR000086; NUDIX_hydrolase.
Pfam; PF00293; NUDIX; 1.
ProDom; PD004109; IPP_isomerase; 1.
Isomerase; Isoprene biosynthesis; Cholesterol biosynthesis; Sterol biosynthesis; Peroxisome; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 743;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                       POTENTIAL.
84B9946E56B82F15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 18;
1; Mismatches
                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Golden hamster).
                                                                                                                              SGD; S0001775; YKR067W.
InterPro; IPR002123; Acyltransferase.
                                                                                                                                                                                             Hypothetical protein; Transmembrane.
TRANSMEM 31 55 POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                    $1 55 PO
69 85 PO
50 54 PO
539 555 PO
743 AA; 83644 MW;
                                                                                                                                                                                                                                                                                                                                                                                     64.3%;
75.0%;
                                                                                EMBL; Z28292; CAA82146.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 VVPCGLHY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMHY 10
                                                                                                             S38143; S38143
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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035586;
                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                              SEQUENCE
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J. Bacteriol. 179:7135-7155(1997).
I-CATRIVITY ATP + xanthosine 5'-phosphate + L-glutamine + H(2)0 = AMP + diphosphate + GMP + L-glutamate.
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-i-SIMILARITY: BELONGS TO THE GMP SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
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Pfam; PF00958; GMP_synt_C; 1.
IIGRRAMs; TIGR00084; QuaA_Cterm; 1.
Ligase; GMP blosypthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 1; Length 308;
                                                                                                                                                   Score 35; DB 1; Length 227; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMP-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
MICROBODY TARGETING SIGNAL.
                                                                                                                                                                                                                           3; Indels
86 86 BY SIMILARITY.
148 148 BY SIMILARITY.
225 227 MICROBODY TARGETING SIGNAL
227 AA; 26317 MW; F500A6586385E803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TP (BY SIMILARITY).
F2DCF6ED202CAEC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000850; AAB85215.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 AA; 34403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.5%;
63.6%;
                                                                                                                                                          62.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                  121 EEVDPNEMHY 130
                                                                                                                                                                                                                                                                                       1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P04079; 1GPM.
                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUAAB OR MTH710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAB_METTH
026806;
   ACT_SITE
ACT_SITE
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                           SEQUENCE
                                                                                                                                                             Query Match
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                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAB_METTH
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                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HERE AND DESCRIPTION OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (EC 1.18.99.1) (NiFeSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                            INTERACT DIRECTLY WITH TRANSLOCATING POLYPEPTIDES TO FACILITATE THEIR TRANSFER AND/OF HELP THEIR FOLDING IN THE ER. IT IS NOT REQUIRED FOR VIABILITY BUT IS ESSENTIAL FOR OPTIMAL GROWTH AT ELEVATED TEMPERATURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PREVENT SECRETION FROM ER (POTENTIAL). 0ACD7EF17540B8E2 CRC64;
                                                                                                                                                                                           Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydrogenlyase large chain).
Desulfovibrio baculatus (Desulfomicrobium baculatus).
Bacteria; Proteobacteria; delta subdivision; Desulfomicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1; Length 426;
Pred. No. 26;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLS1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88058744; PubMed=3316183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000886; ER_target.
PROSITE; PS00014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endoplasmic reticulum; Signal.
SIGNAL 1 17 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 AA; 47201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z50154; CAA90516.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
              STANDARD;
                                                                                        SLS1 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOVIPAGEH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHSL_DESBA
            SLS1_YARLI
Q99158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P13065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
SLS1_YARLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Periplasmic.
-i- MISCELLANEOUS: PERHAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS A TRANSPORT VEHICLE FOR BOTH SUBUNITS.
-i- SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE
                                                                                                                                                                                                           "The crystal structure of a reduced [NiFeSe] hydrogenase provides an image of the activated catalytic center.", Structure 7:557-566(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Menon N.K., Peck H.D. Jr., le Gall J., Przybyla A.E.; "Cloning and sequencing of the genes encoding the large and small subunits of the periplasmic (NiFeSe) hydrogenase of Desulfovibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1CC1; 01-JUN-99.
InterPro; 1PR001501; Ni_hdL.
Pfam; PF00374; NiFSS_HASE; 1.
PROSTTE; PS00507; NI_HGENASE_L_1; 1.
PROSTTE; PS00508; NI_HGENASE_L_2; 1.
Oxidortase; Periplasmic; Nickel; Selenium; Selenocysteine; 3D-structure.

O 0 0 0 1NIT_MET 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                               Garcin E., Vernede X., Hatchikian E.C., Volbeda A., Frey M.,
Fontecilla-Camps J.C.;
                                                                                                                                                                                                                                                                                   -1- COFACTOR: ONE NICKEL ION, TWO 4FE-4S CLUSTERS AND ONE SELENCYSTEINE.
-1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 513; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56683 MW; AC8285A6F80576FC CRC64;
                                                                                                    Menon N.K., Pect H.D. Jr., le Gall J., Przybyla A.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON 1 AND NICKEL.
IRON 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRON 1 AND NICKEL. IRON 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NICKEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NICKEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                  MEDLINE-99306038; PubMed-10378275;
                                                        Bacteriol. 169:5401-5407(1987)
                                                                                                                     J. Bacteriol. 170:4429-4429(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence 15-JUN-2002 (Rel. 41, Last annota: DNA mismatch repair protein mutl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M18271; AAA23375.2; -. PIR; A33101; HQDVLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ferredoxin + H(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 PGGLHYS 303
                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTL_BACSU
P49850;
                                             baculatus
                                                                                       REVISIONS
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SEQUENCE
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METAL
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METAL
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ARAIN-LOG STAIN-LOW WOSZET I., Albertini A.M., Alloni G., KIATIN-LOG STAIN-LOW WOSZET I., Albertini A.M., Alloni G., KATAIN-LOW W., Bortster M.G., Bessieres P., Bolotin A., Borchert S., Runst F., Ogdsawara N., Borsham M., Brignell S.C., Bron S., Berriss R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., R. Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Codni J. J., Connerton I.F., Cammings N.J., Daniel R.A., Bentian K.D., Erington J., Fabret C., Ferrari E., Foulger D., Funier M., Fulita Y., Funier S., Galizzi A., Gallaron P.T., R. Fritz C., Fulita W., Fulita Y., Funier S., Galizzi A., Gallaron N., R. Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., R. A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., R. A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Mosayashi Y., Gotter P., Koningstein G., Krogh S., Kumano M., Mellado R.P., Liu H., Masuda S., Mauel C., Medigue C., R. Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Park S.H., R. Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Raeger M., Ravollik S., Prescort A.M., Packerli M., Portetelle D., Porwollik S., Prescort A.M., Tacconi E., Pujic P., Purnelle B., Rapoport G., Shi B.S., Solfone F., Sonlei M., Yanane K., Scorfone F., Vasanotti A., Tanaka T., Tarkahashi H., Tarkemaru K., Takeuchi M., Tarkemaru K., Tarken H., Wanters P., Wanbutt R., Wandler E., Wadler E., Wedler E., Wedler E., Wedler E., Waller E., Washerchi M., Vannier F., Vasasarotti A., Varannoto H., Yamane K., Yasamoto R., Yasamoto H., Yamane C., Itach C., Rey K., Yata K., Tarch Complete genome sequence of the Gram-positive bacterium Bacillus R., Suhtini S., Shi H., Farker F., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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-!- FUNCTION: THIS PROTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN LEVICTION: THIS PROTEIN IS INVOLVED IN THE PROTEIN THAT REPAIR. MAY ACT AS A "MOLECULAR MATCHAMKER", A PROTEIN THAT PROMOTES THE FORMATION OF A STABLE COMPLEX BETWEEN TWO OR MORE DINA-BINDING PROTEINS IN AN ATP-DEPENDENT MANNER WITHOUT ITSELF BEING PART OF A FINAL EFFECTOR COMPLEX (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                         Ginetti F., Perego M., Albertini A.M., Galizzi A.,
"Bacillus subtilis mutS mutL operon: identification, nucleotide
                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Subtilist; BG11402; mutL.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR002099; DNA_mis_repair.
                                                                                                                                                                                 MEDLINE=96349107; PubMed=8760914;
                                                                                                                                                                                                                                                              sequence and mutagenesis.";
Microbiology 142:2021-2029(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004359; HIS_KIN_sig.
Pfam; PF001119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_c; 1.
TIGRFAMS; TGR00588; mutl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U27343; AAB19236.1; -. EMBL; Z99112; CAB13578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P23367; 1BKN.
  MUTL.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                SEQUENCE FROM N.A.
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Late protein.
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                                                                                                                                                                                                                                                                                   Kryukov V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKNK_BOVIN
P08858;
                                                                                           VLTF_BPT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKNK_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                               VLTF_BPT5
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                                                                                                                                                                                                                                                                                                                                                            MEDINE-94150718; PubMed-7906398;
MEDINE-94150718; PubMed-7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Karsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable phosphorylase B kinase alpha regulatory chain (Phosphorylase
kinase alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                      Gaps
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Hypothetical protein; Glycogen metabolism; Calmodulin-binding.
SEQUENCE 1188 AA; 135558 WW; DE9BB875F3603863 CRC64;
                                                                      ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.9%; Score 33; DB 1; Length 1188; 54.5%; Pred. No. 1.2e+02;
                                                58.9%; Score 33; DB 1; Length 627;
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                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA repair; Complete proteome.
SEQUENCE 627 AA; 70431 MW; 068A0509CC265343 CRC64;
                                                                                                                                                                                    PRT; 1188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
                                                          61;
                                                                       1; Mismatches
                                                             Pred. No.
                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L15188; AAA27954.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 54.5%;
6; Conservative
                                                             54.5%;
                                                             Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                      STANDARD;
                                                                                                                | :|| |||
488 EMIVPLTFHYS 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S44754; S44754
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wohldman P.;
                                                                                                                                                                                        KPBA_CAEEL
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                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-!- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Kaliman A.V., Kryukov V.M., Bayev A.A.;
"The nucleotide sequence of bacteriophage T5 DNA at the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The nucleotide sequence of the bacteriophage T5 ltf gene."; FEBS Lett. 366:46-48(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                986 986 V -> A (IN REF. 2).
1396 AA, 147989 MW; 18CD2192F65FFFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; I
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
                                                                                                                                                                                                                           P13390; 048502;
01-7AN-1990 (Rel. 13, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
00-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                  PRT; 1396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.46
2; Mismatches
                                                                                                                                                                                                                                                                                                                                              L-shaped tail fiber protein (LTF protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=95309401; PubMed=7789514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ001191; CAA04591.1; -. PIR; S01982; S01982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X69460; CAA49220.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 50.0
nes 5; Conservative
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950 EEYAEDGIHYS 960
                                                                                                                                                                                                     STANDARD;
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1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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RESULT 16
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                                                                       Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
NCBI_TaxID=3077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 126
95 95 AMIDATION (G-96 PROVIDE AMIDE GROUP).
126 AA; 13871 MW; 446EF433498EC059 CRC64;
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0
                                                                                                                                                                                                                                                                                                                                                                                                 Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%; Score 32; DB 1; Length 126; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                            -! SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRZ_CHLVU STANDARD; PRT; 267 AA. P56351; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) chloroplast 30S ribosomal protein S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUROKININ B.
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                   SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                    EMBL; M14351; AAA30723.1; -.
EMBL; M14347; AAA30723.1; JOINED.
EMBL; M14348; AAA30723.1; JOINED.
                                                                                                                                                                                                                                                                                                                     EMBL; M14350; AAA30723.1; JOINED.
EMBL; M14350; AAA30723.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=1AM C-27 / Tamiya;
MEDLINE=97303241; PubMed=9159184;
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003635; Neurokinin.
InterPro; IPR002040; Tachykinin.
Probom; PD020370; Neurokinin; I
PROSITE; PS00267; TACHYKININ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                 idae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 EQVVPGGGH 36
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                                                                                                                                                                                                                                                                                                                                          PIR; A25905; A25905.
                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlorella vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                           Amidation;
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SEQUENCE
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Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T., Inamura A., Yoshinaga K., Sugiura M.; "Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: the existence of genes possibly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa, Chórdata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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(START) TRANSITION.

-!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.

-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93275661; PubMed-8502486;
Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
Francke U., Jolicoeur P.;
"The Vin-1 gene, identified by provirus insertional mutagenesis, is
                                                                           involved in childroplast division.";
Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocore 32; DB 1; Length 267;
Pred. No. 40;
4; Mismatches 2; Tran.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7903075340BD900F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G1/S-specific cyclin D2 (Vin-1 proto-oncogene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jocur-1993 (Rel. 27, Created)
01-CCT-1993 (Rel. 27, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                    EMBL, AB001684; BAA57862.1; -.
InterPro; IPR001865; Ribosomal_S2.
Pfam; PR00318; Ribosomal_S2; 1.
PRINTS; PR00395; RIBOSOMALS2.
PROSITE; PS00962; RIBOSOMAL_S2_1; FALSE_NEG.
PROSITE; PS00963; RIBOSOMAL_S2_1; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribosomal protein; Chloroplast.
SEQUENCE 267 AA; 30699 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 EDMIQSGMHF 17
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Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q04827;
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                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                        PROSTIE: PS00292: CYCLINS; 1.

Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene.

CONFLICT 68 68 E -> G (IN REF. 2).

CONFLICT 104 104 C -> V (IN REF. 2).

SEQUENCE 232 232 T -> A (IN REF. 2).

SEQUENCE 288 AA; 32826 MW; 4B522BF4E9835FC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.; "Cyclins D1 and D2 are differentially expressed in human B-lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xiong Y., Menninger J., Beach D., Ward D.C.; *Molecular cloning and chromosomal mapping of CCND genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic organization, chromosomal localization, and independent expression of human cyclin D genes."; Genomics 13:565-574(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                      57.1%; Score 32; DB 1; Length 288; 60.0%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGD2_HUMAN STANDARD; PRT; 289 AA. P30279; Q13955; Q1-APR-1993 (Rel. 25, Created) LARR-1993 (Rel. 25, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                 EMBL; L09752; AAA41010.1; -.
EMBL; D16308; BAA03815.1; -.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92347850; PubMed=1386335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-92347851; Pubmed-1386336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93205384; PubMed=8455931;
                                                                                                                                               Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SMO0385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 8:1049-1054(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-240 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 13:575-584(1992).
                                                                                                                                                                                                                                                                                                                            Local Similarity 60.0 hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G1/S-specific cyclin D2.
                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                          73 EEVFPLAMNY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human D-type cyclins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miyajima
                                                                                                                                                                                                                                                                                                               Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCND2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGD2_HUMAN
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 17
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-i - FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsushime H., Roussell M.F., Ashmun R.A., Sherr C.J.; "Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the cell cycle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of a D-type cyclin from murine erythroleukemia cells.";
Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kiyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyclin; Cell cycle; Cell division; Multigene family. CONFLICT 166 167 KL -> NV (IN REF. 5). CONFLICT 224 224 T -> H (IN REF. 5). SEQUENCE 289 AA; 33067 MW; E4E5FEF476D76D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=91235305; Pubmed=1827757;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=92196134; Pubmed=1372445;
                                                                                                                                                                                                                                                                                                   EMBL; M88083; AAA51928.1; -.
EMBL; M88080; AAA51928.1; JOINED.
EMBL; M88081; AAA51928.1; JOINED.
EMBL; M88082; AAA51928.1; JOINED.
                                                                                                                                                                                                                                      EMBL; M90813; AAA51926.1; -.
EMBL; X68422; CAA48493.1; -.
EMBL; D13639; BAA02802.1; -.
EMBL; BC010958; AAH10958.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00292; CYCLINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00134; cyclin; 1. Pfam; PF02984; cyclin_C; 1. SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 60.0 es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G1/S-specific cyclin D2. CCND2 OR CYL-2.
                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:1583; CCND2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                   PIR; A42822; A42822.
PIR; S26580; S26580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 123833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marks P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGD2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGD2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Cell 65:701-713(1991).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                             -1- SUBUNT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1264:257-260(1995).
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
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-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygil; Neopterygil; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%; Score 32; DB 1; Length 289; 60.0%; Pred. No. 44; 3; Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00114; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PR00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 289 AA; 32897 MW; 58F322771DD1DA3D CRC64;
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15-JUL-1998 (Rel. 36, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
G1/S-specific cyclin D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 AA.
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PIR; A41984; A41984.
MGD; MGI: 88314; CCnd2.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin.
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Matches 6; Conservative
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73 EEVFPLAMNY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (START) TRANSITION.
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Q90459;
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    SO STANDAR DE PRESENTANTE DE PRESENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cockerill M.J., Hunt T., Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (START). TRANSITION.
-!- SUBDUTT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLDENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                    Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%; Score 32; DB 1; Length 291; 60.0%; Pred. No. 44; 1.1ve 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                   3; Indels
                                                                                         Pfam; PF00134; CYClin; 1.
Pfam; PF02984; CYClin; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
CYClin; Cell CYCle; Cell division.
SEQUENCE 291 AA; 33067 MW; FA5274CB1B46D5EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;
                                                                                                                                                                                                               57.1%; Score 32; DB 1;
60.0%; Pred. No. 44;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
G1/S-specific cyclin D1.
                                                                                                                                                                                                                                                                                                                                                                                                 291 AA.
or send an email to license@isb-sib.ch).
                         EMBL; X87581; CAA60885.1; -
ZFIN; ZDB-GENE-980526-176; cycdl.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004366; Cyclin,
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00134; cyclin, 1
Pfam; PF02984; cyclin, 1
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1
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                                                                                                                                                                                            Ouery Match
Best Local Similarity 60.00
The conservative
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                             , 1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                              75 EEVFPLAMNY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMHY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              CGD1_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li H., Grenet J., Kidd V.J.;
"Structure and gene expression of avian cyclin D2.";
Gene 167:341-342(1995).
-- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINEY-THEODYNINE KINASE BOLOGENSTUR COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004366; Cyclin.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
Pfam; PF00134; cyclin_C; 1.
SWART; SM00385; CYCLIN; 1.
SWART; SM00385; CYCLIN; 1.
Cyclin; Cell cycle, Cell division; Multigene family.
SEQUENCE 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;
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01-0cT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
GL/S-specific cyclin D2.
                                                                        ul-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CCND2.
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                                                           291 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 44;
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                                                              PRT;
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                                                           STANDARD;
                                                                                                                                                                                                                                                                                   Gallus qallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (START) TRANSITION
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                           CGD2_CHICK
P49706;
                                                                                                                                                                                                                                                                                                                                                                                      Gallus
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CGD2_XENLA
                                 CGD2_CHICK
RESULT 21
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                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li H., Lahti J.M., Kidd V.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CEK4 AND CDK6 PROTEIN
(START) TRANSITION. INTERACTS WITH THE CDK4 AND CDK6 PROTEIN
KINASES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                       -:- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-:- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                         DALL. CELL 00:37-111(1330).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
[2]
SEQUENCE FROM N.A.
MEDLINE-97380591; PubMed-9237366;
Taleb F., Jessus C.;
"Xenopus cyclin D2: cloning and expression in oocytes and during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; Length 291;
Pred. No. 44;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
CYCLIN; Cell Cyclic, Cell division; Multigene family.
SEQUENCE 291 AA; 32959 MW; 9A290F04F1531E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X83503; CAA58493.1; -.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
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60.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
                                                                                                  early_development.";
Biol. Cell 88:99-111(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G1/S-specific cyclin D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                               (START) TRANSITION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X83503;
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ID CGD1_CHICK
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-1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Medazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xiong Y., Menninger J., Beach D., Ward D.C., Molecular cloning and chromosomal mapping of CCND genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Motokura T., Keyomarsi K., Kronenberg H.M., Arnold A., "Cloning and characterization of human cyclin D3, a cDNA closely related in sequence to the PRADI/cyclin D1 proto-oncogene.", J. Biol. Chem. 267:20412-20415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
                                                                                                                                                                                     ö
                                                                                                                                                   DB 1; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                         Pfam; PF00134; cyclin; 1.

Pfam; PF02984; cyclin_C; 1.

SMART; SM00385; CYCLIN; 1.

PROSITE; PS00292; CYCLINS; 1.

Cyclin; Cell cycle; Cell division; Multigene family.

SEQUENCE 292 AA; 33263 MW; 7B543029DB45A67D CRC64;
                                                                                                                                                                                                                                                                                                                      292 AA.
                                                                                                                                                                                1; Mismatches
                                                                                                                                                   Score 32;
Pred. No.
EMBL; U40844; AAA83271.1; -.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92347851; PubMed=1386336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93015922; PubMed-1383201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=92347850; PubMed=1386335;
                                                                                                                                                  57.18;
60.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human D-type cyclins.";
Genomics 13:575-584(1992).
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                         1 EEVVPXGMHY 10
                                                                                                                                                                                                                                     75 EEVFPLAMNY 84
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
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MEDLINE-92005671; PubMed-1833066;
Lew D.J., Dulic V., Reed S.I.;
"Isolation of three novel human cyclins by rescue of G1 cyclin (Cln)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-92017758; PubMed=1833629;
Withers D.A., Harvey R.C., Faust J.B., Melnyk O., Carey K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
61/S-specific cyclin D1 (FRAD1 oncogene) (BCL-1 oncogene).
CCND1 OR PRAD1 OR BCL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%; Score 32; DB 1; Length 292; 60.0%; Pred. No. 44;
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16E7B1604FEB0029 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclin; Cell cycle; Cell division; Multigene family. CONFLICT 259 259 S -> A (TN REF 1)
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"Characterization of a candidate bcl-1 gene.";
Mol. Cell. Biol. 11:4846-4853(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 44;
1; Mismatches
or send an email to license@isb-sib.ch).
                                                 EMBL; M90814; AAA51927.1; -.
EMBL; M92287; AAA5137.1; -.
EMBL; BC011616; AAH11616.1; -.
EMBL; M88087; AAA51929.1; -.
EMBL; M88084; AAA51929.1; JOINED.
EMBL; M88085; AAA51929.1; JOINED.
EMBL; M88086; AAA51929.1; JOINED.
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InterPro; IPR004367; Cyclin_Cterm.
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292 AA; 32519 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin, 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
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Best Local Similarity 60...
6; Conservative
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PIR; A44022; A44022.
Genew; HGNC:1585; CCND3.
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Cell 66:1197-1206(1991).
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P24385;
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  ACCOORDING TO THE SECTION OF THE SEC
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(START) TRANSITION.

-1. SUBUNIT: INVERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOGNEYARE COMPLEX.

-1. DISEASE: INVOLVED IN B-LYMPHOCYTIC MALIGNANCY (PARTICULARLY MANTLE-CELL LYMPHORA (POLL) BY A CHROMOSOMAL TRANSLOCATION T(11:4) (013:032) THAT INVOLVES CCND1 AND IMMUNOGLOBULIN GENE REGIONS (BCL1 ONCOGENE). ACTIVATION OF CCND1 MAY BE ONCOGENIC BY CHROMOSOMAL TRANSLOCATION T(11:11) (013:032) THAT INVOLVES CCND1 AND IMMUNOGLOBULIN GENE REGIONS (BCL1 ONCOGENE). ACTIVATION OF CCND1 MAY BE ONCOGENIC BY CHROMOSOMAL TRANSLOCATION T(11:11) (013:1915) THAT INVOLVES CCND1 CHROMOSOMAL TRANSLOCATION T(11:11) (013:1915) THAT INVOLVES CCND1 AND THE PARATHYROID HORWOON (PTH) ENHANCER (PRADI ONCOGENE).

-1. DIREARLY SELONGS TO THE CYCLIN PAMILY. CYCLIN D SUBPAMILY.

-1. SIMILARITY: BELONGS TO THE CYCLIN PAMILY. CYCLIN D SUBPAMILY.

-1. DATABASE: NAME-ALIAS Genet. CYCLIN PAMILY. CYCLIN D SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content, is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
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                       MEDLINE-94264323; PubMed-8204893; Rimokh R., Berger F., Bastard C., Klein B., French M., Archimbaud E., Rouault J.-P., Santa Lucia B., Duret L., Vuillaume M.; Renault GCND1 (BCL1/PRAD1) 3' untranslated region in mantle-cell lymphomas and t(11q13) -associated leukemias."; Blood 83:3689-3696(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CDK6 (PLSTIRE) and CDK4 (PSK-J3) are a distinct subset of the cyclin-dependent kinases that associate with cyclin D1."; Oncogene 9:71-79(1994).
-:- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL.CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fram; FFC0134; CYCLID; 1.

PMAN; PFC02036; CYCLIN, 1.

PROSITE; PS00292; CYCLINS; 1.

CYClin; Cell Cycle; Cell division; Multigene family; Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH CDK4 AND CDK6.
MEDLINE-94134440; Pubmed-8302605;
Bates S., Bonetta L., McAllan D., Parry D., Holder A., Dickson C.,
                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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MP -> IA (IN REF. 2).
L -> S (IN REF. 3).
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EMBL; M64349; AAA52136.1; -
EMBL; M73554; AAA88392.1; -
EMBL; Z33022; CAA80558.1; -
EMBL; BC000076; AAH00076.1; -:
EMBL; BC001501; AAH01501.1; -:
EMBL; BC014078; AAH14078.1; -
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InterPro; IPR004367; Cyclin_Cterm.
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Genew; HGNC:1582; CCND1.
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Pfam; PF02984; cyclin_C
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A40034; A40034
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295 AA;
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MIM; 168461; -
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Gencore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:30:25; Search time 25.7857 Seconds

(without alignments)

87.898 Million cell updates/sec

Title: US-09-909-164-7

Sequence: 1 EEVVPXGMHYS 11

Scoring table: BLOSUMGS 11

Scoring table: BLOSUMGS 11

Scoring table: BLOSUMGS 6495, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Manimum DB seq length: 00

Maximum Antch 08

Maximum Match 1008

Listing first 75 summaries
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1: sp_archea:*
2: sp_bacteria:*
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4: sp_lunman:*
5: sp_lunvertebrate:*
6: sp_mammal:*
7: sp_nhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_vertebrate:*
16: sp_bacteriap:*
17: sp_archeap:*

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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

LEG		Description	O8rq86 fusobacteri	09x2e2 thermotoga	Q9hlh8 thermoplasm	099ur5 staphylococ	Q46486 corynebacte	Q8ywp1 anabaena sp	Q9avk4 pisum sativ	057489 bacteroides	Q9pc35 xylella fas	Q40479 nicotiana t	Q91w50 nicotiana s	Q38317 lactobacill	Q9xvk4 caenorhabdi	Q9sa71 arabidopsis	Q8tz07 methanopyru	O27902 methanobact
SUMMARIES		Π	Q8RG86	Q9X2E2	оэнгн8	<b>0990R5</b>	046486	Q8YWP1	Q9AVK4	057489	Q9PC35	040479	O9LW50	038317	Q9XVK4	Q9SA71	Q8TZ07	027902
		DB	16	16	17	16	7	16	10	7	16	10	10	σ	2	10	17	17
		Query Match Length DB	1063	308	322	1057	208	252	819	139	156	233	237	317	425	510	2042	264
	фP	Query Match	67.9	66.1	66.1	66.1	64.3	64.3	64.3	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	60.7
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ALIGNMENTS

	PRT; 1063 AA.		Created)	Last sequence update)	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).	
	PRELIMINARY;		01-JUN-2002 (TrEMBLrel. 21, Created)	(TrEMBLrel. 21, I	(TrEMBLrel, 21, 1	osphate synthase	1
RESULT 1 Q8RG86	Q8RG86	Q8RG86;	01-JUN-2002	01-JUN-2002 (TrEMBLrel.	01-JUN-2002	Carbamoyl-ph	FN0422.
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SEQUENCE FROM N.A.

STAIN-MSBB / DSW 3109;

Na MEDLINE-99287316; PubMed-10360571;

Na Holson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Na Hoft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

NR INGK: TMB22;

TER: TMB22;
                                                                                                                                               APPLINE-21886394; PubMed-11889109; MEDLINE-21886394; PubMed-11889109; Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Greckin J., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Fonstein M., Kyrpides N., Overbeek R.; Fonstein M., Kyrpides N., Overbeek R.; Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25868."; J. Bacteriol. 184:2005-2018(2002).
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SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FTSH protease activity modulator HFLK.
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Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
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SMART; SM00244; PHB; 1.
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                                                                                                                           SEQUENCE FROM N.A.
                                                                 NCBI_TaxID=76856;
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SPECIES=S. aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani M., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Staphlococcus
                                                                                                                                                                                                                                                                                    Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 17; Length 322;
Pred. No. 22;
                                                                                                                                                          Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      322 AA; 36918 MW; B8C239E71009D167 CRC64;
                                                                                 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                 Glucose-fructose oxidoreductase related protein.
TA0250.
                                 322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carbamoyl-phosphate synthase large chain. PYRAB OR SAV1203 OR SA1046.
                                                                  (TrEMBLrel. 16, Created)
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01-JUN-2001 (TrEMBLrel. 17, Last seq
                                 PRT;
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InterPro; IPR004362; MGS_like.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00208; CPSase_L_chain; 2.
                                                                                                                                                                                                                                                                                                                                                 Nature 407:508-513(2000).

EMBL; AL445063; CAC11395.1; -.

InterPro; IPR000683; GFO_IDH_MocA.

Pfam; PF01408; GFO_IDH_MocA.
                                                                                                                                                                                                                                                     STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
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EMBL; AP003361; BAB57365.1; -.
EMBL; AP003132; BAB42298.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.1%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.09
                                                                                                                                                   Thermoplasma acidophilum.
                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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66 VVPDGLHY 73
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 322 AA;
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                                                                01-MAR-2001
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SCARECROW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PERCIES-C.xerosis; STRAIN-M82B;
MEDLINE-96117603; PubMed-8559800;
Tauch A., Kassing F., Kalinowski J., Puhler A.;
The Corynebacterium xerosis composite transposon Tn5432 consists of
Two identical insertion sequences, designated IS1249, flanking the
erythromycin resistance gene ermCX.";
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                                                                                                                      66.1%; Score 37; DB 16; Length 1057; 60.0%; Pred. No. 77;
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                                                                                             1057 AA; 117171 MW; E3E179EF0591F0F8 CRC64;
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208 Aa; 23012 MW; F1504BE1ECDE85A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) Hypothetical 23.0 kDa protein (GcrA).
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
                                  PRINTS; PRO0098; CPSASE.
PROSITE; PS00866; CPSASE.1; 2.
PROSITE; PS00867; CPSASE.2; UNKNOWN.2.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN.1.
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                                                                                                                                   Pred. No. 77;
2; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
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: U21300; AAC95478.1; -.
; AF024666; AAG03390.1; -.
Pfam; PF02786; CPSase_L_D2; 2. Pfam; PF02787; CPSase_L_D3; 1. Pfam; PF02142; MGS; 1.
                                                                                                                                                                                                                                                                                                                                               Corynebacterium xerosis, and
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                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            Corynebacterium striatum
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130 DVIPEGKHYA 139
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190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium.
NCBI_TaxID=1725, 43770;
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Matches 5; Conserv
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                                                                                                                                   Local Similarity
                                                                                    Complete proteome. SEQUENCE 1057 AA
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Q8YWP1
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Q46486
ID Q464
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STRAIN=CV. ALASKA;
MEDLINE=21231727; PubMed=11333309;
Sassa N., Matsushita Y., Nakamura T., Nyunoya'H.;
The Molecular Characterization and in situ Expression Pattern of Pea
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                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.",
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                                                                              Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostoc.
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                                                                                                                                                                                                                                                                                                                                                                                                                  DNA RES. 8:205-213(2001).
EMBL; AP003386; BAB77929-1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 252 AA; 28831 MW; 925572DA5DICA519 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Alr1563.
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SEQUENCE 819 AA; 90372 MW; 41B67BD6DC72A
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45.5%; Pred. No. 94;
iive 4; Mismatches
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EMBL, ABO48713; BAB39155.1; -.
InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR005202; GRAS.
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                                                                                                                                                                                                             MEDLINE-21595285; PubMed=11759840;
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Best Local Similarity
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                                                                                                              Bacteria; Cyanobac
NCBI_TaxID=103690;
                                                                                                                                                                                          SEQUENCE FROM N.A.
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Ouery Match
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                                                                                                                                                            "A multiple site-specific DNA-inversion model for the control of Ompl phase and antigenic variation in Dichelobacter nodosus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                        SEQUENCE FROM N.A.
MEDLINE-96020672; PubMed-7476204;
Moses E.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
                                                                                                                                                                                                                           MEDLINE-96257263; PubMed-8654969;
Billington S.J. Sinistaj M., Cheetham B.F., Ayres A., Moses E.K.,
Katz M.E., Rood J.I.;
"Identification of a native Dichelobacter nodosus plasmid and
implications for the evolution of the vap regions.";
EMBL: U02462; AABL2366.1;
InterPro. PREMO1537; BRCT.
InterPro. PREMO1537; BRCT.
SWART; SM00292; BRCT; I.
PROSITE; PS50172; BRCT; I.
                                        Bacteroides nodosus (Dichelobacter nodosus).
Bateria: Proteobacteria: gamma subdivision; Cardiobacteriaceae;
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139 AA; 15052 MW; E0E110AA4B7D4708 CRC64;
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09PC35;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein xf1950.
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                             ONA ligase (Fragment).
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21 IVPAGVHWS 29
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                                                                                NCBI_TaxID-870;
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                                                                    Dichelobacter
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SEQUENCE
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Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Mania A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira K.C., Palmieri D.A., Paris A.,
Petxoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A da Silva A.C.R., da Silva A.M., da Silva R.M., Jr., da Silva A.M., da Silva R.M., Jr. Stoueira W.J., de Souza A.D.,
A da Silva A.C.R., da Silva M.M., Verloriera W.J., de Souza A.A.,
A da Silva A.C.R., verloriera W.J., de Souza A.A.,
A Vallada H., Van Sluys M.A., Verloriera J.C.;
A Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
The genome sequence of the plant pathogen Xylella fastidiosa.";
Interpro; IRRO2545; Chew.
SMART; SM00260; Chew.
SMART; SM00260; Chew.
Hypothetical protein; Complete proteome.
SEQUENCE 156 As; 17144 WW; D8358619C6671A5D CRC64;
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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"Ethylene-inducible DNA binding proteins that interact with an ethylene responsive element.";
Plant Cell 7:173-182(1995).
EMBL; D38126; BAA07324.1; --
HSSP; 080337; 2GCC.
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CE 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Created)
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STRAIN-BY4; TISSUE-LEAF;
MEDLINE-95276459; PubMed-7756828;
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ProDom; PD001423; TF_AP2; 1.
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Best Local Similarity 60.00,
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Matches 5; Conservative
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62.5%;
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Matches 6; Conservative
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nes 5; Conservative
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                                                                                                                                              Kitajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
"Characterization of gene expression of NSERFs, transcription factors of basic PR genes from Nicotiana sylvestris.";
Plant Cell Physiol. 41.817-824(2000).
EMBL; AB016264; BAA97122.1;
HSSP; 080337; 2GCC.
Interpro; IPR001471; TE_ERF.
Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
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MEDLINE-33231538; PubMed-8472961;
Fremaux C., De Antoni G., Raya R., Klaenhammer T.;
"Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99384014; PubMed=10452953;
Altermann E., Klein J., Henrich B.;
"Primary structure and features of the genome of the Lactobacillus gasseri temperate bacteriophage phi-adh.";
Gene 236:333-346(1999).
                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids 1; Solanales; Solanaceae; Nicotiana.
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Henrich B., Binishofer B., Blaesi U.;
Primary structure and functional analysis of the lysis genes of
Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
                                                                                                                                                                                                                                                                                                                                       ;
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Pred. No. 41;
1; Mismatches 3; Indels
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   237 AA; 26243 MW; 01BC3EEB51E46298 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Ethylene-responsive element binding factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AA
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                                                   Nicotiana sylvestris (Wood tobacco)
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MEDLINE-20399450; PubMed-10945353;
                                                                                                                                                                                                                                                                                                            62.5%;
60.0%;
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Engel G., Altermann E., Klein J., Henrich B.;
Engel G., Altermann E., Klein J., Henrich B.;
Structure of a genome region of the Lactobacillus gasseri temperate phage phi adh covering a repressor gene and cognate promoters.";
Gene 210:67-70(1998).
Gene 210:67-70(1998).
InterPro; IPR00263; GH_25.
InterPro; IPR003646; SH3_bac.
Fram; PF01183; Glyco_hydro_25; 1.
ProDom; PD004620; GH_25; 1.
SWART; SW00287; SH3D; 1.
SWART; SW00287; SH3D; 1.
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                    Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Last annotation update)
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56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
science 281:2012-2018(1998).
EMBL; Z81109; CAB03241.1; -.
InterPro; IPRO00719; Euk_pkinase.
Pfam; PRO0069; pkinase; 1.
Probom; PD000001; Euk_pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last annota
T518.1 protein.
T518.1.
Arabidopsis thaliana (Mouse-ear cress).
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Pred. No.
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                          Gaps
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbiniao O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.; "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and amonophyly of archeal methanogens."; Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                              62.5%; Score 35; DB 10; Length 510; 60.0%; Pred. No. 92;
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                                                                                                                                                                                                                     510 AA; 55089 MW; 0DC63CC41F4712F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Predicted protein of the CobN/Mg-chelatase family
                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2042 AA.
                                                                                                                                                                                                                                                                      2; Mismatches
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STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; Pubmed=11930014;
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75.0%;
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21,
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01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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12 EEVKPPGIHF 21
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                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                                                                SEQUENCE FROM N.A
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                                       NCBI_TaxID-3702;
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White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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                                                                                                                                           Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Reagle P., Lumm W., Pothler B., Qiu D.,
Spadadfora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M.,
Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
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                               Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              60.7%; Score 34; DB 17; Length 264; 62.5%; Pred. No. 74;
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Pred. No. 79;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               264 AA; 28858 MW; 366BAE4E4D992C21 CRC64;
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279 Aa; 31140 MW; DCEA100E0AEE8831 CRC64;
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13, Last sequence update)
20, Last annotation update)
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InterPro; IPR000878; Cor/por_Metransf.
InterPro; IPR004551; Dphthn_synthase.
                 Methanobacterium thermoautotrophicum.
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                                                                                                                STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00590; TP_methylase; 1.
TIGRFAMS; TIGR00522; dph5; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein DR0271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 60.7%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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NCBI_TaxID=1299;
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Matches 5; Conservative
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01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                 NCBI_TaxID=187420;
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 264 AA;
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Q9RXN9
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4 VPXGMHYS 11

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252
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MEDLINE=2108290;
PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
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MEDLINE-20036896; PubMed-10567266;
Milte O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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Pred. No. 80;
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                                                                                                                                                                           .-OCT-2001 (TrEMBLrel. 18, Created)
1-OCT-2001 (TrEMBLrel. 18, Last sequence update)
1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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PRINTS; PR00603; CYTOCHROMEC1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
COMPLETE proteome.
SEQUENCE 285 AA; 30961 WW: 3110chron111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL, AP003000; BAB49770.1; -.
InterPro; IPR000345; Cytc.heme_bind.
InterPro; IPR002326; Cyt.C1.
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55.6%;
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NCBI_TaxID=1299;
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                     PRELIMINARY;
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100 VPLGRHYS 107
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01-JUN-2002
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinsshi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mortobiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                     Gaps
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SERVAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                            60.7%; Score 34; DB 16; Length 350; 60.0%; Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                  Indels
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                 37121 MW; 37601D08B2FB6116 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 AA; 39873 MW; 7A995A55116077B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL079355; CAB45581.1; -
InterPro; IPR000977; DNA_ligase.
Pfam; PF01068; DNA_ligase; 1.
PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
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                    EMEL, AE001932; AAF10353.1; ...
HSSP; P07547; 1DQS.
TIGR; DR0777; ...
Interpro; IPR002658; DHQ_synthase.
Pfam; PF01761; DHQ_synthase, 1.
Pfam; PF01761; AAF, 37121 MW; 37601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel, 12, 01-JUN-2002 (TrEMBLrel, 21, Putative DNA ligase. SCO6707 OR SC4C6.17C.
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Science 286:1571-1577(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XAM3;
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
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Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              | | | ||||||
EAVAYGMHYA 261
                                                                                                                                                                                                                                                                                                                                                                           2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
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Query Match
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Q9Y0Y6;
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016912
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                                                                                                                                                                                                                                                                                                                                                         Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
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                      Indels
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                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                      1;
  le+02;
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                  1; Mismatches
  Pred. No.
                                                                                                                                                                                                                                                                                                                                       Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                         Created)
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
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MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0111; pelA; 1.
Cell division; Complete proteome.
SEQUENCE 360 AA; 40814 MW; 2A
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InterPro; IPR005141; eRF1_2.
InterPro; IPR005142; eRF1_3.
InterPro; IPR004405; PelA.
Pfam; PF03463; eRF1_1; 1.
Pfam; PF03464; eRF1_2; 1.
ilarity 71.48;
Conservative
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Query Match
Best Local Similarity 45.5.5.
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EDLVPMGSHHT 108
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                                                                                                                                                                                                                                                                                              Cell division protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus halodurans.
                                                         4 VPXGMHY 10
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20 IPPGMHY 26
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                    027679;
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027679
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Q9KBA1
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton D., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Bightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan R., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                        halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:417-431(2000).
BMBL; AP001514; BAB05746.1;
Hypothetical protein; Complete proteome.
SEQUENCE 425 AA; 47639 MW; 914824B1FB65E3DE CRC64;
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Rhabditidae; Peloderinae; Caenorhabditis.
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus
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                                                                                                                                                                                                                                                                                                              Score 34; DB 16; Length 425;
Pred. No. 1.2e+02;
2; Mismatches 2; Indels
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50.0%; Pred. No. 1.4e+02;
Live 2; Mismatches 3; Indels
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Graves T., Wohldmann P., Gillam B.;
Graves T., Wohldmann P., Gillam B.;
"The sequence of the legans cosmid F10D2.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022972; AAC48234.1;
InterPro; IPR004121; Sre.
Pfam; PR03125; Sre; 1.
SEQUENCE 495 AA; 58190 MW; OC61139C138EEE4C CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 AA
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                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 60.0
Matches 6; Conservative
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403 EELLIEGMHY 412
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218 ENIVPTGKHH 227
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Best Local Similarity
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DI OL-NOV-1999 (TERBELLE, 12, Last sequence update)

DI OL-NOV-1999 (TERBELLE, 12, Last sequence update)

DI OL-NOW-1999 (TERBELLE, 12, Last sequence update)

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EMBL; AF275348; AAG27217.1; -.
Hypothetical protein.
SEQUENCE 678 AA; 75850 MW; A17B09E30512FE3C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.7%; Score 34; DB 12; Length 678; 50.0%; Pred. No. 2e+02;
Score 34; DB 5; Length 637;
Pred. No. 1.9e+02;
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                                2; Indels
                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 75.9 kDa protein.
                                                                                                                                                                   678 AA.
                               1; Mismatches
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 60.7%;
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                                6; Conservative
                                                                                                                                                                   PRELIMINARY;
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263 VVPDAVHYS 271
                                                            3 VVPXGMHYS 11
   Query Match
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

2			Description	່ບ	۲ ،	Hepatitis C virus	<b>r</b> 3	Hepatitis C virus	۲,	U	r 1	υ	Hepatitis C virus
SOFTWANTES			ID	~	ABB80528	ABB80529	ABB80561	ABB80562	ABB80538	ABB80542	ABB80543	ABB80521	ABB80522
			DB	23	23	23	23	23	23	23	23	23	23
			re Match Length DB ]	11	11	11	11	11	11	11	11	11	11
	æ	Query	Match	96.3	96.3	96.3	96.3	96.3	87.0	87.0	87.0	85.2	85.2
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ALIGNMENTS

RESULT 1 ABB80524 ID ABB80524 standard; peptide; 11 AA.

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. carbonyl forming keto-amide linkage with 7 "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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100.0%; Pred. No. vo.
... 0; Mismatches
                                                                                  /note= "N-terminal acetyl"
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                                                                                                          "Norvalyl
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 64; 69pp; English.
                                                                                                                           residue
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                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-361643/39
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                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4
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                                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                          /note= "C-terminal amide"
                                                                                                                                                                                                                                               'note= "D-form residue"
                                                                                                                                                        Location/Qualifiers
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/note= "Norvalyl carbonyl forming keto-amide linkage with
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketodmide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-361643/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus protease -
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  Modified-site
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Synthetic.
                                                                                                                                                                        Sequence
                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                  virucide
                                                                                                                                                                                                                                                                   RESULT 7
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                                                                                                                                                                                                                                         Dp
                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have a medicament to treat useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                           Gaps
                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18
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                                                                                                                                                                                                                                                      96.3%; Score 52; DB 23; Length 11; 100.0%; Pred. No. 0.0015; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "C-terminal amide"
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                                                                               Brunck TK,
                                                                                                                                                                                                                                                                                                                                                    ABB80538 standard; peptide; 11 AA.
                                                                                                                                                Claim 17; Page 65; 69pp; English.
                         19-JUL-2001; 2001WO-US23169
                                            21-JUL-2000; 2000US-220101P
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                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                         1 EEVVPXGMDYS 11
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                                                                             Lim-wilby M, Levy OE,
                                                             (CORV-) CORVAS INT INC
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                                                                                             WPI; 2002-361643/39
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         31-JAN-2002
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                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                   RESULT 6
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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Brunck TK;
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                                                                                                                                                                                                                             Claim 17; Page 64; 69pp; English.
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                                                      WPI; 2002-361643/39.
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Matches 10; Conserv
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                                                                                                                                                                             virus protease
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Matches 10;
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                          The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                             "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
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                                                                                                                        DB 23; Length 11; 0.014;
                                                                                                                                          1; Indels
                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             "C-terminal amide"
                                                                                                                        Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       "D-form residue"
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        Claim 17; Page 65; 69pp; English.
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                                                                                                                        87.0%;
90.9%;
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                                                                                                                   Query Match 07.0
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                       Sequence
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virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A paramaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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Pred. No. 0.014
0; Mismatches
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Best Local Similarity
Matches 10; Conserv
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us-09-909-164-8.rag

"Norvalyl carbonyl forming keto-amide linkage with

residue 7"

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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
                                                                                                                                                     note= "N-terminal acetyl"
                                                                                                                                                                                                                             /note= "C-terminal amide"
                                                                                                                                                                                                         "note= "D-form residue"
                                                                                                                                   Location/Qualifiers
ABB80525 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US23169.
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                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                 (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                   virus protease
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Modified-site
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                                                                                                               Synthetic.
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                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
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Pred. No. 0.022;
); Mismatches 1; Indels
                                                                                                                                                                                                                                    'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                          "C-terminal amide"
                                                                                                                                                                                                                                                                                      "D-form residue"
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                                                                            ABB80522 standard; peptide; 11 AA.
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Brunck TK;

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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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RESULT 11 ABB80525

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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                          /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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Pred. No. 0.022;
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             "N-terminal acetyl"
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have
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                                                                                                                                         "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                 'note= "N-terminal acetyl"
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Matches 10; Conservative
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(CORV-) CORVAS INT INC
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                                                                                                                   peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31
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Pred. No. 0.022;
0; Mismatches 1; Indels
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                                                                                     Brunck TK;
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                                                                                                                                                 Claim 17; Page 65; 69pp; English.
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90.9%;
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                                                                 (CORV-) CORVAS INT INC
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WO200208251-A2.
                                                                                                                                     virus protease
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.2%; Score 46; DB 23; Length 11; 90.9%; Pred. No. 0.022;
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Lim-wilby M, Levy OE, Brunck TK;
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                                                                                                                                                                                                                                                 Claim 17; Page 65; 69pp; English.
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hes 10; Conservative
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                                                               WPI; 2002-361643/39
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                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #37.
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                                                                                                                                            Score 46; DB 23; Length 11;
Pred. No. 0.022;
0; Mismatches 1; Indels
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                     Claim 17; Page 65; 69pp; English.
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Matches 10; Conservative
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmacceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                               Score 46; DB 23; Length 11;
Pred. No. 0.022;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                11 AA;
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(first entry)

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ABB80564 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                              "Valyl carbonyl forming keto-amide linkage with
                                         Gaps
                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                      Length 11;
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                     DB 23;
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90.9%; Pred. No. 0.022;
ive 0; Mismatches 1;
                   Score 46; DB 23;
Pred. No. 0.022;
0; Mismatches
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/note= "C-terminal amide"
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                                                                                                                      ABB80563 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                         residue
                    85.2%;
90.9%;
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                                                                                                                                                          (first entry)
                                     Conservative
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                                                        1 EEVVPXGMDYS 11
                                                                         1 EEVVPXGMSYS 11
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Best Local Similarity
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11 AA;
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 Sequence
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                                                                                                                                                                                                                                                                                      "Leucyl carbonyl forming keto-amide linkage with residue 7"
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                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
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                                                                                                                                                                                                                                                                                           /note=
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.

1 EEVVPXGMSYS 11

us-09-909-164-8.rag

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha Retoanide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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"2-aminoisobutyryl carbonyl residue forming a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47
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                    keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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/note= "C-terminal amide"
                                                      "C-terminal amide"
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                                                                                                                                                                                                                               (CORV-) CORVAS INT INC
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Best Local Similarity
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                                                                                                                                                                                /note= "Norleucyl carbonyl forming keto-amide linkage
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                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis {\tt C}
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                                                                                                                                                 'note= "N-terminal acetyl"
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/note= "C-terminal amide"
                                                                                                                                                                                                    with residue 7"
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es 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Alpha-propynyl-glycinyl-carbonyl residue forming a keto-amide linkage with residue 7"
                                                                                                                                                                                                                                    Gaps
                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis \mathsf{C}
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0.022;
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                                                                                                                                                                                                                 Score 46;
Pred. No.
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                                           Brunck TK;
                                                                                                                                                                                                                                                                                                          ABB80568 standard; peptide; 11 AA.
                                                                                                          Claim 17; Page 65; 69pp; English.
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90.9%;
       21-JUL-2000; 2000US-220101P.
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nes 10; Conservative
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                        (CORV-) CORVAS INT INC.
                                        Lim-wilby M, Levy OE,
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/note=
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                                                                                                                                                                                               11 AA;
                                                                                            virus protease
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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activity useful for treating disorders associated with hepatitis C
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0.022;
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Pred. No.
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                                                                     Claim 17; Page 65; 69pp; English.
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virucide
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Search completed: June 10, 2003, 13:39:07 Job time : 32.3571 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:31:45 ; Search time 9.64286 Seconds Run on:

(without alignments)
33.564 Million cell updates/sec

1 EEVVPXGMDYS 11 US-09-909-164-8 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched: 262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Issued_patents_AA:*
1: /cgn2_6/ptodate/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodate/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 4, Appli	Sequence 5, Appli	24,	Sequence 11, Appl	7,	Sequence 7, Appli	Sequence 76, Appl	82	14,	8	œ	Sequence 6, Appli	Patent No. 5177197	23,	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 21, Appl	21,	21,			Sequence 22, Appl		Sequence 22, Appl	
SUMMAKIES	ΙD	US-08-853-948B-4	US-08-853-948B-5	US-09-697-367-24	US-08-429-054A-11	US-08-718-777-7	US-09-051-341-7	US-08-569-147-76	US-08-569-147-82	US-08-963-851-14	US-08-070-165F-8	US-08-885-418-8	0S-06-383-630-6	5177197-51	US-08-580-988A-23	US-08-460-694-4	US-08-460-744-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	US-08-246-361A-21	US-08-463-772-21	PCT-US93-05000-21	US-08-926-842B-20	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22
	Query Match Length DB	341 4	348 4	368 4	1068 2	1068 2	1068 3	140 4	140 4	59 4	378 1	378 2	801 4	65 6	102 2	152 2	152 3	152 3	• •		189 2			231 3			236 3	236 5
æ	Query Match I	66.7	66.7	66.7	66.7	66.7	66.7	63.0	63.0	61.1	61.1	61.1	61.1	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3
	Score	36	36	36	36	36	36	34	34	33	33	33	33	32	32	32	32	32	32	32	. 32	32	32	32	32	32	32	32
	Result No.	1	7	ю	4	വ	0	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

equence 21, equence 6, equence 4, equence 4, equence 4, equence 6, equence 5, equence 23, equence 6,	Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 8, Appli Sequence 2, Appli Sequence 19, Appl Sequence 19, Appl Sequence 20, Appl Sequence 20, Appl	equence equence equence equence equence equence equence equence tent No.	Sequence 8, Appli Sequence 5, Appli Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5124, Ap Sequence 5124, Ap Sequence 5124, Ap Sequence 3003, Ap Sequence 4, Appli Sequence 4, Appli Sequence 2003, Ap
926-842B-2: 464-517-6 463-772-6 246-361A-4 593-05000-4 464-517-23	-361A -772- -05000 -120- -120- -694- -517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-517- -1-	S-08-460-744-2 S-08-460-744-2 S-08-947-492-8 S-08-947-492-8 CT-0893-05000- CT-0893-05000- CT-0893-05000- T-0893-05000- T-0893-05000- T-08-1772-4 S-08-463-772-4 S-09-411-628-1	08-770-761 08-770-761 08-770-761 08-770-761 08-770-761 08-246-361 08-46-361 08-46-361 09-085-199 09-085-199 09-134-001 09-39-913
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20000000000000000000000000000000000000		4 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

## ALIGNMENTS

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GENERAL INCORNATION:
APPLICANT: AKIHAMA, TOYOTA
APPLICANT: AKIHAMA, TOYOTA
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 0049-0235-0
CURRENT APPLICATION NUMBER: US/08/853,948B
CURRENT APPLICATION NUMBER: 1997-05-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN OF: 2.1
SEQ ID NO 4: 2.1
SEQ ID NO 4: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, Asn, Asp, OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe,
                                        ; Sequence 4, Application US/08853948B
; Patent No. 6210943
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Citrus unshiu
RESULT 1
US-08-853-948B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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STRANDEDNESS:
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                          RESULT 4
US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-718-777-7
                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: ARIHAMA, TOYOTA
APPLICANT: ARIHAMA, TOYOTA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
TITLE OF INVENTION: THE SAME
TITLE OF INVENTION: THE SAME
CURRENT APPLICATION NUMBER: US/08/853,948B
CURRENT APPLICATION NUMBER: US/08/853,948B
CURRENT FILING DATE: 1997-05-09
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 348
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0
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                                                                                                  Gaps
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0
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0
                                                     66.7%; Score 36; DB 4; Length 341; 66.7%; Pred. No. 14; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 36; DB 4; Length 368;
66.7%; Pred. No. 16;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORANTION:
APPLICANT: Orozco Jr., Emil M.
APPLICANT: Caini, Perry G.
APPLICANT: Gaini, Perry G.
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
TILE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REPRENCE: BB1166 US NA
CURRENT APPLICATION NUMBER: US/09/697,367
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/084,529
PRIOR FILING DATE: 1998-MAY-07
PRIOR FILING DATE: 1998-MAY-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: MICROSOFT Office 97
LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 4
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                      Sequence 5, Application US/08853948B Patent No. 6210943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09697367
Patent No. 6323015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 66.7%;
Similarity 66.7%;
6; Conservative ;
                                             Query Match
Best Local Similarity 66.7
Matches 6, Conservative
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228 VIPPGMDFS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Citrus unshiu
                                                                                                                           3 VVPXGMDYS 11
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234 VIPPGMDFS 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VVPXGMDYS 11
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Matches 6; Conserv
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US-09-697-367-24
                                                                                                                                                                                                                                   US-08-853-948B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-853-948B-5
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APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: VAN ASSCHE, TONI; GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
TITLE OF INVENTION: A PREPARATION METHOD AND CDMA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
TORRESPONDENCE ADDRESS:
ADDRESSE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 53;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-July-1990
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 842,337
FILING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-July-1991
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Charles A. Muserlian
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1137
TELECOMMUNICATION INFORMATION:
Sequence 11, Application US/08429054A
Patent No. 5917126
                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08718777; Patent No. 5981852
GENERAL INFORMATION:
APPLICANT: Van Assche, C.
APPLICANT: Bruneau, J. M.
APPLICANT: Voelker, T.
APPLICANT: Gervals, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WORDPERFECT : CURRENT APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Unknown MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 VIPPGMDFS 443
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                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                NEW YORK
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                                                                                                                                                                                                                                                           NEW YORK
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-569-147-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  US-09-051-341-7
                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Patent No. 6124528

GENERAL INFORMATION:
APPLICANT: Shewmaker, C. K.
TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE.
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ANDERS: 14
CORRESPONDENCE ANDERS: ADDRESSE: Rae-Venter Law Group, P.C.
STREFT: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
CITY: Palo Alto
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSITCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.072.02US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                ADDRESSEE: Law Offices of Barbara Rae-Venter
STREET: 260 Sheridan Avenue, Suite 440
  MODIFICATION OF SUCROSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                      SYNTHASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/051,341
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                  PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415)328-4400
TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1068 amino acids
                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                         NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 VIPPGMDFS 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS 11
                                                                                                                                    Palo Alto
California
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94306
                                                                                                                                                                                            94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-051-341-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-718-777-7
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                         STATE:
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/569,147 FILING DATE: 25-March-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & ADDRESSEE: No. 6180377ris, LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMANISED ANTIBODIES
                                                                                                                                                                                                             CGNE.110.02US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 566-3100
TELEPHONE: (215) 566-3100
INFORMATION FOR SEO ID NO: 76:
SEQUENCE CHARACTERISTICS:
PCI/US96/17351
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-CCT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-CCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      FILING DATE: 12-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter. Ph.D.,
REGISTRATION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 76, Application US/08569147; Patent No. 6180377
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CGNE TELECOMMUNICATION INFORMATION: TELEPHONE: (415)328-4400 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.08;
75.08;
                                                                                                                                                                                                                                                                                                                                            1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 140 amino acids
amino acid
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APPLICANT:
TITLE OF INVENTION: HUMA
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-569-147-76
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 VIPPGMDFS 443
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                                                                                                                                                                                                                                                                                                                                                             amino acid
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Gaps

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Sequence 8, Application US/08070165F
Patent No. 5750365
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew I
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08885418
Patent No. 595528
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION:
ACCORDESPONDENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: S2052 Davis Medical Research Center, 480 West .
                                                                                                              Score 33; DB 4; Length 59;
Pred. No. 7.5;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Ing-Ming Chiu
STREET: S2052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DAYS: APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEPAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE GHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
                                                   ; ORGANISM: Enterococcus faecalis US-08-963-851-14
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45.5%;
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ZIP: 43210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                         Query Match
Best Local Similarity 45...
For Si Conservative
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Matches 6; Conservative
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38 EKHIPGGLEYS 48
                                                                                                                                                                                      1 EEVVPXGMDYS 11
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; MOLECULE TYPE: protein
US-08-070-165F-8
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| 139 PPGMDYS 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Columbus
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                 US-08-070-165F-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-885-418-8
                                   TYPE: PRT
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                 LENGIH:
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         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08963851
| Patent No. 6300116
| GENERAL INFORMATION:
| APPLICANT: VAN DER OSTEN, CLAUS
| APPLICANT: ANDERSEN, CARSTEN
| APPLICANT: BAUKIER, TORDEN
| APPLICANT: BAUKIER, PETER
| APPLICANT: BAUGIN, PETER KAMP
| TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
| FILE REFERENCE: 4946,200-US
| CURRENT APPLICATION NUMBER: US/08/963,851
| NUMBER OF SEQ ID NOS: 35
| SOFFWARE: FESTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 618037771S, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                    Sequence 82, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 140 amino acids TYPE: amino acid
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-147-82
                                                                           122 VVPTGFDY 129
                                     3 VVPXGMDY 10
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122 VVPTGFDY 129
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   6;
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Matches
                                                                                                                                  RESULT 8
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US-09-383-630-6
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TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
FACTOR RECEPTOR ASSOCIATED
CHONDRODYSPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.1%; Score 33; DB 2; Length 378; 85.7%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS DOS version 6.2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
ATTORNEY AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
TELECHOMUNICATION INFORMATION:
TELECHONE: 972-3-562553
TELEPRAX: 972-3-562554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-Aug-1999
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09383630A; Patent No. 6265632; GENERAL INFORMATION:
                                                                                                                                                                                                                                        CLASSIFICATION: 435
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (614)-293-8093
TELEFRAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                         : 378 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear; MOLECULE TYPE: protein US-08-885-418-8
                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 PPGMDYS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PXGMDYS 11
Columbus
                                        USA
                       Ohio
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-383-630-6
                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Sequence 23, Application US/08580988A
Patent No. 5856161
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Méthods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
LENA; HELLDIN, CARL-HENBIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
RELING DATE: 27-FEB-1990
SEQ ID NO:51:
LENGTH: 65
                                                                                                                                                            Score 33; DB 4; Length 801; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 6; Length 65; Pred. No. 13; Aismatches 3; Indels
                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM: MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATUR SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Benjamin Aaron Adler, Ph.D., J.D.
                                                       STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/580,988A FILING DATE: January 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Dr. Benjamin A. Adler
8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.3%;
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                              Query Match 61.1%;
Best Local Similarity 85.7%;
Matches 6; Conservative C
SEQUENCE CHARACTERISTICS:
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                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 KEICPGGMGYT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                               | ||||||
566 PPGMDYS 572
                                                                                                                                                                                                                                                    5 PXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                            RESULT 13
5177197-51
;Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-580-988A-23
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us-09-909-164-8.rai

20 EEVFPLAMNY 29

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Pred. No. 22;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI CYCLIN and 1ts CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New YORK AVenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.3%; Score 32; DB 2;
60.0%; Pred. No. 35;
tive 1; Mismatches
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721C1P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-221
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MCCOnathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-460-694-4
; Sequence 4, Application US/08460694
; Patent No. 5858655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 amino acids
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                        internal
                                                                                                                                                                                                                         MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMDY 10
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                                                                                                                                                                                                                                                                                  ANTI-SENSE: no FRAGMENT TYPE: 1 ORIGINAL SOURCE: US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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1 EEVVPXGMDY 10

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Gaps
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                                                                                                                                                   APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERME, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.: 1100 NEW YORK AVE., NW, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION UNESTED #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
NAME: 
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                       Sequence 4, Application US/08460744
Patent No. 6107541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGIGSRATION NUMBER: 35,279
REFERENCE/COCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.3%;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMDY 10
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                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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US-08-460-744-4
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Indels

60.0%; Pred. No. 41; tive 1; Mismatches

6; Conservative

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Best Local Similarity
                           Matches
                                                                                                                                                                     RESULT 19
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APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND
TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
NUMBER OF SEQUENCES: 34
CORRESPONDEMESS: 34
CORRESPONDEMESS: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                  59.3%; Score 32; DB 3; Length 152; 60.0%; Pred. No. 35; tive 1; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                          ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: ATRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 330
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGIGSTRATION UNDRER: 33,208
REFERENCE/DOCKET UNDRER: 5998-0016
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
11-MAR-1991
11-MAR-1991
11-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-193-977-7; Sequence 7, Application US/08193977; Patent No. 5625031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 173 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: single TOPOLOGY: not relevant MOLECULE TYPE: peptide '-667-7118-4
                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 60.v
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                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMDY 10
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                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                             CLASSIFICATION:
                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94301
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US-08-246-361A-21
; Sequence 21, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
    APPLICANT: BEACH, David H.
    TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
    NUMBER OF SEQUENCES: 50
    Sequence 21, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.38; Score 32; DB 2; Length 189; 60.08; Pred. No. 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
APPLICATION NUMBER: US 07/701,514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MIJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Matthew P. Vincent REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 60.0
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-464-517-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                     ZIP: 02109
                                                                                                                                                                                                                                    MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
US-08-464-517-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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59.3%; Score 32; DB 1; Length 173;

Query Match

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Gaps
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GENERAL INFORMATION:
APPLICANT: MITOTIX
TILLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.3%; Score 32; DB 3; Length 189; Best Local Similarity 60.0%; Pred. No. 46; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Particia
RESISTRATION NUMBER: 32,27
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSHL91-02A
                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-7401
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two ...
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 EEVFPLAMNY 83
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Patent No. 606501
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.3%; Score 32; DB 2; Length 189; 60.0%; Pred. No. 46; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                        FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-07/963,308
FILING DATE: 16-CCT-1992
PRIOR ROPELICATION DATA:
APPLICATION NUMBER: US-07/988,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-07/701,514
                                                                                                                                                                                                                            SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILLING DATE: 19-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATCHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 6; Conserv
                       USA
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                                                                                                       COUNTRY:
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TELEFAX: 616-861-9540 INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 189 amino acids TYPE: AMINO ACID

MOLECULE TYPE: protein

unknown

TOPOLOGY:

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1: 236 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.3
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-517-22
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COMPUTER READABLE FORM:
MEDIUM.TYPE: Floppy
                                                                                                                                                                                                                                   SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                      STREET: bu su
                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                 02109
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                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Sa-No. 6030807ueira, Isabel
APPLICANT: de Lencastre, Herminia
TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION: AAPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.3%; Score 32; DB 3; Length 231; 55.6%; Pred. No. 58;
                                        Score 32; DB 5; Length 189;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,842B
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600-1-089 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       ; Sequence 20, Application US/08926842B
; Patent No. 6030807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIECATION:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-

TELECOMMUNICATION INFORMATION:

TELEFHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:

LENGTH: 231 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   υS-08-926-842B-20
                                            59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.v.-
                        Query Match
Guery Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                       1 EEVVPXGMDY 10
                                                                                                                                                              74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | |:|||
41 IKPSGVDYS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: ESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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        PCT-US93-05000-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                           RESULT 23
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Gaps
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APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.3%; Score 32; DB 2; Length 236; 60.0%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/08/246,361A
19-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/246,361A PITANG AMPRICATION NUMBER: US/08/246,361A
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701
FILING DATE:
                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/ABENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Matthew P. Vincent
RECISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/08246361A Patent No. 5998582
                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: LAHIVE & COCKFIELD 60 State Street
ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
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Search completed: June 10, 2003, 13:51:32 Job time : 10.6429 secs

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June 10, 2003, 13:46:50; Search time 15 Seconds (without alignments) 75.710 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                              392085
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       392085 segs, 103240269 residues
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                Run on:
                                                                                                                                                                                                              Title:
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Maximum Match 100% Listing first 75 summaries Post-processing: Minimum Match 0% Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Published Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_WINK_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_WINK_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_ENEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	10,	χ,	4, A		Sequence 9, Appli	Sequence 27, $Appl$	Sequence 5111, Ap	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 14, Appl	Sequence 4881, Ap	9	526,		Sequence 526, App	Sequence 526, App		Sequence 420, App
SUMMARIES	QI	US-10-217-700-10	US-10-217-700-8	US-10-217-700-4	US-10-217-700-11	US-10-217-700-9	US-09-813-408-27	US-09-815-242-5111	US-10-027-806-4	US-10-034-623-4	US-10-027-801-4	US-09-948-080-14	US-09-738-626-4881	US-09-815-242-10697	US-09-978-295A-526	US-09-978-697-526	US-09-978-192A-526	US-09-999-832A-526	US-09-978-189-526	US-10-174-590-420
	88	6	σ,	σ	σ	σ	σ	10	6	6	σ	10	σ	10	σ	6	6	σ	σ	6
	% Query Match Length DB	1049	1068	1081	1083	1084	440	1062	3472	3472	3472	59	283	299	736	736	736	736	736	736
,	& Query Match	66.7	66.7	66.7	66.7	66.7	64.8	63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1
	Score	36	36	36	36	36	35	34	34	34	34	33	33	33	33	88	33	33	33	33
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## ALIGNMENTS

APPLICANT: Holaday, A. Scott
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSCENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 2002-08-12 ; Sequence 10, Application US/10217700 ; Publication No. US20030070191A1 ; GENERAL INFORMATION: US-10-217-700-10 RESULT 1

Gaps

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1; Indels

Best Local Similarity 66.7%; Pred. No. 1e+02; Matches 6; Conservative 2; Mismatches

3 VVPXGMDYS 11 |:| ||:| 445 VIPPGMDFS 453

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| Publication No. US20030070191A1
| Publication No. US20030070191A1
| Publication No. US20030070191A1
| APPLICANT: Haigler, Candace H.
| APPLICANT: Holaday, A. Scott
| TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
| FILE REFERENCE: 201304/1000
| CURRENT APPLICATION NUMBER: US/10/217,700
| CURRENT PILING DATE: 1090-09-10
| EARLIER FILING DATE: 1999-09-10
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE FILE REFERENCE: 201304/100
FILE REFERENCE: 201304/100
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                        Query Match 66.7%; Score 36; DB 9; Length 1049; Best Local Similarity 66.7%; Pred. No. 96; Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 98;
2; Mismatches 1; Indels
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Craterostigma plantagineum US-10-217-700-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10217700
Publication No. US20030070191A1
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66.78;
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Best Local Similarity 66.7
Matches 6; Conservative
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436 VIPPGMDFS 444
                                                                                                                                                         ; ORGANISM: Oryza sativa
US-10-217-700-10
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LENGTH: 1068
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US-10-217-700-8
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LENGTH: 1081
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                                                                                                                                       TYPE: PRT
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66.7%; Score 36; DB 9; Length 1081;

Query Match

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                                                                                                       APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: 09/10/217,700
CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
BARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 2002-06-12
EARLIER PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 9; Length 1083; llarity 66.7%; Pred. No. 1e+02; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                            ; Sequence 11, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  us-10-217-700-9
. Sequence 9, Application US/10217700
. Publication No. US20030070191A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 27, Application US/09813408
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Arabidopsis thaliana US-10-217-700-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 6; Conservative
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483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VVPXGMDYS 11
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453 VIPPGMDFS 461
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US-10-217-700-9
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Matches 6; Conserv
RESULT 4
US-10-217-700-11
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US-09-813-408-27
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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US-IU-U34-023-4
Sequence 4, Application US/10034623
Sequence 4, Application No. US20020198365A1
Publication No. US20020198365A1
GENERAL INNORMATION:
APPLICANT: Schleper. Christa
APPLICANT: Schleper. Christa
APPLICANT: Schleper. Christa
APPLICANT: Schleper. Christa
APPLICANT: Schleper. 2001-12-21
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
                                              us-iu-uz/-aud-4

Sequence 4, Application US/10027806

Sequence 4, Application US/10027806

Sequence 4, Application US/10027806

Sequence 4, Sequence 4, Sequence 4, Sequence 4, Sequence 4, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sept. Sequence 8, Sept. Sequence 8, Sept. Sequence 8, Sept. Sequence 8, Sequence 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.0%; Score 34; DB 9; Length 3472; Best Local Similarity 45.5%; Pred. No. 9.1e+02; Indels Matches 5; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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45.5%; Pred. No. 9.1e+02;
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GENERAL INFORMATION:
APPLICANT: Feldman, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Cenarchaeum symbiosum ; US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.5%
Best Local Similarity
5, Conservative
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2294 EDVIPRGISFS 2304
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Publication No. US20030049619A1
GENERAL INFORMATION:
APPLICANT: Delagrave, Simon
APPLICANT: Marrs, Barry
APPLICANTON: Methods For The Synthesis Of Polynucleotides
TITLE OF INVENTION: Of Polynucleotides
FILE REFERENCE: HERO041
FILE REFERENCE: HERO041
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEO ID NOS: 85
SOFTWARE: Patentin version 3.0
SEO ID NO 27
LENGTH: 440
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APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xumanoto, Robert T.
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FILE REFERENCE: ELITER, 011A
CURRENT FILES ELITER, 011A
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR APPLICATION NUMBER: 60/25,931
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5111, Application US/09815242
Patent No. US20020061569Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Aeropyrum pernix
US-09-813-408-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 66.7
Matches 6; Conservative
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SEQ ID NO 10697
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APPLICANT: Schieper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
CURRENT ENPERENCE: DCORP.002A
CURRENT APPLICATION UNDER: US/10/027,801
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
SOFTWARE: FASTER for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: HALKIER, TORDEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVENTION: PROTERSE VARIANTS AND COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/948,080
PRIOR APPLICATION NUMBER: US/08/963,851
PRIOR PLING DATE: 1997-11-04
SOFTWARE: FASTSEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.1%; Score 33; DB 10; Length 59;
45.5%; Pred. No. 15;
tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09948080; Patent No. US20020102702A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4881, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Enterococcus faecalis
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Best Local Similarity 45.5%;
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ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                       1 EEVVPXGMDYS 11
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OCHTAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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                                                                                                                                             SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-948-080-14
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APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Prokaryotes
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-24
PRIOR PLING DATE: 2000-05-26
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40.0%; Pred. No. 94;
tive 4; Mismatches 2; Indels
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 90/259162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
SOFTWARE: PALENTION NUMBER: JP 00/280988
SOFTWARE: PALENTION NOWER: JP 00/280988
SOFTWARE: PALENTION NOWER: JP 00/280988
SOFTWARE: PALENTIN VET: 3.0
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4881
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Best Local Similarity
These 6; Conservat
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Best Local Similarity
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Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                       Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kliyavin, Ivar J.
Kuo, Sophia S.
Napler, Mary A.
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FILING DATE: 1998-03-26
                                                                                                                                                                                                                                                       Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                     Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                        Goddard, Mary E. Goddard, Audrey
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Paoni, Nicholas F.
                                                                             Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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                                                                       Eaton, Dan
US-09-978-295A-526
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PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-30
PRIOR PLING DATE: 1998-03-31
PRIOR PLING DATE: 1998-04-01
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-15
PRIOR PRILING DATE: 1998-04-15
PRIOR PRILING DATE: 1998-04-15
PRIOR PRILING DATE: 1998-04-22
PRIOR PRILICATION NUMBER: 60/08332
PRIOR P

APPLICATION NUMBER: 60/083495

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT PAPLICATION NUMBER: US/09/978,697

CURRENT APPLICATION NUMBER: 2001:10-16
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PRIOR FILING DATE: 2001-07-30
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-07-10-19
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR PELING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/077641
PRIOR PELING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/07804
PRIOR PELING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078936
PRIOR PELING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR PELING DATE: 1998-03-20
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Shelton, David L.
Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Kljavin, Ivar J.
Kuo, Sophia S.
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Filvaroff, Ellen
                         Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Ashkenazi, Avi
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                                                                                                                             PRIOR FILING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08354
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
PRIOR PRING DATE: 1998-04-29
PRIOR PRING DATE: 1998-04-29
PRIOR PRING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084441
PRIOR PLING DATE: 1998-05-05
PRIOR PRIOR DATE: 1998-05-07
PRIOR PRIOR DATE: 1998-05-07
PRIOR PRIOR DATE: 1998-05-07
PRIOR PRIOR DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PPLING DATE: 1998-05-07
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PRIOR PILLING DATE: 1998-05-15
PRIOR PELLING DATE: 1998-05-15
PRIOR PELLING DATE: 1998-05-15
PRIOR FILLING DATE: 1998-05-15
PRIOR FILLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08573
PRIOR APPLICATION NUMBER: 60/08573
PRIOR APPLICATION NUMBER: 60/08579
PRIOR APPLICATION NUMBER: 60/085697
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
                                   APPLICATION NUMBER: 60/083496
FILING DATE: 1998-04-29
                                                                                                    APPLICATION NUMBER: 60/083499
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083545
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Best Local Similarity 70.0
Matches 7; Conservative
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PRIOR APPLICATION NUMBER: 60/079656 PRIOR FILING DATE: 1998-03-26 PRIOR APPLICATION NUMBER: 60/079664 PRIOR FILING DATE: 1998-03-27

APPLICATION NUMBER: 60/079689 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079728

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PRIOR FILLING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR APPLICATION NUMBER: 60/081195
PRIOR APPLICATION NUMBER: 60/081195
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PRIOR PILING DATE: 1998-04-08
PRIOR PELING DATE: 1998-04-09
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PRIOR PELING DATE: 1998-04-2
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R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080338
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080333
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/081040
R FILING DATE: 1998-04-08
R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079786

R TILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079920

R FILING DATE: 1998-03-30

R FILING DATE: 1998-03-30

R FILING DATE: 1998-03-30

R APPLICATION NUMBER: 60/080105

R R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080107

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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083392
FILING DATE: 1998-04-29
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/080194
FILING DATE: 1998-03-31
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Gaps ö 61.1%; Score 33; DB 9; Length 736; 70.0%; Pred. No. 2.6e+02; ive 0; Mismatches 3; Indels Sequence 526, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Ferrara, Napoleon PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-05-05
PRIOR FILING DATE: 1998-05-05
PRIOR FILING DATE: 1998-05-05
PRIOR PELICATION NUMBER: 60/084414
PRIOR APPLICATION NUMBER: 60/084414
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08463
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08463
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PRIOR PELING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/08559
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559 PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR PELLING DATE: 1998-04-29
PRIOR PELLING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08350
PRIOR PELLING DATE: 1998-04-29
PRIOR PELLING DATE: 1998-04-30
PRIOR FILING DATE: 1998-05-05
PRIOR FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/085580 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085573 PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION UNDBER: 60/085704 PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085697 Ferrara, Napoleon Filvaroff, Ellen Query Match
Best Local Similarity 70.0. 331 EPVVVYGMDY 340 1 EEVVPXGMDY 10 RESULT 16 US-09-978-192A-526 qq οy

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APPLICANT:

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PRIOR
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APPLICANT: Tumms, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065364
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PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
                                                            Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR APPLICATION NUMBER: 60/07/641

DR FILING DATE: 1998-03-11

DR APPLICATION NUMBER: 60/07/649

DR FILING DATE: 1998-03-12

DR APPLICATION NUMBER: 60/07/649

DR APPLICATION NUMBER: 60/07/8004

DR FILING DATE: 1998-03-12

DR APPLICATION NUMBER: 60/07/8064

DR FILING DATE: 1998-03-20

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DR APPLICATION NUMBER: 60/07/8936

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DR APPLICATION NUMBER: 60/07/8936

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DR APPLICATION NUMBER: 60/07/8939

R APPLICATION NUMBER: 60/07/8939
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APPLICATION UNMBER: 60/079663
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/079689
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Shelton, David L.
Stewart, Timothy A.
              Gerber, Hanspeter
Gerritsen, Mary E.
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Wei-Qiang
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APPLICANT:
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PRIOR FILING DATE: 1998-03-31
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PRIOR PLING DATE: 1998-03-31
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PRIOR PLING DATE: 1998-03-31
PRIOR PLING DATE: 1998-03-31
PRIOR PLING DATE: 1998-04-01
PRIOR PLING DATE: 1998-04-08
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PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-28
PRIOR PLING DATE: 1998-04-29
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JANT: Moto, Scotint 3.

LACONTY: Moto, Mo
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APPLICATION UNMBER: 60/079920
APPLICATION DATE: 1998-03-30
APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
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Godowski, Paul J.
Grimaldi, J. Christopher
                                                                              R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-30
R FILING DATE: 1998-04-30
R TRILING DATE: 1998-05-05
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R PILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/085700
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085689
FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
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APPLICATION NUMBER: 60/085704
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Desnoyers, Luc
Eaton, Dan
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Best Local Similarity 70.v.
Thos 7; Conservative
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US-09-999-832A-526
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PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
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PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-08
PRIOR PLING DATE: 1998-04-08
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PRIOR PELING DATE: 1998-04-15
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PRIOR PELING DATE: 1998-04-15
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PRIOR PILING DATE: 1998-04-15
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OR APPLICATION NUMBER: 60/081838

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R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/083742
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R APPLICATION NUMBER: 60/083742
R FILING DATE: 1998-06-05
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
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FILING DATE: 1998-05-06
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PRIOR APPLICATION NUMBER: 60/084637
PRIOR PILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-15
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PRIOR PILING DATE: 1998 UO-13
PRIOR PILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08582
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR PAPLICATION NUMBER: 60/08559
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
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Gao, Wei-Qiang,
Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 526, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
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Best Local Similarity 70.0
Matches 7; Conservative
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APPLICANT: Baker Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMDY 10
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APPLICANT:
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Pan, James; Paoni, Nicholas F

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APPLICANT: SLEWALL, TAUNCHLY A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
ITTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITTLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-015
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/07791
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-13
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR PELICATION NUMBER: 60/078936
PRIOR PELICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079656
PRIOR PELING DATE: 1998-03-27
PRIOR PAPLICATION NUMBER: 60/079669
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079669
PRIOR PILING DATE: 1998-03-27
PRIOR PAPLICATION NUMBER: 60/079969
PRIOR PILING DATE: 1998-03-37
PRIOR PAPLICATION NUMBER: 60/079920
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1998-03-37
PRIOR APPLICATION NUMBER: 60/080107
PRIOR PILING DATE: 1998-03-37
PRIOR APPLICATION NUMBER: 60/080107
PRIOR PILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
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R APPLICATION NUMBER: 60/077450
R APPLICATION NUMBER: 60/077632
R APPLICATION NUMBER: 60/077632
R APPLICATION NUMBER: 60/077641
R APPLICATION NUMBER: 60/077641
R APPLICATION NUMBER: 60/077641
R APPLICATION NUMBER: 60/077649
R APPLICATION DATE: 1998-03-11
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APPLICATION NUMBER: 60/080165
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
   APPLICANT:
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PRIOR APPLICATION NUMBER: 60/08134
PRIOR FILING DATE: 1998-04-01
PRIOR PELICATION NUMBER: 60/081070
PRIOR PELICATION NUMBER: 60/081049
PRIOR PELICATION NUMBER: 60/081071
PRIOR PELICATION NUMBER: 60/081071
PRIOR PELICATION NUMBER: 60/08129
PRIOR PELING DATE: 1998-04-05
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-21
PRIOR PELING DATE: 1998-04-21
PRIOR PELING DATE: 1998-04-22
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 19

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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: APPLICANT: APRENDED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Pred. No. 2.6e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 420
LENGTH: 736
                                                                                                                                                                                                  Sequence 420, Application US/10176758; Publication No. US20030008353A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 420, Application US/10175737
Publication No. US20030013153A1
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70.0%;
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Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Matches 7; Conservative
                                                              331 EPVVVYGMDY 340
                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P.
                               1 EEVVPXGMDY 10
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US-10-176-758-420
                                                                                                                                                                                                                                                                                                        Chen,Jian
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US-10-175-737-420
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                                                                                                                                                                          US-10-176-758-420
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US-10-175-737-420
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LENGTH: 736
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APPLICANT:
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APPLICANT:
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APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Alang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PASTORICA2
CURRENT APPLICATION NUMBER: US, 10/174, 590
CURRENT APPLICATION NUMBER: US, 10/174, 590
FILO APPLICATION TEMOVED - See File Wrapper or Palm
SEQ ID NO 4.20
LENGTH: 736
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61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels
                                    PRIOR PETLICATION NUMBER: 60/084598
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-15
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                          APPLICATION NUMBER: 60/084598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
     FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 70.0
Matches 7; Conservative
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Smith, Victoria
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; ORGANISM: HOMO Sapien
US-10-174-590-420
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US-10-174-590-420
PRIOR
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Gaps

61.1%; Score 33; DB 9; Length 736;

Query Match

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Pan,James
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US-10-175-752-420
US-10-175-738-420
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LENGTH: 736
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: APPLICANTON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C7
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
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           Best Local Similarity 70.0%; Pred. No. 2.6e+02; Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps
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CURRENT FILING DATE: 2002-06-19
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 420
LENGTH: 736
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                                                                                                                                                                                   ; Sequence 420, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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ORGANISM: Homo Sapien
                                                                   1 EEVVPXGMDY 10
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US-10-173-706-420
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LENGTH: 736
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US-10-173-706-420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin T.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C60
CURRENT PPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
PLIOT APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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  Length 736;
61.1%; Score 33; DB 9; Length 736 70.0%; Pred. No. 2.6e+02; tive 0; Mismatches 3; Indels
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 420
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                                                                                                                                                                                                                                 ; sequence 420, Application US/10175752; publication No. US20030022295A1; GENERAL INFORMATION:
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Wood, William I.
Zhang, Zemin
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           Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                   331 EPVVVYGMDY 340
                                                                                             1 EEVVPXGMDY 10
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US-10-175-752-420
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; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-420

Query Match

Query Match

Best Local Similarity 70.0%; Pred. No. 2.6e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMDY 10

Db 331 EPVVVXGMDY 340
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Search completed: June 10, 2003, 14:35:42 Job time : 16.0714 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds

(without alignments)
94.297 Million cell updates/sec

Title: US-09-909-164-8
Perfect score: 54
Sequence: 1 EEVVPXGMDYS 11

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Winimum DB sea length: 0

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1	Description	hypothetical prote	served hyp	V1 protein - tobac	sucrose-phosphate		unknown protein F2	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	hypothetical prote	peptidoglycan-bind	probable alkaline	hypothetical prote	probable membrane	af)		plastocyanin precu	plastocyanin b pre	06-methylguanine-D	6-O-methylguanine-	hypothetical prote	probable hexosyltr	L-lactate dehydrog	ABC transporter AT	phenylalanine-tRNA	succinate dehydrog	disease resistance
CT TATELLOS	£ i	S54619	D69551	A42452	S72649	S72650	G96764	JC4783	JQ1329	T09837	T04062	T04103	T24111	н87660	H72784	T20173	F69009	B49132	S00210	S38255	S58208	D98182	AG3104	F72745	669290	669350	E86665	A70164	F81138	T48898
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	Length DB	156	363	102	341	348	460	1049	1068	1081	1083	1084	425	433	440	1150	1474	2747	66	155	168	290	290	296	357	366	565	266	587	906
s Ouerv	'	74.1	70.4	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.8	64.8	64.8	64.8	64.8	64.8	•	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0
	Score	40	38	36	36	36	36	36	36	36	36	36	35	35	35	35	35	35	34	34	34	34	34	. 34	34	34	34	34	34	34
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ALIGNMENTS

RESULT 1

S54619
hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N.A.Lternate names: hypothetical protein 02612; hypothetical protein YOL303.3
C; Species: Saccharomyces cerevisiae
C; Date: 08-140-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C; Accession: S54619; S66879
R; de Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A; Reference number: S54617
A; Accession: S54619
A; Molecule type: DNA
A; Residues: 1-156 cDEB>
A; Re

A;Molecule type: DNA A;Residues: 1.156 CDEN> A;Cross-references: EMEL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS A;Experimental source: strain S288C

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R; Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A; Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate s
A; Reference number: S72648; MUID:96439842; PMID:8842155
A; Accession: S72649
A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                              A.Molecule type: mRNA
A.Residues: 1-341 < KOWS
A.Cross-references: EMBL:AB006319; NID:92588891; PIDN:BAA23215.1; PID:92588892
A.Experimental source: Efruit, cv. Miyagawa-Wase
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
C.Genetics:
A.Genetics:
C.Function:
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Pred. No. 17;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson G:Accession, E.; Overbeek, R.; Gocayne, J.D.; Neidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Vonter, J.C.
Smith, H.O.; Woese, C.R.; Vonter, J.C.
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A.Reference number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: tobacco yellow dwarf virus
C:Species: tobacco yellow dwarf virus
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C:Accession: A42452
A:Ritle: The nucleotide sequence of the infectious cloned DNA component of tobacco yellc
A:Reference number: A42452
A:Residues: 1.102 < ANORNA
A:Residues: 1.103 < ANORNA
A:R
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C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S72649
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                             Score 40; DB 2; Length 156;
Pred. No. 1;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
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                                                                                   A; Map position: 15R
C; Superfamily: hypothetical protein YOR013w
                                                                                                                                                                                                                         74.18;
                                              A;Cross-references: SGD:S0005539
                                                                                                                                                                                                                                                              Best Local Similarity 77.8
Matches 7; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                         Query Match
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C; Genetics:
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us-09-909-164-8.rpr

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A;Molecule type: protein
A;Residues: 71-74;206-212;471-481;872-892 <WOR1>
C;Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-pl
C;Comment: This enzyme is involved in the regulation of carbon partitioning in the
C;Cumcnion:
A;Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D
A;Residues: 1-1068 <WOR>
A;Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
                                                                                                                                                                                                                                                                                                                                                         A; Pathway: sucrose blosynthesis
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A; Molecule type: DNA
                                                                                        A; Accession: PQ0260
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C; Function:
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C; Species: Oryza sativa (rice)
C; Species: Oryza sativa (rice)
C; Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
C; Accession: JG4783
R; Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
R; Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
R; Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
R; Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
R; Totos-170, 217-222, 1996
A; Meference number: JG4783
A; Molecule type: mRMA
A; Residues: 1-1049 cVAL>
A; Rober number: JG58-18175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A; Note: UDPglucose-fructose-phosphate glucosyltransferase; Sucrose-phosphate form UDPglucose and C; Genetics:
A; Genet
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C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: JO1329; P00260
E; Porcession: JO1329; P00260
B; Porcession: JO1329; P00260
B; Porcession: JO1329; MUID: 92338837; PMID: 1840396
                    A; Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome lof the plant Arabidopsis.
A; Accession: G96764
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1460 <STO>
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C;Genetics:
A;Gene: F25P22.17
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%; Score 36; DB 2; Length 460;
70.0%; Pred. No. 23;
Live 0; Mismatches 3; Indels
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66.7%;
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nes 6; Conservative
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Matches 7; Conservative
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C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homoloc; Superfamily: sucrose-phosphate synthase homoloc; Keywords: q1ycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;178-666/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Pathway: sucrose biosynthesis
C.Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homo]
C.Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:176-674/Domain: sucrose/sucrose-phosphate synthase homology <SSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D. Plant Physiol. 115, 113-121, 1997
A;Title: Analysis of CDNA clones encoding sucrose-phosphate synthase in relation A;Reference number: Z16874; MUID:97451773; PMID:9306694
A;Accession: T09837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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A;Molecule type: mRNA
A;Residues: 1-1081 <ING>
A;Cross-references: EMBL:Y11795; NID:g2190349; PIDN:CAA72491.1; PID:g2190350
A;Experimental source: ABA-treated callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Craterostigma plantagineum
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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                                                                                                                                 Score 36; DB 1; Length 1068; Pred. No. 59;
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                                                                                                                                        h 66.7%;
Similarity 66.7%;
6; Conservative
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                                                                                                                                                                              Best Local Similarity
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C; Accession: T04062
R; Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, March 1999
                                         C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                A; Residues: 1-1083 <BEV>
A; Cross-references: EMBL:AL049487
A; Experimental source: cultivar Columbia; BAC clone F28M11
C; Genetics:
                                                                                                                                                                                                                        A; Reference number: Z15184
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A; Molecule type: mRNA

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C:Species: Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
B: H87660
B: Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.;
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Aritle: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE005673; NID: 913425020; PIDN: AAK25284.1; GSPDB: GN00148 C; Genetics: A; Gene: CC3322
                                                                                                                                                                                                                        peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
64.8%; Score 35; DB
Best Local Similarity 54.5%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 EVILPPGFDYS 276
                                      335 EQIVPGGLQY 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T. Plant Sci. 112, 207-217, 1995
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that A;Reference number: 215212
                              A; Note: F28M11.40
C; Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
F; 230-714/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: Sps1
A;Map position: 1
A;Map position: 1
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Reywords: glycosyltransferase; hexosyltransferase
C;Reywords: glycosyltransferase; hexosyltransferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein R10D12.10 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T2411
R; Percy, C.
R; Percy, C.
A; Accession: T2411
A; Accession: T2411
A; Accession: T2411
A; Accession: T2411
A; Molecule type: DNA
A; Residues: 1-425 <WIL>
A; Molecule type: DNA
A; Residues: 1-425 <WIL>
A; Molecule type: DNA
A; Residues: 1-425 <WIL>
A; Molecule type: Companion of the molecule type: DNA
A; Residues: 1-425 <WIL>
A; Molecule type: Companion of the molecule type: Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
C;Species: Oryza sativa (rice)
C;Date: 23.Apr.1999 #sequence_revision 23.Apr-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                         66.7%; Score 36; DB 2; Length 1083; larity 66.7%; Pred. No. 60; Conservative 2; Mismatches 1; Indels
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A;Cross-references: EMBL:D45890; PIDN:BAA08304.1
A;Experimental source: subsp. Japonica
C;Genetics:
                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 60;
2; Mismatches
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A; Introns: 23/3; 56/3; 113/3; 257/2
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Best Local Similarity 66.7%;
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Best Local Similarity 50.00,
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Best Local Similarity
6; Conservē
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Gaps

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3; Indels

DB 2; Length 433;

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probable alkaline proteinase APE0263 - Aeropyrum pernix (strain KI)
C;Species: Aeropyrum pernix
C;Species: 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: H72784
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawarabayasi, Y.; Hino, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, JNR Res: 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                            A; Accession: H72784
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-440 < KAW>
A; Cross references: DDBJ: AP000058; NID: 95103388; PIDN: BAA79178.1; PID: 95103657
A; Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 29-0ct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1996
A;Reference number: Z19232
A;Accession: T20173
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: subtilisin; subtilisin homology
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Best Local Similarity 66.70,
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120 EVLPWGVDY 128
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A;Cross-references: GB:L04959; NID:g157411; PIDN:AAF01345.1; PID:g6013474
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:12
                                                                      A; Accession: A49132
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-2704, 'VT', 2707, 'ANNV' <FI2>
A; Cross-references: GB:L04958; NID:g157410; PIDN:AAF01346.1; PID:g6013475
A; Cross-reference extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:12.
C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRBS Lett. 226, 17-22, 1987
A.Title: Complete amino acid sequence of poplar plastocyanin b.
A.Fitle: Complete amino acid sequence of poplar plastocyanin b.
A.Reference number: S00210
A.Recession: S00210
A.Recession: S00210
A.Residues: 1-99 CDIM>
C.Superfamily: plastocyanin
C.Superfamily: plastocyanin
C.Superfamily: chloroplast; copper: electron transfer; metalloprotein
F;37,84,87,92/Binding site: copper (His, Cys, His, Met) (type 1) **status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plastocyanin precursor - barley
C;Species: Hordeum vulgare (barley)
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
C;Accession: 338255; S00206
C;Accession: S38255; Gausing, K.
Eur. J. Biochem. 217, 97-104, 1993
A;Title: In vitro binding of nuclear proteins to the barley plastocyanin gene prom
A;Reference number: S38255; MUID:94039081; PMID:8223592
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A;Experimental source: strain NK 1558
R;Nielsen, P.S.; Gausing, K.
FEBS Lett. 225, 159-162, 1987
A;Title: The precursor of barley plastocyanin: sequence of cDNA clones and gene ex.
A;Reference number: S00206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Populus nigra var. italica (Lombardy poplar)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Apr-2000
C;Accession: S00210
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                     Length 2747;
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                                                                                                                                                                                                                                                                                     Score 35; DB 2; Length 274 Pred. No. 2.7e+02; 3; Indels
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                                                                                                                                                                                                                                                                                             64.8%;
54.5%;
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Best Local Similarity
6; Conserva
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A;Residues: 1-155 <NIE1>
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Best Local Similarity
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A; Residues: 1-1150 <WIL>
A; Cross-references: EMB1: Z81486; PIDN: CAB03994.1; GSPDB: GN00023; CESP: C53A5.2
A; Cross-references: EMB1: Z81486; PIDN: CAB03994.1; GSPDB: GN00023; CESP: C53A5.2
A; Experimental source: clone C53A5
B; Matthews, L.
Submitted to the EMBL Data Library, August 1996
A; Accession: T23867
A; Accession: T23867
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1150 <WIL>
A; Residues: 1-1150 <WIL>
A; Residues: 1-1150 <WIL>
A; Experimental source: clone R02D5
C; Genetics: A; Genetics: A; App Position: 5
A; That position: 5
A; Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 65
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C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila sequence_revision 25-Apr-1997 #text_change 01-Dec-2000
C; Accession: B49132, A49132
R; Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
Development, 116, 985-1000, 1992
A; Fitle: The fat facets gene is required for Drosophila eye and embryo development.
A; Reference number: A49132; MUID:93202020; PMID:1295747
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Matches 5; Conservative
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A;Molecule type: nucleic acid
A;Residues: 1-2747 <FIS>
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1238 DVLPAGLDY 1246
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Matches 6; Conserv
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C;Keywords: duplication
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6-0-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (str
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-K. ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: F72745
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawarabayasi, Y.; Hino, Y.; Furahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J
BNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aer
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable hexosyltransferase (EC 2.4.1.-) AF0327 [similarity] - Archaeoglobus fulgidus probable hexosyltransferase (EC 2.4.1.-) AF0327 [similarity] - Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C; Accession: G69290 RSCHenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Doc R.Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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                                                                                                                                                                                                                                                                                                                                                                      A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AG3104
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45253.1; PID:g17742937; GSPDB:GN00187
                                                                                                             C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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Pred. No. 35;
2; Mismatches 3; Indels
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C;Genetics:
A;Gene: APEO493
C;Superfamily: Aeropyrum pernix hypothetical protein APEO493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein APEO493 - Aeropyrum pernix (strain K1)
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50.0%;
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Conservative
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                       C; Accession: AG3104
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A;Description: mediates the transfer of electrons from cytochrome b6/f to photosystem I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Wolecule type: mRNÅ
A:Residues: 1-168 <REI>
A; Cross-references: EMBL:Z50186; NID:g929814; PIDN:CAA90565.1; PID:g929815
C; Superfamily: plastocyanin
C; Keywords: copper; electron transfer; metalloprotein
F;106,153,156,161/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted
                        C; Superfamily: plastocyanin
C; Keywords: chloroplast; copper; electron transfer; metalloprotein
F;1-58/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;59-155/Product: plastocyanin #status predicted <MAT>
F;55,140,143,148/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Populus nigra (black popular)
C; Accession: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-May-2000
C; Accession: 58208
R; Reichert, J.; Jenzelewski, V.; Haehnel, W.
Submitted to the EMBL Data Library, July 1995
A; Description: Kinetic studies of recombinant poplar plastocyanins.
A; Reference number: 558208
A; Status: preliminary
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                                                                                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                                                                                              63.0%;
54.5%;
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A;Map position: linear chromosome
                                                                                                                                                                                                                                   Best_Local Similarity 54.59
Matches 6; Conservative
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Best Local Similarity
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0; Gaps

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Gaps .; 0

2; Indels

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Lactate dehydrogenase, cytochrome-type (11dD) homolog - Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Date: 05-Dec-1997 #text_change 17-Mar-2000 C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000 B; Marchard H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson B; Klenk, H.P.; Clayton, R.D.; Coeayne, J.D.; Weidman, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 344-370, 1997 Ash. Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C. Ashither The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69250; MuID:98049343; PMID:9389475 Ashacession: G69350 Ashacession: G69350 Ashacession: Ashacessio
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69250
A; Accession: G6920
A; Accession: G6920
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-357 < KLE>
A; Residues: 1-357 < KLE>
A; Cross-references: GB: AE001082; GB: AE000782; NID: 92689405; PIDN: AAB90909.1; PID: 9265031
C; Superfamily: probable hexosyltransferase ytxN
C; Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
*Residues: 1-36 cKLE>
A;Cross-references: GB:AE001049; GB:AE000782; NID:g2689372; PIDN:AAB90435.1; PID:g26498C
C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.0%; Score 34; DB 1; Length 357; Best Local Similarity 55.6%; Pred. No. 44; Matches 5; Conservative 3; Mismatches 1; Indels
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289 EKVVPTGVD 297
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Search completed: June 10, 2003, 13:49:13 Job time: 13.2143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 10, 2003, 13:25:04; Search time 4.5 Seconds Run on:

(without alignments) 101.387 Million cell updates/sec

1 EEVVPXGMDYS 11 US-09-909-164-8 54 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 75 summaries Post-processing: Minimum Match 08 Maximum Match 100%

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description			•			~		-				_		•		_				-		٠.			P19102 xenopus lae	•		-			_	ത	P30280 mus musculu
ID	CARB_FUSNN	Y11K_TYDVA	SPS_ORYSA	SPS_MAIZE	SPS2_CRAPL	FAF_DROME	KHL1_HUMAN	PLAS_ORYSA	PLAS_HORVU	PLAT_POPNI	SYFB_BORBU	Y939_METUA	PANC_PSEAE	HMPA_VIBCH	ACDM_RAT	ECB2_HALEL	ECB1_HALEL	ECE2_HUMAN	FGR3_MOUSE	CEK2_CHICK	SULH_SCHPO	ENV_SFV3L	RPOC_VIBCH	ZEP1_HUMAN	ET2A_XENLA	PLAS_DAUCA	HES3_RAT	ARAD_ECOLI	ARAD_SALTY	HIS9_THEMA	CGD2_RAT	CGD2_HUMAN	CGD2_MOUSE
DB	<u> </u>	Н	Н	Н	Н	-	П	Н	Н	٦	Н	-	~1	Н	Н	Н	Н	Н	-	Н	٦	Н	Н	-	Н	Н	Н	Н	Н	Н	H	Н	1
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% Query Match	70.4	66.7	2.99	66.7	66.7	64.8	63.8	63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	60.2	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3
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0459 10755 3706 9706 93782 3169 9281 4385	rattu rattu methi xenoj xenoj sacci	P15032 escherichia 000291 homo saplen P38681 neurospora 061137 mus musculu P22064 homo saplen 004351 clostridium 014766 homo saplen 000918 rattus norv		USBOOT MENTANCOCCU P10941 Cryphonectr P34338 caenorhabdi P58869 methanosarc P31906 bradyrhizob Q27667 methanobact P44677 haemophilus P53998 Kluyveromyc Q75355 homo sapien P46810 mycobacteri Q99qt4 staphylococ Q55154 synechocyst P23622 neurospora
CGD1_BRARE CGD1_XRNLA CGD2_CHICK CGD2_KRNCA CGD1_CHICK CGD1_CHICK CGD1_CHICK CGD1_HUMAN	CGD1 CGD1 CGD1 MTBA ET2E HNFE			1 YCLO_METUA 1 YHAL_CRYPA 1 YK14_CREEL 1 MTBA_METAC 1 HYPE_BRATA 1 LE11_METTH 1 TOLE_HARIN 1 LET1_KLUIA 1 ENP3_HUMAN 1 GUAA_WYCLE GUAA_MYCLE GIDA_STRAM 1 DNK1_SYNY3 1 CY14_NEUCR
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ALIGNMENTS

STRAIN=ATCC 25586;
MEDLINE-21886394; PubMed=11889109;
MEDLINE-21886394; PubMed=11889109;
MEDLINE-21886394; PubMed=11889109;
MEDLINE-21886394; PubMed=11889109;
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.";
J. Bacteriol. 184.2005-2018(2002).
-: CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) PRT; 1058 AA. Fusobacterium nucleatum (subsp. nucleatum). Bacteria; Fusobacteria; Fusobacterium. STANDARD; NCBI_TaxID=76856; CARB OR FN0422. CARB_FUSNN Q8RG86; CARB_FUSNN RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                            -I-PATHWAY: Arginine blosynthesis.
-I-PATHWAY: Pyrimidine blosynthesis; first step.
-I-SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

AACT MW; ED7037AF7771E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0098; CPGASE.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manganese; Complete proteome.

1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-92188538; PubMed-1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Pred. No. 7.8;
3; Mismatches 1; Indels
   phosphate + L-glutamate + carbamoyl phosphate.
COFACTOR: Binds three manganese ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tobacco yellow dwarf virus (strain Australia) (TYDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssDNA viruses; Geminiviridae; Mastrevirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALLOSTERIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                            SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AA.
                                                                                                                                                                                                                                                                                  EMBL, AE010554; AAL94625.1; ALT_INIT.
INCEPTO; IPR00543; CPRSe_L.
INTERPTO; IPR005443; CPRSe_L.D2.
INTERPTO; IPR005480; CPRSe_L.D3.
INTERPTO; IPR005481; CPRSe_L.D3.
INTERPTO; IPR005481; CPRSe_L.N.
Pfam; PF00289; CPRSe_L.CAnin; PF6m; PF02786; CPRSe_L.CAnin; PF6m; PF02786; CPRSe_L.CAnin; PF6m; PF02786; CPRSe_L.D3; 1.
Pfam; PF02786; CPRSe_L.D3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 EIVPNGLNYS 199
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546
1058
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832 83
1058 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y11K_TYDVA
P31619;
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PATHWAY: SUCTOSE SYNTHASIS.
-i- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
-i- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.
-CAPALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + Sucrose 6-phosphate.
-I- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
"The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants."; virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                            PIR; A42452; A42452.
InterPro; IPR002621; Gemini_mov.
Pfam; PF01708; Gemini_mov; 1.
Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A40ECFIE0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14)
(UDP-glucose-fructose-phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,.
Herrera-Estrella L.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1049 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. Indica-IR36; TISSUE=Leaf;
MEDLINE=96235138; Pubmed=8666248;
                                                                                                                                                                                                                                                         EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 QVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 170:217-222(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPS_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
SPS_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRIN-CV. PIONEER 3184; TISSUE-Leaf;

X MEDLINE-92338837; PubMed-1840396;

A WEDLINE-92338837; PubMed-1840396;

A WEDLINE-92338837; PubMed-1840396;

A WEDLINE-92338837; PubMed-1840396;

A WEDLINE-92338837; PubMed-1840396;

I leaf carbohydrate partitioning.";

L leaf carbohydrate partitioning.";

L plant Cell 3:121-130(1991).

C -1- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREOFER PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE ELBA.

C -1- CATALYTIC ACTIVITY: UDP-Glucose + D-fructose 6-phosphate = UDP + SUCROSE 6-phosphate.

C -1- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- DEVELOPMENTAL STAGE: GERMINATING SEEDS OR MATURE LEAVES.
-i- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate synthase (EC 2.4.1.14) (UDP-glucosyltransferase).
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                 66.7%; Score 36; DB 1; Length 1049; 66.7%; Pred. No. 20;
                                                                                                                                                                                                                           1; Indels
                                                                                            22 29 POLY-GLY.
695 698 POLY-GLU.
775 779 POLY-AGG.
1049 Aa; 116455 MW; ED862E2819AA4B04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 25
                                Interpro; IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 22 29 POLY-GIY.
                                                                                                                                                                                                       Pred. No. 20;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- PATHWAY: Sucrose synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M97550; AAA33513.1; -.
                  EMBL; U33175; AAC49379.1; -.
                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                          29
698
779
                                                                                                                                                                                                                                                                                                      436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                 3 VVPXGMDYS 11
                                                                                                                                                                                                           Best Local Similarity
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P31927:
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                         Query Match
                                                                                              DOMAIN
                                                                                                                DOMAIN
                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                 Matches
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                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- PATHWAY: Sucrose synthesis.
-i- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
-i- PTW: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiales incertae sedis; Torenleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation; Multigene family.
                                                       Gaps
                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sucrose 6-phosphate.
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Pred, No. 21;
2; Mismatches 1; Indels
                           66.7%; Score 36; DB 1; Length 1068; 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                    PRT; 1081 AA.
                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ARG
                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y11795; CAA72491.1; -.
                                                                                                                                                                                                                                                                                                Craterostigma plantagineum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 66.7
hes 6; Conservative
                   Query Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VVPXGMDYS 11
                                                                                                                  435 VIPPGMDFS 443
                                                                                      3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4153;
                                                                                                                                                                                                                                                                                                                                                        Craterostiqma
                                                                                                                                                                                     SPS2_CRAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                    004933;
                                                                                                                                                                        SPS2_CRAPL
                                                                                                                                                            RESULT 5
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us-09-909-164-8.rsp

1394 EVIVPDGODFS 1404

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELORMENT. 116:985-1000(1992).

-1- FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A ROLLE IN COMPOUND EXE ASSEMBLY AND OGGENESIS RESPECTIVELY. IN THE LARVAL FYE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE THIS PROTEIN FOR SHORT-RANGE CELL INTERACTIONS THAT DREWINT THE MYSTERY CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR
                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-Dobable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
(Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease
FAF) (Deubiquitinating enzyme FAF) (Fat facets protein).
                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Muscomorpha; Ephydroidea; Endopterygota; Diptera; Brachycera;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1-CATALYICA ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 = ubiquitin + a thiol.
-1-ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1-TISSUE SPECIFICITY: EXE DISKS AND OVARIES.
-1-SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCRRVIIKKLVESKDEEDATSATTAATTEVTTSPATAS
QRQQL --> VTRANNV (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93202020; PubMed-1295747;
Fischer-Vize J.A., Rubin G.M., Lehmann R.;
"The fat facets gene is required for Drosophila eye and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 1; Length 2747;
Pred. No. 91;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; lrnvvi, 1, 1, Pfam; Pro0443; UCH-1; 1, Pfam; Pro0443; UCH-2; 1, PROSITE; PS00973; UCH_2_1; 1, PROSITE; PS00973; UCH_2_2; 1, PROSITE; PS50235; UCH_2_3; 1, UCH_2_3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vision; Alternative splicing.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.8%;
54.5%;
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InterPro; IPR001394; UCH-2.
                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ubl conjugation pathway.
Developmental protein, vi
ACT_SITE 1677 1677
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2747 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1986
2705
                                                                                                                 01-NOV-1997
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                                        FAF_DROME
P55824;
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VARSPLIC
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FAF_DROME
                                        $\frac{1}{2} \frac{1}{2} \frac
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                                                                                                                                                                                                                                                                                                                                            Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                     MEDLINE=20347694; PubMed=10888605;
Koob M.D., Nemes J.P., Benzow K.A.;
"The SCA8 transcript is an antisense RNA to a brain-specific
transcript encoding a novel actin-binding protein (KLHLL).";
Hum. Mol. Genet. 9:1543-1551(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: CYtoplasmic.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
-!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
KHII_HUMAN STANDARD; PRT; 748 AA. Q9NR65; Q9P238; Q9HX44; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF252283; AAF81719.1; -.
EMBL; AF25279; AAF81716.1; -.
EMBL; AB040923; BAA96014.1; ALT_INIT.
EMBL; AL353738; CAC16128.1; -.
Genew; HGNC:6352; KLHL1.
                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=20277482; PubMed=10819331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat
                                                                                                                                                                                                                                                                                                                                                                                             for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 179-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0501; KELCHREPEAT.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
Cytoskeleton; Actin binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR000210; BTB_POZ.
InterPro: IPR001798; Kelch.
Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch; 6.
                                                                           Kelch-like protein 1.
KLHL1 OR KIAA1490.
                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC: (
MIM; 605332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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6; Conservative

Best Local Similarity

Matches

Gaps

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3; Indels

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PLAS_HORVU
P08248;
                    SEQUENCE
                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                 PLAS_HORVU
METAL
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                            HIHIHIMA WARAHAN DARCCCCCCCCCCCRIII ARK CARTAR CART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                           1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIRAIN—CV. Japonica;
MEDLINE—89386623; PubMed=2780537;
MEDLINE—89386623; PubMed=2780537;

"The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";

"The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";

"The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";

"The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";

"The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";

"The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";

"The amino acid sequence of plastocyanin from rice (Oryza sativa, and rice (Oryza sativa, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00156; COPPERBLUE.
PRODOM; PR00125; COPPER_BLUE; 1.
PROSITE: PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
                                                                             Score 34.5; DB 1; Length 748;
Pred. No. 29;
1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                82680 MW; C11C43D8282F9FF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                P20423; Q9SBB8;
01-FBB-1991 (Rel. 17, Created)
12-UN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASTOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHLOROPLAST
  KELCH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000923; BlueCu_1.
InterPro; IPR001235; Copper_blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Ilpoom; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00127; copper-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF093636; AAC78108.1; -.
                                                                                      63.9%;
80.0%;
                                                                                                                 Local Similarity 80.0 nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                     127 EEVVP-GMDF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
154
154
                                                                                                                                                                                                    1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S06105; S06105.
JT0352; JT0352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00289; 2PCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 58-154.
                                748 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee J.-S.;
                                                                                                                                                                                                                                                                                                                                                                                                        PLAS_ORYSA
                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSIT
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
           REPEAT
                                                                                                                                                                                                                                                                                                                                                                             PLAS_ORYSA
                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV, NK 1558;
MEDLINE=94039081; PubMed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
promoter region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter region. 217:97-104(1993).

-i. FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-i. SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nielsen O.S., Gausing K.; "The predursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues."; FEBS Lett. 225:159-162(1987).
                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloropiast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide. 58 CHLOROPIAST.
                                                                       Score 34; DB 1; Length 154;
Pred. No. 6.8;
                                                                                                                            3; Indels
147 147 COPPER (BY SIMILARITY).
154 AA; 15577 MW; E45725D25B5F400D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASTOCYANIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLASTOCYANIN
                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COPPER
COPPER
COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y00704; CAA68696.1; --
EMBL; 228347; CAA82201.1; --
PIK; S00206; S00206.
HSSP; P00208; ZPCF.
InterPro; IPR000923; BlueCu_1.
InterPro; IPR001355; Copper_blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00127; copper-bind; 1. PRINTS; PR00156; COPPERBLUE. PRODOM; PD001235; COPPER_BLUE; 1. PROSITE; PS00196; COPPER_BLUE: 1.
                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequ
                                                                            63.0%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare (Barley).
                                                                                                                               Conservative
                                                                                                                                                                                                                                 100 EDAVPSGVDVS 110
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
155
155
140
143
                                                                                                                                                                                 1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-cv. Bomi;
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B.
-1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast; Electron transport; Copper; Thylakoid; Membrane; Transit peptide; Multigene family.

CHLOROPLAST.
                                                      Score 34; DB 1; Length 155; Pred. No. 6.9;
                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. Italica; TISSUB-Leaf;
Reichert J., Jenzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
 COPPER (BY SIMILARITY).
T -> N (IN CV. NK 1558).
DAA7EABE5F6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F20DA6EA2038AEEA CRC64;
                                                                                                                                                                                                                   01-0CT-1989 (Rel. 12, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JDN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASTOCYANIN-LIKE
                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLASTOCYANIN B.
                                                                                                                                                                                                                                                          Plastocyanin B, chloroplast precursor.
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00299; IPIC.
InterPro: IPR000923; Bluecu_1.
InterPro: IPR000923; Bluecu_1.
Pfam: PF00127; copper_blue.
PRINTS; PR00125; Copper_blue.
ProDom; PD001255; Copper_blue;
PRODOM; P0001295; Copper_blue; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPPER
                                                                                                                                                                                                                                                                                     Populus nigra (Lombardy poplar).
                           15709 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 CC
16981 MW;
                                                   63.0%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z50186; CAA90565.1; -.
PIR; S00210; S00210.
                                                                             6; Conservative
                                                                                                                             101 EDAVPSGVDVS 111
                                                                                                                                                                                              STANDARD;
                                                                                                      1 EEVVPXGMDYS 11
148 1
120 1
155 AA;
                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 70-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
106
153
156
                                                                                                                                                                                            PLAT_POPNI
P11970;
                         SEQUENCE
                                                    Query Match
              VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
 METAL
                                                                  Best Loc
Matches
                                                                                                                                                                               PLAT_POPNI
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METAL
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                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine-tRNA ligase beta chain) (PheRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 35210 / B31;

STRAIN-ATCC 35210 / B31;

MEDLINE-98065943; Pubmed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A., Quackenbush J., Salzberg S., Hanson M.,

Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,

Garland S., Fujii C., Cctton M.D., Horst K., Roberts K., Hatch B.,

"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Barbour A.G., Hinnebusch J.; "Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and thioredoxin reductase gene of Borrella burgdorferi."; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natúre 390:580-586(1997).
-!- CATÂLYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) - AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLUTAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
CHAIN FAMILY. SUBFAMILY 2.
                                        ;
0
   Score 34; DB 1; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diphosphate + L-phenylalanyl trnå(Phe).
                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                                                                                                                         Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                       . 566 AA.
                                     2; Mismatches
                      Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03484; B5; 1.
TIGRFAMS; TIGR00471; pher_arch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005147; B5.
InterPro; IPR004531; PheT_arch.
63.0%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE001153; AAC66870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U82978; AAB41019.1; -.
                                     6; Conservative
                                                                                           |: || |:| |
112 EDAVPSGVDVS 122
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
                                                                      1 EEVVPXGMDYS 11
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
SEQUENCE 566 AA
                                                                                                                                                                                                                                                                                                                      PHET OR BB0514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; BB0514;
                                                                                                                                                                                             SYFB_BORBU
P94283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              burgdorferi
                                                                                                                                                          RESULT 11
SYFB_BORBU
                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                              δ
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63.0%; Score 34; DB 1; Length 566;

Query Match

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cholerae.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9KMY3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMPA_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
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            ö
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SERIALVALL. I, DEM 2661 / ATCC 43067;

MEDLINE-96337999; Pubmed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Startavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fultmann J.L., Nguyan D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus

Jannaschii."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Pantoate--beta alamine ligase (EC 6.3.2.1) (Pantothenate synthetase)
(Pantoate activating enzyme).
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.1%; Score 33; DB 1; Length 276; 45.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
              Indels
                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67537; AAB98946.1; -.
TIGR; MJ0939; -.
Hypothetical Protein; Complete proteome.
SEQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
              1;
                                                                                                                                                (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 AA
                                                                                                                         276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
            Mismatches
  85.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
                                                                                                                                                                                    Hypothetical protein MJ0939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                Conservative
                                                                                                                                                                                                              Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 EEITENGMEHS 151
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
                                                             169 VPFGMDY 175
                                     4 VPXGMDY 10
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                 NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=287;
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                                                                                                                                                01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PANC_PSEAE
Q9HV69;
                                                                                                                                                                          16-OCT-2001
                                                                                                                          Y939_METJA
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                                                                                                                           qq
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Nature 406:477-483(2000).

Nature 406:477-483(2000).

Nature 406:477-483(2000).

Nature 406:477-483(2000).

Nature 406:477-483(2000).

Nature 108:477-483(2000).

Nature 108:477-483(20
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MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Gill S.R., Helt D.H., Red T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                   AERINATIC 15692 / PAO1;
MEDLINE-2043737; Pubmed-10984043;
MEDLINE-2043737; Pubmed-110984043;
MEDLINE-2043737; Pubmed-110984043;
MEDLINE-2043737; Pubmed-110984043;
MICKEY M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brioth K.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Reizer J., Saier M.H., Hancock R.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an Auture 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP + diphosphate + (R)-pantothenate.
-:- PATHWAY: Pantothenate biosynthesis; last step.
-:- SIMILARITY: BELONGS TO THE PANTOTHENATE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TONA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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15-JUN-2002 (Rel. 41, Last annotation update)
Flavohemoprotein (Hemoglobin-11ke protein) (Flavohemoglobin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 283;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligase; Complete proteome.
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004886; AAG08116.1; -.
InterPro; IPR003721; Pantoate_ligase.
Pfam; PF02569; Pantoate_ligase; 1.
IGRFAMs; TIGR00018; panC; 1.
Pantothenate_biosynthesis; Ligase; Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Best Local Similarity bo...
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 EEMYPDGMD 104
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Acyl-CoA dehydrogenae, medium-chain specific, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 262:10104-10108(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G., Ikeda Y., Mole J., Rosenberg L.E., Tanaka K.; "Molecular cloning and nucleotide sequence of cDNA encoding the entire precursor of rat liver medium chain acyl coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
IRON (HEME PROXIMAL LIGAND)
(BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
DDA3490FAE28823A CRC64;
                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01033; GLOBIN; I.
Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
-!- SIMILARITY: TO A NUMBER OF FAD/NAD(P) FLAVOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                            IRON (HEME DISTAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                         Oxygen transport; Transport; Complete proteome.
DOMAIN 1 136 GLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 30;
                                                                                                                                                                                                TIGR; VCA0183; ...,
InterPro: IPR001834; Cyt_B5_reductase.
InterPro: IPR0010934; FPN_Cyt_redctse.
InterPro: IPR0010971; Globin.
InterPro: IPR001433; Oxred_FAD/NAD(P).
InterPro: IPR001433; Oxred_FAD/NAD(P).
InterPro: IPR001221; Phe_hydroxylase.
Pfam; PF000175; NAD_binding; 1.
Pfam; PF00970; FAD_binding; 1.
PRINTS; PR00371; FPNCR.
PRINTS; PR00410; PENCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.1%; Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87280028; PubMed=3611054;
                                                                                                                                                                 EMBL; AE004358; AAF96096.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44191 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 EVTPEGSDY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVVPXGMDY 10
                 OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268
394 AA;
                                                                                                                                                                                   P39662; 1CQX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dehydrogenase.";
                                                                                                                                                                                               VCA0183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACDM_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACADM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
ACDM_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
a
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                                             -i- SUBCELLULAR LOCATION: Mitochondrial matrix.
-i- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-COA DEHYDROGENASES OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORMS A HYDROGEN-BOND WITH THE FLAVIN N(5) OF THE FAD COFACTOR (BY SIMILARITY).

BASE (BY SIMILARITY).

2CF076F8C919BDB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Dlaminobutyrate--pyruvate aminorransferase (EC 2.6.1.46) (L-diaminobutyric acid transaminase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goller K., Ofer A., Galinski E.A.; "Construction and characterization of an NaCl-sensitive mutant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aspartate 4-semialdehyde + L-alanine.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF ECTOINE (1,4,5,6-TETRAHYDRO-2-METHYL-4-PYRINIDINE CARBOXXLIC ACID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                  -! - SIMILARITY: BELONGS TO THE ACYL-COA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Halomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.1%; Score 33; DB 1; Length 421; 50.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism; Mitochondrion; Transit peptide.
TRANSIT 26 421 ACYL-COA DEHYDROGENASE, MEDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halomonas elongata impaired in ectoine biosynthesis.";
FEMS Microbiol. Lett. 161:293-300(1998).
-!- CATALYTIC ACTIVITY: L-2,4-diaminobutanoate + pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                 Interpro, IPR001552; Acyl-Coa_dh.
Pfam: PF00441; Acyl-Coa_dh; 1.
Pfam: PF02770; Acyl-Coa_dh_M; 1.
Pfam: PF02771; Acyl-Coa_dh_N; 1.
PROSITE: PS00072; Acyl-Coa_dh_I; 1.
PROSITE: PS00073; Acyl-Coa_DH_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=DSM 2581T;
MEDLINE=98231640; PubMed=9570121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46555 MW;
                                                                                                                                                                                                                                                                                  EMBL; J02791; AAA40670.1; -.
                               -!- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||::| ||
58 EEIIPVAPDY 67
                                                                                                                                                                                                                                                                                                   PIR; A28436; DERTCM.
                                                                                                                                                                                                                                                                                                                     HSSP; P11310; 1EGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halomonas elongata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECB2_HALEL
052250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halomonas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
ECB2_HALEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
 QQ
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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canovas D., Vargas C., Calderon M.I., Ventosa A., Nieto J.J., "Characterization of the genes for the biosynthesis of the compatible solute ectoine in the moderately halophilic bacterium Halomonas elongata DSM 3043.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TETRAHYDRO-2-METHYL-4-PYRMIDINE CARBOXXLIC ACID).
-1- SUBGNIT: HOMOHEXAMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-WAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Diaminobutyrate--pyruvate aminotransferase (EC 2.6.1.46) (L-diaminobutyric acid transaminase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF ECTOINE (1,4,5,6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Aminotransferase; Pyridoxal phosphate.
BINDING 267 267 PYRIDOXAL PHOSPHATE (POTENTIAL).
SEQUENCE 421 AA; 46166 MW; A4A2E21596E1E16C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Halomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                    61.1%; Score 33; DB 1; Length 421; 58.3%; Pred. No. 32; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                     Pfam; PE00202; aminotran_3; 1.
TIGREAMS; TIGRO0709; dat; 1.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-DSM 3043;
MEDLINE-99123891; PubMed-9924816;
                                                                                                                                                                                                                                 HSSP; P12995; 1QJ3.
InterPro; IPR000954; Aminotran_3.
InterPro; IPR004637; Dat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ011103; CAA09484.1; -. HSSP; P12995; 1QJ3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                               EMBL; AF031489; AAC15882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 EEVILKPRGLDY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVV--PXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINOTRANSFERASES.
                       AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halomonas elongata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECB1_HALEL
Q9ZEU7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halomonas.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECB1_HALEL
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       SQ PR PR DR DR DR SQ CCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human endothelin converting enzyme-2 (ECE2): characterization of mRNA species and chromosomal localization.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
Trp-!-Val-22 bond in the precursor.
-:- SUBCELLULAR LOCATION: Type II membrane protein.
-:- ALTERNATIVE PRODUCTS: 3 isoforms; ECE-2A (shown here), ECE-2B and ECE-2C; are produced by alternative splicing.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
Lorenzo M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,
Marsden P.A.;
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-9829045; PubMed=9628581; Magase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
61.1%; Score 33; DB 1; Length 423; 58.3%; Pred. No. 32;
                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                               ECE2_HUMAN STANDARD; PRT; 787 AA.
060344; Q96NX4; Q96NX3;
30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).
                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000718; Peptidase_M13.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochim. Biophys. Acta 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF428263; AAL30386.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF192531; AAG28399.1; -.
                                                                                                                                                                                                          Sest Local Similarity 58.3
Astches 7; Conservative
                                                                                                                                                                                          1 EEVV--PXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P08473; 1DMT.
MEROPS; M13.003; -.
                                                                                                                                                                                                                                                                                                                                                                                      ECE2 OR KIAA0604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF428264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                    ECE2_HUMAN
                                                                                                                                                                Matches
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    DR DR DR Z
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                                                                                                                                EXTRACELLULAR (POTENTIAL).

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

PROTON DONOR (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

MORRHAHVPQLARREDMOVERIALD.).

AGREDDMYNESSECHTUNDUTS.
                                                                                                                                                                                                                                                                                                                                                                                          AGERDPWIVSSEGVHIVDQVLS -> MNVALQELGAGSNMV
                                                                                                                                                                                                                                                                                                                                                                                                                                       MOARHAHVPOLRWETMDVRKLDFPSASFDVVLEKGTLDALL
                                                                                 CYTOPLASMIC (POTENTIAL),
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGR3_MOUSE STANDARD; PRT; 801 AA.

G01851; Q63834; Q61564;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibroblast growth factor receptor 3 precursor (EC 2.7.1.112) (FGFR-3)
FGFR3 OR MFR3 OR SAM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGERDPWTVSSEGVHTVDQVLSE -> MNVALQELGAGSN
                                                                                                                                                                                                                                                                                                                                                                                                       EYKRATLRDEDAPETPVEGGASPDAM (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation of the complementary DNA encoding a mouse heparin-binding growth factor receptor with the use of a unique kinase insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Pfam; PF01431; Peptidase_M13; 1.
PRINTS; PR00786; NEPRILYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane; Signal-anchor; Alternative splinting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ornitz D.M., Leder P.; "Ligand specificity and heparin dependence of fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Katoh O., Hattori Y., Sasaki H., Sakamoto H., Fujimoto K.,
Fujii T., Sugimura T., Terada M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC2D2B0F0EBF7239 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IN ISOFORM ECE-2C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.1%; Score 33;
Best Local Similarity 70.0%; Pred. No. 6
Matches 7; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor receptors 1 and 3.";
J. Biol. Chem. 267:16305-16311(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-92355591; PubMed-1379594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
MEDLINE-93177694; PubMed-8382556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  787 AA; 89221 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer Res. 53:1136-1141(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 EPVVVYGMDY 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.";
                                                                                                                                                            ACT_SITE
METAL
                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 19
FGR3_MOUSE
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                                                                                                                                                                                                                           TYPOSINE PHOSPDATE.

1- SUBCELLULAR LOCATION: Type I membrane protein.

1- ALTERNATIVE PRODUCTS: 2 isoforms; J/IIIC (shown here) and 2/IIIb; are produced by alternative splicing.

1- TISSUE SPECIFICITY: IN EMBRYO, EXPRESSED IN HEART, LUNG, KIDNEY, SKIN, HEAD AND LIVER BUT NOT IN MUSCLE. IN ADULT, HIGHEST LEVELS IN BRAIN. ALSO EXPRESSED IN LIVER, LUNG, KIDNEY, TESTIS, OVARY AND UTERUS. VERY LOW LEVELS IN HEART, THYMUS, SPLEEN AND MUSCLE.

1- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYO FROM MID-GESTATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
Receptor; Glycoprotein; Tyrosine-protein kinase; App-binding;
Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTÏAL.
FIBROBLAST GROWTH FACTOR RECEPTOR 3.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ??·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMO0408; IGC2; 3.
SMART; SMO0219; TyrKc; 1.
PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001109; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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SIGNAL 1 20 POTENTIA
CHAIN 21 801 FIBROBLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M81342; AAA39535.1; -.
EMBL; S56291; AAB25535.1; -.
EMBL; L26492; AAA21490.2; -.
HSSP; P11362; IFCK.
MGD; MG1:95524; Fgfr3.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003006; Ig_MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; 1g; 4.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD00001; EUK_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003598; Ig_c2.
InterPro; IPR001245; Tyr_pkinase.
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2229
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TRANSMEM
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NP_BIND
BINDING
ACT_SITE
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                                                                                                                                                                             ö
                                            AWLVVLP -> SWISENVEADARLRLANVSEROGGEYLCRA
TNFIGVAEKAFWLRVHGPQA (IN ISOFORM 2).
                N-LINKED (GLCNAC. .) (POTENTIAL).
TAGANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIGFSHHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOW; 1.
PROSITE; PS0011; PROFEIN_KINASE_DOW; 1.
RROSITE; PS0011; PROFEIN_KINASE_DOW; 1.
Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 87:5812-5816(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
--- SUBCELLUIAR LOCATION: Type I membrane protein.
--- SIMILARITY: BELONGS TO THE FIBROBLASI GROWTH FACTOR RECEPTOR
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasquale E.B.; A distinctive family of embryonic protein-tyrosine kinase
                                                                                                                                            61.1%; Score 33; DB 1; Length 801; 85.7%; Pred. No. 64;
                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine kinase receptor CEK2 precursor (EC 2.7.1.112).
                                                                                                              68BC110212691705 CRC64;
                                                                                 P -> L (IN REF. 2)
MISSING (IN REF. 2
                                                                                                                                                                                                                                                                                                                           806 AA.
                                                                                                                                                                                0; Mismatches
                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interprist IPR000719; Buk_pkinase.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003598; Ig_C2.
Interpro; IPR001245; Tyr_pkinase.
Pfam; PF00047; Ig; 3.
Pfam; PF00069; pkinase; 1.
PrintTs; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00408; IGC2; 3.
SMART; SM0219; TYRKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-90332672; PubMed=2165604;
                                                                                                                 87758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M35195; AAA48664.1; -.
                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A35963; A35963.
                                                                                                                                                                                                                                   | ||||||
| 566 PPGMDYS 572
                                                                                                                                                                                                               5 PXGMDYS 11
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P11362; 1FGK
                                                                                                                 801 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptors."
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P18460;
                                                                                                  CONFLICT
     CARBOHYD
CARBOHYD
                                     VARSPLIC
                                                                                    CONFLICT
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MEDLINE-21848401; PubMed-11859360;

MEDLINE-21848401; PubMed-11859360;

MEDLINE-21848401; PubMed-11859360;

MEDLINE-21848401; PubMed-11859360;

MOOD V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squros J., Peat N., Hayles J., Bakham D., Bowman S.,

Brooks K., Brown D., Brown D., Davis P., Feltwell T., Fraser A.,

Collins M., Connor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,

Rentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

A Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

Rentles K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

A James K., Jones L., Jones M., Leather S., McLean J.,

Rutherford K., Rutter S., Saunders D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Saunders D., Quail S., Warren T., Whitehead S.,

Rydorav J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Meltjens I., Vanstreels E., Rieger M., Schaefer M., Hilbert H.,

Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                              PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
        TYROSINE KINASE RECEPTOR CEK2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 806;
                                                                                                                  ASP/GLU-RICH (HIGHLY ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                 CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                 SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
17-JUL-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             877 AA.
                                                                                                                                    KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   . 64
                                                                                                                                                                                BY SIMILARITY
                                            POTENTIAL.
                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No
                                                                                                                                                    ATP (BY
ATP (BY
                                                                                                                                    PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                       89730 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    61.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                         219
256
288
309
322
                                                                                                                     141
755
480
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611
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107
833
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 PPGMDYS 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                        288
309
322
806 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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[70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULH_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPBC3H7.02
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CARBOHYD
SEQUENCE
                                                                                                                                                                                    ACT_SITE
MOD_RES
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                            DOMAIN
TRANSMEM
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                                                                                                                                                                                                                     DISULFID
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BINDING
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                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski GV, Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                -1- SUBCELLULAK LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
-1- SIMILARITY: CONTAINS 1 STAS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic organization and expression of simian foamy virus type 3
                                                                                                                                                                                      -1- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 877; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56995A8493371E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92124734; PubMed-1310187;
Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
Neumann-Haefelin D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simian foamy virus (type 3 / strain LK3) (SFV-3).
Viruses; Retroid viruses; Retroviridae; Spumavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ENV Polyprotein (Coat polyprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 982 AA
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InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
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STRAINELI TOY N16961 / Serotype 01;
MEDLINE-20406833; Pubmed-10952301;
Heidelberg J. F., Eisen J. A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Godson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tetterlin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:477-483(2000).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
10-JUN-401-ected RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
beta' chain) (RNA polymerase beta' subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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| PIR; C40820; VCLJLK. |
| InterPro; IPR005070; Foamy_env. |
| A piam; PRO3408; Foamy_virus_ENV; 1. |
| W Coat protein; Transmembrane; Polyprotein; Glycoprotein. |
| TRANSMEM 68 8 I (POTENTIAL). |
| FT TRANSMEM 955 975 II (POTENTIAL). |
| FT TRANSMEM 955 975 II (POTENTIAL). |
| FT CARBOHYD 17 17 N-LINKED (GLCNAC. ) (POTENTIAL). |
| FT CARBOHYD 25 25 N-LINKED (GLCNAC. ) (POTENTIAL). |
| FT CARBOHYD 109 N-LINKED (GLCNAC. ) (POTENTIAL). |
| FT CARBOHYD 1141 N-LINKED (GLCNAC. ) (POTENTIAL). |
| FT CARBOHYD 1141 N-LINKED (GLCNAC. ) (POTENTIAL). |
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| FT CARBOHYD 1141 N-LINKED (GLCNAC. ) (POTENTIAL). |
| FT CARBOHYD 1141 N-LINKED (GLCNAC. ) (POTENTIAL). |
| FT CARBOHYD 1141 N-
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  (SFV-3).";
Virology 186:597-608(1992).
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44 EEVIPTRMD 52
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Best Local Similarity
6; Conserve
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827
982 AA;
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Q9KV29;
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                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-EPI) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
HIVEPI OR ZNF40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution.";
Blochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                          (RNA)(N).
SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN (By similarity).
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
 OF DNA INTO RNA USING THE FOUR RIBONUCLEUSIDE TRIFHUSFRALES SUBSTRATES (By similarity).

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fan C.M., Maniatis T.; "A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 2087-2142.
MEDLINE=92232684; PubMed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E., Gronenborn A.M.;
DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammanla; Eutheria; Pinlades; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                             61.1%; Score 33; DB 1; Length 1401; 50.0%; Pred. No. 1.2e+02; .ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                     Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                      1401 AA; 155021 MW; DFDB0F2B5514504F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2717 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90169514; PubMed=2106471;
                                                                                                                                                                                                                                                           Interpro; IPR000722; RNA_pol_A.
Interpro; IPR002879; RNA_pol_A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 2113-2142.
                                                                                                                                                                                                                      EMBL; AE004121; AAF93502.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ::|| |: ||
581 QIVPKGLPYS 590
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                                                                                                                                                                                                                                                   VC0329;
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P15822;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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"High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1.";
Biochemistry 31:3907-3917(1992).
-:- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC, INTERLEBERIOL-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Nuclear.
-i- INDUCTION: BY WITGGEN AND PHORBOL ESTER.
-i- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00355; ZnF_C2H2; 4.
PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
Nuclear protein; Repeat; 3D-structure.
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Pred. No. 2.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C2HC-TYPE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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TRANSFAC; T00497; -.
Genew; HGNC:4920; HIVEP1.
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Matches 6; Conservative
                                                                                                                                                                                                                                             IN T-CELL ACTIVATION.
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3ZNF; 15-JAN-92.
4ZNF; 15-JAN-92.
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                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-92158632; PubMed-1741266;
Burdett L.A., Q1 S.M., Chen Z.Q., Lautenberger J.A., Papas T.S.;
"Characterization of the cDNA sequences of two Xenopus ets-2 proto-
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92088972; PubMed-1751411;
Wolff C.M., Stiegler P., Baltzinger M., Meyer D., Ghysdael J.,
Stehelin D., Befort N., Remy P.;
"Cloning, sequencing, and expression of two Xenopus laevis c-ets-2
                            C-ETS-2A protein.
ETS2A OR ETS-2A.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                           Wolff C.M., Stiegler P., Baltzinger M., Meyer D., Ghysdael J., Stehelin D., Befort N., Remy P.; "Isolation of two different c-ets-2 proto-oncogenes in Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 170 POINTED.
366 446 ETS-DOMAIN.
472 AA; 53894 MW; E0E8088B5E6BF111 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.2%; Score 32.5; D
Best Local Similarity 58.3%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 18:4603-4604(1990).
                                                                                                                                                                                                                               Nucleic Acids Res. 20:371-371(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                              TISSUE-OOCYTE;
MEDLINE-90356411; Pubmed-2201951;
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PIR; $28824; $28824.
HSSP, P14921; 2STT.
TRANSFAC; T02041; ...
INCEPPIC; IPR000418; Ets.
INCEPPIC; IPR00341; HSF_ETS.
INCEPPIC; IPR033118; SAM_PNT.
                                                                                                                                                                                                                                                               SEQUENCE OF 121-472 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00464; EESDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
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DOMAIN 87 170 I
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                                                                                                          Xenopodinae; Xenopus.
                                                                                                                          NCBI_TaxID=8355;
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SEQUENCE
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1;

Gaps

Indels

1 EEVVPXGMD-YS 11

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49 EQAVPTGLDSYS 60
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Search completed: June 10, 2003, 13:40:19 Job time : 5.5 secs

· us-09-909-164-8.rspt

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:30:25 ; Search time 25.7857 Seconds (without alignments) 87.898 Million cell updates/sec Run on:

US-09-909-164-8 Title: Perfect score:

54 1 EEVVPXGMDYS 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database :

SPTREMBL_21:*
1: Sp_archea:*
2: sp_bacteria:*
3: sp_tung:*
4: sp_tuman:*
5: sp_tung:*
5: sp_tung:*
5: sp_mammal:*
5: sp_mammal sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* sp_rodent:* sp_virus:* sp_plant:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

	Description	Q12479 saccharomyc 030260 archaeoglob 080266 fusobacteri 022081 citrus unsh 022096 citrus unsh 0804568 arabidopsis 090547 arabidopsis 090547 arabidopsis 090510 arabidopsis 043010 oryza sativ	Q99904 eriocheirs Q8xpa8 clostridium O52367 rhizobium t Q9xxk4 caenorhabdi Q9a382 caulobacter
SUMMARIES	. QI	Q12479 Q30260 Q30260 Q202081 Q22096 Q9W568 Q9C9T7 P93782 Q9SN30 Q43010	QQQQQ4 Q8XPA8 O52367 Q9XVK4 Q9A382
	DB	100 110 110 110 110 110 110 110 110 110	16 17 19 19 19 19 19 19 19 19 19 19 19 19 19
	% Query Match Length DB	156 363 363 341 341 4452 1047 11083 11083	219 219 253 298 425 433
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	Score	4 w w w w w w w w w w w w w w w w w w w	
	Result No.	1100843701	112 13 14 15

09yfi3 aeropyrum p 052680 escherichia 08xx15 ralstonia s 09b5p46 carcinus ma 09u6a3 callinectes 017704 caenorhabdi 052673 escherichia 05266 escherichia 077146 methanobact 098x29 rhizobium l	omo sapien rosophila rosophila royra sati royranana archaeoglo archaeoglo archaeoglo rhizobium richoderma	095cini lactococcus 095zy8 neisseria m 092sy4 arabidopsis 09fik8 arabidopsis 095zy3 arabidopsis 09n5al arabidopsis 09m5al arabidopsis 09m5al arabidopsis 09m5al arabidopsis 09m5al arabidopsis 090xy3 arabidopsis 0910y8 pseudomonas 074056 cenarchaeum 09xx4 cenis famil 097vx9 sulfolobus	Q97x12 sulfolobus Q8sw14 encephalito Q9de16 bracipydanio 065890 cyclotella 000404 homo sapien Q40129 lycopersico Q9p916 pyrobaculum Q9c610 arabidopsis Q97yb8 sulfolobus Q97yb8 sulfolobus Q97yb8 sulfolobus Q97ye9 sulfolobus Q91ye9 homo sapien Q97tv4 sulfolobus Q91w4 sulfolobus Q91w4 sulfolobus Q91w4 sulfolobus Q91w4 sulfolobus Q91ys sulfolobus Q94ys sulfolobus Q94br8 simian foam	
09YFI3 552680 08XZL5 08XZL5 595P46 5906A3 117704 027146 027146	3019.17 99VSY8 09SBB8 08SU5 08U7J0 09YET8 029920 029451 029451 098FXI	09CIN1 09JSY4 09JSY4 09JSY4 09JSY4 09JSY3 09JSY3 09JOX8 074056 09JSYR9 09JVS 09JUS 09JUS 09JUS 09JUS 09JUS 09JUS 09JUS	097XJ2 088WL4 088WL4 008WL4 00658916 0010404 001129 099916 097189 097787 097787 097787 097774 099788 099888	
114 115 116	0.00000000	0377 6 000000	F 80 0F 80 FF FFFF RIBIT	
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114 22 22 22 24 25 24 24	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	00000000000000000000000000000000000000	

ALIGNMENTS

	PRT; 156 AA.		01, Created)	Last sequence update)	Last annotation update)	
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	PRELIMINARY		(TrEMBLrel.	(TrEMBLrel.	(TrEMBLrel.	
LT 179	12479	012479;	01-NOV-1996	01-NOV-1996 (TrEMBLrel	01-JUN-2002 (TrEMBLrel.	ORF YOR013W.
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;
Maddine-980494343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Kichardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischann R.D., Ougkerbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M.,
                                                                                                                                                                                                                                                                                                                                        STRAIN=FY1679;
MEDLINE-94019318; PubMed-8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Saccharomyces cerevisiae (Baker's yeast).
Sukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLING-94166519; PubMed-7764548;
MEDLING-94166519; PubMed-7764548;
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
Molecular cloning of a gene, DHSI, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Blochem. 58:391-395(1994).
EMBL: 784920; CAA69201.1; ---
SCD; SO005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              "CYC2 encodes a factor involved in mitochondrial import of yeast cytochrome c."; Mol. Cell. Biol. 13:6442-6451(1993).
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0
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                                                                                                      De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                            Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                   De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
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Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AF2411.
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                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      STRAIN=FY1679;
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Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosida II; Sapindales; Rutaceae; Citrus.
NCBL_TAXID-55188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rapatral V., Anderson I. Tranova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Wallunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586."; J. Bacteriol. 184:2005-2018(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                         Query Match 70.4%; Score 38; DB 17; Length 363; Best Local Similarity 54.5%; Pred. No. 12; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 16; Length 1063;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ligase; Complete proteome.
SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;
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                                                                                                                                                                                        0E976EAE788F4803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                QBRGB6;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1063 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteriu; Fusobacterium.
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                                                                                                                                  InterPro; IPR002103; Bac_luciferase.
Pfam; PF00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE7
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01-JAN-1998 (TrEMBLrel. 05, Greated)
01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last ann
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STRAIN=ATCC 25586;
MEDLINE=21886394; Pubmed=11889109;
                                                                                                     EMBL; AE001109; AAB91255.1; -.
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                       TIGR; AF2411;
                                  Venter J.C.;
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O22081
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NCBI_TaxID=3702;
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        RESULT 6
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                                                                                                                                    STRAIN-CV. MIYAGAWA-WASE; TISSUE-JUICE SACS AND SEGMENT EPIDERMIS; Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; "Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; Plant Sci. 140:169-178(1999).
EMBL: AB006319; BAA23215.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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           SEQUENCE FROM N.A.
STRAIN-CV. MIXAGAWA-WASE; TISSUE-JUICE SACS AND SEGMENT EPIDERMIS;
MEDLINE-96439842; PubMed-8842155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Komatsu A., Takanokura Y., Omura M., Akihama T.; "Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
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                                               Kometsu A., Takanokura Y., Omura M., Akihama T.; Takanokura Y., Omura M., Akihama T.; Cloning and molecular analysis of CDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
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Last annotation update)
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                                                                                                                                                                                                                                                                                   66.7%; Score 36; DB 66.7%; Pred. No. 29; ive 2; Mismatches
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MEDLINE-96439842; PubMed-8842155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sucrose-phosphate synthase (Fragment)
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01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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EMBL; AB006660; BAA22071.1; -.
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228 VIPPGMDFS 236
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Matches 6; Conserv
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SEQUENCE
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STRAIMCY. COLUMNIA;

MEDLINE-21016719; PubMed=11130712;

MEDLINE-21016719; PubMed=11130712;

Mittee O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Mittee O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Feng B., Fujii C.Y.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A Kim C.J., Kroo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Milischer J., Miranda M., Niguyen M., Niguran W.C., Osborne B.I.,

Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
                                                                                                                                                                                                                                                                                                                                        Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Kazilin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakuzai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                        Arabidopsis thaliana (Mouse-ear Cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR419606; AR4131931; --
InterPro; IPR002471; Prol.endopep_ser.
InterPro; IPR000379; Ser_estrs_site.
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SEQUENCE 452 AA; 49682 MW; A159955B21742C4A CRC64;
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01-MAR-2002 (TrEMBLrel. 17, Last sequence update)
Hypothetical 50.6 kDa protein.
F25522.17.
                                                              01-WAR-2002 (TrEMBLrel. 20, Last sequence update) 01-UUN-2002 (TrEMBLrel. 21, Last annotation update) At1g73750/F25F22_17.
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                                                  01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity 70.v-
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PRELIMINARY;
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"Differential Expression of Two Genes for Sucrose-Phosphate Synthase
in Sugarcane: Molecular Cloning of the cDNAs and Comparative Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Saccharum.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 36; DB 10; Length 460; 70.0%; Pred. No. 41; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Gene Expre ssion."; submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. EMBL; ABO0137; BAA19241.1; InterPro: IPR001296; Glycos_transf_1. Fram: PF00534; Glycos_transf_1; 1. Glycos_transf_are. From: From:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1047 AA; 116379 MW; DOEDB34961E1D83D CRC64;
                                                                                                                                           EMBL; AC012679; AA652073.1; -.
InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR000379; Ser_estrs_site.
PROSITE; PS007008; PRO_ENDOPEP_SER; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 460 AA; 50564 MW; E94B27B5C4B249EC CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
F28M11.40 OR AT4G10120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1047 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                     Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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414 VIPPGMDFS 422
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Best Local Similarity
7; Conserve
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                                                                                         thaliana.
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Plant Sci. 112:207-217(1995).
-!- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.
-!- PATHWAY: ANAEROBIC GLYCOLSIS; FINAL STEP.
-!- SUBMINIT: HOWOTETRAMER (BY SIMILARITY).
EMBL; D45890; BAA08304.1; -.
InterPro; IPR001296; Glycos_transf_1.
InterPro; IPR00157; L_LDH.
Pfan; PP00534; Glycos_transf_1; 1.
PROSITE; PS00064; L_LDH: 1.
Glycolysis; NAD; Oxidoreductase.
SEQUENCE 1084 AA; 119417 MW; 4D0D79AFEDD2F92B CRC64;
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                             Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza,
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Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Fujimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1084;
                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (RAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049487; CAB39764.1;
EMBL; AL161516; CAB78135.1;
EMBL; AL161516; CAB78135.1;
EMBL; AL161516; CAB78135.1;
FinterPro; IPR001296; Glycos_transf_1.
Figm; PF00534; Glycos_transf_1.1
Glycosyltransfearaev; Transfearaev.
SEQUENCE 1083 AA; 122688 MW; EFC126FCA2137BB1 CRC64;
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66.7%; Pred. No. 1.1e+02;
66.7%; Pred. No. 1.1e+02;
                                                                                                                EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
L-lactate dehydrogenase (EC 1.1.1.27) (LDH).
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Matches 6; Conservative
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hes 6; Conservative
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483 VIPPGMDFS 491
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[1]
SEQUENCE FROM N.A.
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                 SEQUENCE FROM N.A.
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Q43010;
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RESULT 11

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                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoldeae, Oryzeae, Oryza.
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Weibrauch D., Towle D.W.;
"Na+/H+-exchanger and Na+/K+/2Cl- -cotransporter are expressed in gills of the euryphaline Chinese crab Eriocheir sinensis.";
Comp. Biochem. Physiol. 126:S158-S158 (2000).
EMBL: AF301160; AAG39938-1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STAIN-CV. NIPPONBARE:
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Suparia sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0678F11.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003437; BAB86107.1;
SEQUENCE 1100 AA; 121170 MW; 084F4604BA389CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 10; Length 1100;
Pred. No. 1.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Na+/K+/ZCl-cotransporter (Fragment).

Eriocheir sinensis (Chinese mitten crab).

Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
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Pred. No. 29;
1; Mismatches 1; Indels
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative sucrose-phosphate synthase.
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PRT; 1100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-MJUN-2002 (TrEMBLrel. 21, Last ann
Hypothetical protein CPE0057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
66.7%;
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Atches 6; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 VIPPGMDFS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=39947;
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SEQUENCE
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-i- COFACTOR: ZINC (BY SINTLARITY:
-i- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                    Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shina T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
NCBI_TaxID=398;
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Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 16; Length 253;
Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              il protein; Complete proteome.
253 AA; 27714 MW; 814DF79D3E0D7486 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Aryl-alcohol dehydrogenase homolog (Fragment).
                                                                                                                                                                                                                                                                               flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, ACO03185; BAB79763.1;
InterPro; IPR000205; NAD_binding.
InterPro; IPR000594; ThiF_domain.
Pfam; PF00899; Thif; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 27714 MW; 814DF79D3E0D7486 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 AA.
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HSSP; P07846; 1SDG.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR0002085; Adh_zn_family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.8%;
50.0%;
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Best Local Similarity 50.0°
Matches 5; Conservative
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Best Local Similarity 50...
For 5; Conservative
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EEIIPDDVDY 117
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Plasmid pRtrCFN299a.
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STRAIN=13 / TYPE A;
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                                                                                                                                                                                   PubMed=11792842;
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Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Nierman W.C., Newton A., Stephens C., Phadke N.D.,
Deboy R.T., Dodson W.C., Newton A., Stephens C., Phadke N.D.,
Ely B.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
HSSP: P41052; ILTM.
                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.8%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 61; 2; Indels 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                       Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                              Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
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                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pertidoglycan-binding protein, putative.
                   425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 AA.
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EMBL, 281109; CAB03241.1; -
InferPro: IPR000719; ENL_pkinase.
ProDom; PD00069; pkinase; 1.
ProDom; PS00001; EUL_pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                               Created)
                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01471; PG_binding_1; 1.
                                      01-NOV-1999 (TrEMBLrel. 12, Cr
01-NOV-1999 (TrEMBLrel. 12, La
01-NAR-2002 (TrEMBLrel. 20, La
R10D12.10 protein.
R10D12.10.
Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Transferase.
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                              SEQUENCE FROM N.A.
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                              09XVK4;
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09A382;
              Q9XVK4
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Q9XVK4
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                                            Gaps
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Punahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Kl.";
BMBL, AP000088; BAA79178.1;
HSSP; P00782; 258T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Escherichia.
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        DB 16; Length 433; 62;
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                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
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SEQUENCE 440 AA; 44680 MW; E43E6E2174B6F07E CRC64;
                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last annotation update)
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                                         2; Mismatches
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              64.8%; Score 35; 54.5%; Pred. No.
                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
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PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000209; Peptidase_S8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00082; Peptidase_S8; 1. PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ECOR-50;
Wang Y.-D., Zhao S., Hill C.W.;
                                                                                                                                                                                                                                                                                      Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
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01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-DEC-2001 (TrEMBLrel. 19,
Core protein (Fragment).
Query Match
Best Local Similarity 54.5.
                                                                                            266 EVILPPGFDYS 276
                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                   1 EEVVPXGMDYS 11
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                                                                                                                                                              Q9YFI3
Q9YFI3;
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052680
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"Cloning and sequencing a Na+/K+/2cl- cotransporter from gills of the euryhaline blue crab Callinectes sapidus.";
Am. Zoologist 38:114A-114A(1998).
"Sequence and expression analysis of the Na+/K+/2Cl- cotransporter in the euryhaline crabs Callinectes sapidus and Carcinus maenas."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AV03548, AAK62044.1; InterPro; IPR002293; AA/rel_prmeasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Callinectes sapidus (Blue crab).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Callinectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.8%; Score 35; DB 5; Length 1031; 75.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                            64.8%; Score 35; DB 5; Length 745; 75.0%; Pred. No. 1.1e+02; ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-GILL;
Substance D.;
Substance (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF190129; AAF05702.1; -
InterPro; IPR002293; AA/rel_prmeasel.
InterPro; IPR004842; KCl_cotransport.
InterPro; IPR002443; NaKCl_transport.
InterPro; IPR002443; NaKCl_transprter.
FIGNRAMS; TIGREAMS; TIGREAMS; TIGREAMS; TIGREAMS; 113699 MW; F67773021AB05D71 CRC64;
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                                                                                                                                                                           745 AA; 81249 MW; 08AE2D3E1F70C7BE CRC64;
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                      Pfam; PF00324; aa_permeases; 1.
NON TER 1
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01-JAN-1998 (TrEMBLrel. 05,
01-NOV-1998 (TrEMBLrel. 08,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Na+/K+/2Cl-cotransporter.
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                                                                                                                                                                                                                                  Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                               625 VPQGLDYS 632
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SEQUENCE
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                                                                                                                                         NON_TER
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017704
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 21
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                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arlat M., Billault A., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2002 (TrEMBLrel. 20, Created)
1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable SUBSTATE-binding periplasmic (PBP) ABC transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.8%; Score 35; DB 16; Length 517; 66.7%; Pred. No. 76;
                                                                                                                          64.8%; Score 35; DB 2; Length 511; 60.0%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                               2; Indels
         "Rhs elements comprise three subfamilies.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF044506; AAC62388.1; -.
NON_TER 511 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 AA; 57349 MW; 861EE836F645F2DA CRC64;
                                                                                        511 AA; 55877 MW; C85402569450DBFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Na+/K+-ZCl.-cotransporter (Fragment).
Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             745 AA.
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                                                                                                                                                                                                                                                                                                                                  517 AA
                                                                                                                                                               2; Mismatches
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MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AL646064, CAD15082.1; -. InterPro, IPR000914; SBP_bac_5. Pfam; PF00496; SBP_bac_5; 1.
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Weihrauch D., Towle D.W.;
                                                                                                            Query Match
Best Local Similarity 60.0%
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Matches 6; Conservative
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381 EQVNPEGLDY 390
                                                                                                                                                                                                    1 EEVVPXGMDY 10
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316 VVPQGVDYA 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=305;
                                                                      NON_TER
SEQUENCE
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Pred. No. 2.4e+02; 2; Mismatches 2; Indels

60.08;

Best Local Similarity 60.0 Matches 6; Conservative

382 EQVNPEGLDY 391

1 EEVVPXGMDY 10

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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Caratton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
John M., Gershaw J., Kirsten T., Hillier L., Jier M., Johnston L.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston B.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Wang Y.D., Zhao S., Hill C.W.;
"Rhs elements comprise three subfamilies which diverged prior to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacterlaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.8%; Score 35; DB 2; Length 1410;
                                                                                                Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 281486; CAB03994.1;
EMBL; 278015; CAB01994.1;
EMBL; 278015; CAB01937.1;
EMBL; Z81486; CAB01437.1;
EMBL; Z81486; CAB01437.1;
InterPro; IPR001201; PAP_22A_core.
InterPro; IPR001201; PAP_22A_core.
InterPro; IPR0003101; PAP_21A_CORE.
InterPro; IPR0003102; Unk_Met10.
Pfam; PR02475; Met_10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1150 AA; 133001 MW; BA130A251C1A12F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acquisition by Escherichia coli.";
J. Bacteriol. 180:4102-4110(1998).
EMBL; APO44503; AAC22478.1; -.
InterPro: IPR001826; RHS.
Pfam: PP03527; RHS; 1.
PRINTS; PR00394; RHSPROTEIN.
SEQUENCE 1410 AA; 158739 MW; 39ECB9FRC97FCB15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1410 AA.
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562 VLPVGIDYS 570
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Escherichia coli.
                                 NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                   Wang Y.D., Zhao S., Hill C.W.; "Rhs elements comprise three subfamilies which diverged prior to
                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
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                                                                                                                                                                                                                                                                             acquisition by Escherichia coli.";

EMBL; AFC44501; A672471.1;

EMBL; AFC44501; A672471.1;

InterPro; IPR000130; Zn_MTpeptdse.

FRAN; PR03527; RHS; 1.

PRNNTS; PR00344; RHSSPOFIN.

PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.

SEQUENCE 1420 AA; 159215 MW; E7851E4D48740621 CRC64;
                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
                                    PRT; 1420 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                    MEDLINE=98361897; PubMed=9696756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative membrane protein.
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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es 6; Conserv
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                                                                                                                             Escherichia coli.
                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                            Core protein.
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027146;
                               052666
RESULT 24
052666
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DR InterPro; IPR001434; DUF11.

DR Pfam; PF0145; DUF11; 9.

KW Complete proteome.

SQ SEQUENCE 1474 AA; 153713 MW; 11D4D27BD86255F0 CRC64;

Query Match

64.8%; Score 35; DB 17; Length 1474;

Best Local Similarity 55.6%; Pred. No. 2.5e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps

QY 2 EVVPXGMDY 10

1238 DVLPAGLDY 1246
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Search completed: June 10, 2003, 13:46:32 Job time : 28.7857 secs

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June 10, 2003, 13:24:45 ; Search time 31.3571 Seconds
(without alignments)
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 75 summaries
                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1 EEVVPXGMSYS 11
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A. SIDS2/gcgdata/geneseq/genesegp-embl/AA1980.DAT:*
SIDS2/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*
SIDS2/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*
SIDS2/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*
SIDS2/gcgdata/geneseq/genesegp-embl/AA1983.DAT:*
SIDS2/gcgdata/geneseq/genesegp-embl/AA1984.DAT:*
SIDS2/gcgdata/geneseqy-embl/AA1984.DAT:*
SIDS2/gcgdata/geneseqy-embl/AA1986.DAT:*
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SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:*
SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* A_Geneseq_101002:* 10: 112: 113: 114: 116: 119: 220: 220: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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24	Result		Query	Query			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	No.	Score	Match	Length	B :	ID	Description
	-	50	96.2	11	23	ABB80521	Hepatitis C virus
	7	20	96.2	11	23	ABB80522	Hepatitis C virus
	e	20	96.2	11	23	ABB80525	Hepatitis C virus
Ç	4	20	96.2	11	23	ABB80526	Hepatitis C virus
٢	2	20	96.2	11	23	ABB80559	٠,
1	9	50	96.2	11	23	ABB80563	۲,
	7	50	96.2	11	23	ABB80564	Hepatitis C virus
-	8	20	96.2	11	23	ABB80565	
	6	20	96.2	11	23	ABB80566	Hepatitis C virus
	10	20	96.2	11	23	ABB80567	Hepatitis C virus

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ALIGNMENTS

ABB80521 standard; peptide; 11 AA. RESULT 1 ABB80521 ID ABB8

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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0.0011;
hes 0;
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100.0%; Pred. No. ...
0; Mismatches
                                                                 /note= "N-terminal acetyl"
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                                                                                                                                'note= "D-form residue"
                                       Location/Qualifiers
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                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US23169.
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Best Local Similarity 100.
Matches 11; Conservative
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            Synthetic.
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                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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                                                                                                                                                                                       /note= "N-terminal acetyl"
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                                    08-OCT-2002 (first entry)
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Best Local Similarity 100.
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            ABB80521;
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Length 11; Indels

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21-JUL-2000; 2000US-220101P.
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Matches 11; Conservative
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                                                                                 Levy OE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
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                                                                                                                                                                                                                                                                                                                                    Score 50; DB 23; Length 11;
Pred. No. 0.0011;
0; Mismatches 0; Indels
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         /note= "D-form residue"
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100.0%; Pre
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                                                                                    19-JUL-2001; 2001WO-US23169.
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Les 11; Conservative
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 Misc-difference 8
                                                                                                                                                                                                                                                                                                                    11 AA;
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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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Pred. No. 0.0011;
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100.0%; Pre
                                                                                                                     Brunck TK;
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21-JUL-2000; 2000US-220101P.
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Synthetic
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                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\sf C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
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Pred. No. 0.0011;
0; Mismatches 0; Indels
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/note= "C-terminal amide"
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                                               Brunck TK;
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100.0%; Pre
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                                                                                                                                                                  Claim 17; Page 65; 69pp; English.
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Matches 11; Conservative
                                              Levy OE,
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               (CORV-) CORVAS INT INC
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                                                                         WPI; 2002-361643/39.
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                                                                                                                                       virus protease -
                                                                                                                                                                                                                                                                                                                     11 AA;
                                          Lim-wilby M,
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                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                              pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Leucyl carbonyl forming keto-amide linkage with residue 7\,\mathrm{m}
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                         96.2%; Score 50; DB 23; Length 11; 100.0%; Pred. No. 0.0011; ive 0; Mismatches 0; Indels
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Claim 17; Page 65; 69pp; English.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                      11 AA;
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Levy OE,
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Matches 11; Conserv
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                                                                                                                    virucide.
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        RESULT 9
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                                      Gaps
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                Score 50; DB 23; Length 11;
Pred. No. 0.0011;
0; Mismatches 0; Indels
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100.0%; Pred. No. v.
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nes 11; Conservative
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                                                          1 EEVVPXGMSYS 11
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                          Local Similarity
nes 11; Conserv
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11 AA;
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 Sequence
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46
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ABB80566 standard; peptide; 11 AA
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcomnide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                        /note= "Alpha-propynyl-glycinyl-carbonyl residue forming a keto-amide linkage with residue 7"
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Matches 11; Conservative
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                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
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/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 23; Length 11;
Pred. No. 0.0075;
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Brunck TK;
                                                                                                                                                                                  Claim 17; Page 64; 69pp; English.
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Lim-wilby M, Levy OE,
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    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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Pred. No. 0.0075;
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                                   Claim 17; Page 64; 69pp; English.
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virus protease
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with RCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                   Gaps
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                                                                                                                             Score 46; DB 23; Length 11;
Pred. No. 0.0075;
0; Mismatches 1; Indels
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                                                                                                                     Query Match
Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                         ABB80527;
                                                                                                                                                                                                                         virucide
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                                                                     RESULT 18
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                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C professe -
  is useful for treating disorders associated with hepatitis C virus
                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
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                                                     Score 46; DB 23; Length 11;
Pred. No. 0.0075;
0; Mismatches 1; Indels
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illarity 90.9%; Pred. No. 0.012;
Conservative 0; Mismatches 1
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11
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                                                                                                                                                                                                            ABB80523 standard; peptide; 11 AA.
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                                                        88.5%;
90.9%;
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                                                                                    Conservative
                                                                                                              1 EEVVPXGMSYS 11
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Best Local Similarity
Matches 10; Conserv
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nes 10; Conserv
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                                                                                    datches
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide compound having hepatitis C virus protease inhibitory .ty useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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Pred. No. 0.012;
0; Mismatches 1; Indels
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11
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                                                                                                                                  ABB80527 standard; peptide; 11 AA.
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Best Local Similarity 90.9
Matches 10; Conservative
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"Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                           "N-terminal acetyl"
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                                                                                                                                                 "C-terminal amide"
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                                   Location/Qualifiers
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                                                                                                                                                                        WO200208251-A2
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Modified-site
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          Synthetic
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Best Local
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                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis \mathsf{C}
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                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #15.
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0; Mismatches
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/note= "C-terminal amide"
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90.9%;
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              ABB80535;
                                                                                                     virucide.
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(CORV-) CORVAS INT INC.
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virucide.
         31-JAN-2002
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                                                                                                                                                                                                                                        peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis {\tt C}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 23; Length 11;
Pred. No. 0.012;
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          /note= "D-form residue"
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90.9%;
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hes 10; Conservative
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                                                                                                                                                                                          Lim-wilby M, Levy OE,
                                                                                                                                                                  (CORV-) CORVAS INT INC
                                                                                                                                                                                                                   WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                      virus protease -
Misc-difference 8
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                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80558 standard; peptide; 11 AA.
                                                                                                                                                                   Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 65; 69pp; English.
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90.9%;
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19-JUL-2001; 2001WO-US23169.
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Matches 10; Conservative
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                                                                                                                                                                   Lim-wilby M, Levy OE,
                                                                                                              (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                          peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis {\sf C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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11
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                   Lim-wilby M, Levy OE, Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80560 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residue 7"
                                                                                                                                                                     Claim 17; Page 65; 69pp; English.
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORV-) CORVAS INT INC
                                                       WPI; 2002-361643/39
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                  virus protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\cal C}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 23; Length 11; Pred. No. 0.012;
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                                                                                                                     Claim 17; Page 65; 69pp; English.
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.5
Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         11 AA;
                                                                 virus protease
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CC virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A CC pharmaceutical composition comprising the peptide as an active ingredient CC is useful for treating disorders associated with hepatitis C virus.

XX

SQ sequence 11 AA;

Query Match

Bast Local Sinilarity 90.9%; Pred. No. 0.019;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DD 1 EEVVPXCMSXS 11

DD 1 EEVVPXCMSYS 11
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Search completed: June 10, 2003, 13:39:08 Job time: 32.3571 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:45 ; Search time 9.64286 Seconds (without alignments)
33.564 Million cell updates/sec

Title: US-09-909-164-9
Perfect score: 52
Sequence: 1 EEVVPXGMSYS 11

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database : Issued_Patents_AA:* 1: /cgn2_6/ptodata/1/laa/5A_COMB.p

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 73, Appl	Sequence 236, App	236,	oce	õ	Patent No. 5177197			99		(1	4	4	4	7, 4	21,		21,	21,	22,	22,	à	22,		Sequence 6, Appli	Sequence 4, Appli	Sequence 4, Appli
SUMMAKIES	ID	US-09-228-986-73	-23	US-08-871-355A-236	US-09-201-945-236	5177197-51	5177197-1	5177197-30	-952-6	US-09-521-650-66	US-09-168-888-66	US-08-580-988A-23	US-08-460-694-4	US-08-460-744-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	US-08-246-361A-21	US-08-463-772-21	PCT-US93-05000-21	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22	US-08-464-517-6	US-08-463-772-6	US-08-246-361A-4	PCT-US93-05000-4
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	& Query Match Length DB	947	45	45	45	65	410	1394	10	10	10	102	152	152	152	173	189	189	189	189	236	236	236	236	280	280	289	285
	% Query Match	65.4	63.5	63.5	ω,	63.5	63.5	63.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	H.							61.5		61.5		61.5	H
	Score	34	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
	Result		2	ım	4	'n	G	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

equence 23, aguence 20, aguence 19, aguence 19, aguence 20, aguenc	sequence 7, Appl. sequence 7, Appl. sequence 7, Appl. sequence 14, Appl. Sequence 2, Appl. sequence 2, Appl. sequence 23, Appl. sequence 68, Appl. sequence 68, Appl. sequence 11, Appl. sequence 1, Appl. sequence 2, Appl.
PCT-US93-0500 US-08-464-517 US-08-246-3611 US-08-246-3611 US-08-246-3617 PCT-US93-0500 US-08-460-694 US-08-460-694 US-08-464-517 US-08-464-517 US-08-464-517 US-08-464-517 US-08-464-517 US-08-463-772 US-08-463-772 US-08-463-772 US-08-463-772 US-08-463-772 US-08-463-772 US-08-463-772 US-08-463-772 US-08-947-492 US-08-947-492 US-08-947-492 US-08-947-492 US-08-947-492 US-08-9770-761 US-08-770-761 US-08-770-761 US-08-770-761 US-08-770-761	US-08-9 US-08-08-08-08-08-08-08-08-08-08-08-08-08-
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8000118m4506V8000118m444444444600118m45000000000000000000000000000000000000	57 59 60 60 60 60 60 70 70 70 70 70 70 70

ALIGNMENTS

RESULT 1
US-09-228-986-73
US-09-228-986-73
Sequence 73, Application US/09228986
Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Selected from Plant Cells
TITLE OF INVENTION: Compositions Selected from Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT PRILIG DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 73
LENGTH: 947
TYPE: PRY
TYPE: PRY
TYPE: PRY
TYPE: PRY
GRANISM: Phius radiata
US-09-228-986-73

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Ouery Match 65.4%; Score 34; DB 4; Length 947; Best Local Similarity 66.7%; Pred. No. 1e+02; Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 5.1;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CAPRICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                Sequence 236, Application US/08637759B
Fatent No. 5876931
GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCE: 501
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-871-355A-236
Sequence 236, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
INMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 4.5.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY_AGBWT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/POCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
EENTH: 45 amino acids
wvor: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: use
ZIP: 30309-3450
COMPUTER READABLE FORM:
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                                                                                                 686 VMPSGISYS 694
                                                                        3 VVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         Georgia
                                                                                                                                                                                                                                                                                                                                                                                    CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                RESULT 2
US-08-637-759B-236
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Score 33; DB 3; Length 45;
Pred. No. 5.1;
1; Mismatches 3; Indels
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: U9-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION TARA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: RPMS 101 CON
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8794
INFORMATION FOR SEQ 1D NO: 236:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 236, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES:
ADDRESSEE: Patrea L. Pabst
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
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COMPUTER: IBM PC compatible
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60.0%;
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ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSY 10
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Best Local Similarity
Local 6; Conserva'
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                                                                               Georgia
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: USA
                                                          CITY: Atlanta
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                                                                                                   USA
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                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KANZAKI, TETSUTO:OLOFSSON, ANDERS; MOREN, ANITA;
"WERNSTEDT, CHRESTER HELLMAN, ULE; MIYAZONO, KOHEI; CLAESSON-WELSH,
"LELDIN, CARL-HENRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      **HERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, ANDERS; MOREN, ANITA; LENA; HELLLIN, CARL-HERRIK TILEDEN, CARL-HERRIK TILEDEN, CARL-HERRIK TILEDEN, CARL-HERRIK SEQUENCE EXPRESSING; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.5%; Score 33; DB 6; Length 410; Best Local Similarity 45.5%; Pred. No. 63; Matches 5; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.5%; Score 33; DB 6; Length 65; 45.5%; Pred. No. 7.8; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 4
Pred. No. 5.1;
1; Mismatches
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FILING DATE: 27-FEB-1990
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APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                              REFERENCE/DOCKET NUMBER: RPMS 101
                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
                                                           31,284
                                                                                                                                                                                                                                                                                                                                                                        63.58;
60.08;
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                     LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.5
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                    linear
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Best Local Similarity
Matches 5; Conserv
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5177197-51
;Patent No. 5177197
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5177197-1
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5177197-51
                                                                                                                                                                                                                                                                                                                                US-09-201-945-236
                                                                                                                                                                                                                                                                    TOPOLOGY:
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APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
TITLE OF INVENTION: Other Enzymes and the Use Thereof
CURRENT FILING DATE: 1999-07-21
EARLIER FILING DATE: 1999-07-21
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SEQ ID NO 66
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                               APPLICANT: KANZÁKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
WERNSTEDT, CHRISTER:HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
LENA;HELDIN, CARL-HENRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%; Score 33; DB 6; Length 1394; 45.5%; Pred. No. 2.6e+02; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.5; 2; Indels ive 3; Mismatches 2; Indels
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US-09-521-650-66
; Sequence 66, Application US/09521650
; Patent No. 6315429
; Patent No. 6315429
; APPLICANT: Weber, Eckard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 66, Application US/09357952 Patent No. 6248904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 45...
5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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399 KEICPGGMGYT 409
                                           399 KEICPGGMGYT 409
1 EEVVPXGMSYS 11
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                                                                                                                                        5177197-30
;Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQ ID NO:30:
; LENGTH: 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-357-952-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                               5177197-30
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Sequence 23, Application US/08580988A

Patent No. 5856161

GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
CORRESPONDENCE BEDISHIN A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Patent No. 5888655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD1 Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 2;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILLING DATE: January 3, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
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60.0%;
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LENGTH: 102 amino acids
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or: internal
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MOLECULE TYPE:
DESCRIPTION: protein
                                      1 DDIVPCSMSY 10
              1 EEVVPXGMSY 10
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORIGINAL SOURCE:
US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
                                                                                                                                                   US-08-580-988A-23
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                                                                                  TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the TITLE OF INVENTION: Use Thereof CURRENT PRINCE: 1735 029002

FILE REFRENCE: 1735 029002

CURRENT APPLICATION NUMBER: US/09/521,650

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: US/0601,582

EARLIER PILING DATE: 1998-10-09

EARLIER FILING DATE: 1997-10-10

EARLIER FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 142

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
TITLE OF INVENTION: Hear Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Soreening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Soreening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Soreening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Soreening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Soreening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Soreening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Soreening Assays for Caspases and Other Enzymes and the
FAILER FILING DATE: 1998-10-09
CURRENT FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-3-03
NUMBER OF SEQ ID NOS: 142
SEQ ID NO 66
LENGTH: 10
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US-09-521-650-66
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US-09-168-888-66
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Patent No. 6342611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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50.0%;
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                     APPLICANT: Keana, John F.W. APPLICANT: Drewe, John A. APPLICANT: Zhang, Han-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.5
Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0°
Matches 5; Conservative
APPLICANT: Cai, Sui Xiong
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1 DDIVPCSMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTR:

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
TILNG PATE: 02-UUN 1995
TILNG PATE: 02-UUN 1995
                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02/09/1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCONALHY. Evelyn H.
REGISTREATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Arnold, Andrew TITLE OF INVENTION: PRAD1 Cyclin and its CDNA NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REPERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6107541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: '202-371-2540 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-460-694-4
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                          Washington
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                                                                                     COUNTRY:
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Pred. No. 33;
1; Mismatches 3; Indels
                                                                                                                         Score 32; DB 3; Length 152;
Pred. No. 33;
                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ARNOLD, ANDREW TITLE OF INVENTION: Prad1 Cyclin and Its CDNA NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/07667711B Patent No. 6110700 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08193977
Patent No. 5625031
GENERAL INFORMATION:
APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PEPTIDE INH
                                STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%;
60.0%;
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152 amino acids
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not relevant
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Best Local Similarity 60.v
                                                                                                                                              3est_Local Similarity 60.0
4atches 6; Conservative
                                                                     ; MOLECULE TYPE: peptide US-08-460-744-4
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                   amino acid
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                                                                                                                             Query Match
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 P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN PAPILLOMAYIRUS E7 ONCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08464517
Fatent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: Boston
CITY: Boston
STATE: MA
ZIP: O2109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 173; 38;
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                                                                                                               Score 32; DB Pred. No. 38; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
                                                             STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/464,517
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: P34CDC2 C TITLE OF INVENTION: PAPILLOMA NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS: ADDRESSE: RED & ROBINS STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0°
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-193-977-7
                                                                                                                                                                                                                                                                                                                                                                                           single
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                                                                                                                                                                                                                                                                                                                                                                                                      linear
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PRIOR APPLICATION NURBER: US 07/701,514

**PLING TOREST IS-W-1991

**ATTORNEY ACREST INFORMATION:
**NAME: NARLENGE W. VINCENT

**NAME: NARLENGE W. VINCENT

**NAME: NARLENGE W. VINCENT

**NAME: NARLENGE W. VINCENT

**TELERRANTION NURBER: 36,709

**NAME: NARLENGE W. VINCENT

**TELERRANTION NURBER: 36,709

**NAME CHARACTERISTICS: 11:
**SEQUENCE CHARACTERISTICS: 21:
**SEQUENCE CHARACTERISTICS: 3: Indels 0; Gaps

**NAMECH: 189 anino acids

**SEGUENCE CHARACTERISTICS: 3: Indels 0; Gaps

**OURTY NARLENGE W. SECUENCE: 3: Indels 0; Gaps

**PRIOR APPLICATION NUMBER: 105 0
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                              Sequence 21, Application US/08463772
Patent No. 6065501
APPLICANT: BEACH, David H.
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 3; Length 189;
Pred. No. 42;
1; Mismatches 3; Indels
                                                                       61.5%; Score 32; DB 2; Length 189; 60.0%; Pred. No. 42; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/463,772
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                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
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60.0%;
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Best Local Similarity 60.0°
                                                                     Query Match 61.5
Best Local Similarity 60.0
Matches 6; Conservative
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TOPOLOGY: linear
; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-246-361A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-463-772-21
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MEDIUM TYPE: Floppy
                                                                                                                                                   1 EEVVPXGMSY 10
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                                                                                                                                                                        amino acid
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CITY: Boston
STATE: MA
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US-08-463-772-21
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Gaps
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Patent No. 5865640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
ITILE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                    D-Type Cyclin and Uses Related Thereto
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                                                                       E: Hamilton, Brook, Smith & Reynolds, P.C. Two Militia Drive
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US93/05000 FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-YAX-1992
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
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APPLICATION NUMBER: US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 616-861-9540 INFORMATION FOR SEQ ID NO: 21:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 189 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown; MOLECULE TYPE: protein PCT-US93-05000-21
APPLICANT: MITOTIX
TITLE OF INVENTION: D-1
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                              STREET: Two Militia I
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ZIP: 02109
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                                                                               ADDRESSEE:
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                                                                                                                                                         COUNTRY:
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US-08-463-772-22
US-08-463-772-22
Sequence 22, Application US/08463772
Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INFORMATION:
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                      DB 2; Length 236;
54;
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Pred. No. 54; 1; Mismatches
                                                                                                                                                      Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
RECISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                    61.5%;
60.0%;
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60.0%;
                236 amino acids
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Best Local Similarity 60.v-
                                                                                                                                                                                         Conservative
                                                                       ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-246-361A-22
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                                  TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 6; Conserv
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Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH,
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB
Pred. No. 54;
1; Mismatches
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NAME: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGBNT INFORMATION:
REGISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEFAHONE: (617) 227-7400
TELEFAHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MI-004C
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-517-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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20 EEVFPLAMNY 29
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CLASSIFICATION:
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ZIP: 02109
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Gaps

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-517-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥
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                                                                            APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BACCH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%; Score 32; DB 5; Length 236; 60.0%; Pred. No. 54; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
RESULT 23
PCT-US93-05000-22
Sequence 22, Application PC/TUS9305000
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 236 amino acids
AMINO ACID .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown ; MOLECULE TYPE: protein PCT-US93-05000-22
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 60 secor
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ZIP: 02109
                                                                                                                                                                                                                                          RY: US
02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/963,308

PRIOR APPLICATION NUMBER: US 07/963,308

PRILING DATE: 16-027-1992

PRILING DATE: 16-027-1992

PRILING DATE: 26-MAY-1992

PRILING DATE: 26-MAY-1992

PRILING DATE: 36-MAY-1992

PRILING DATE: 36-MAY-1992

PRILING DATE: 36-MAY-1992

PRILING DATE: 36-MAY-1992

PRILING DATE: 37-MAY-1992

PRILING PRILICATION NATA: 37-MAY-1992

PRILING PRILICATION NATA: 37-MAY-1993

PRILING PRILICATION NA
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-772-6

Query Match
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVYPXGMSY 10

| | | | | | | | | |
| Db 75 EEVFPLAMNY 84

Search completed: June 10, 2003, 13:51:33
Job time: 10.6429 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:46:50 ; Search time 15 Seconds (Without alignments) 75.710 Million cell updates/sec Run on:

1 EEVVPXGMSYS 11 US-09-909-164-9 52 Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

392085 seqs, 103240269 residues Searched:

392085 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database

. cgn2_6/ptodata/2/ptupaa/US07_NEW_PUB.pep:*
. cgn2_6/ptodata/2/ptupaa/US07_NEW_PUB.pep:*
. cgn2_6/ptodata/2/ptupaa/US07_NEW_PUB.pep:*
. cgn2_6/ptodata/2/ptupaa/US08_PUBCOMB.pep:*
. cgn2_6/ptodata/2/ptupaa/US09_PUBCOMB.pep:*
. cgn2_6/ptodata/2/ptupaa/US09_PUBCOMB.pep:*
. cgn2_6/ptodata/2/ptubpaa/US09_PUBCOMB.pep:*
. cgn2_6/ptodata/2/ptubpaa/US10_NEW_PUB.pep:*
. cgn2_6/ptodata/2/ptubpaa/US09_PUBCOMB.pep:*
. cgn2_6/ptodata/2/ptubpaa/US09_PUBCOMB.pep:*
. cgn2_6/ptodata/2/ptubpaa/US09_PUBCOMB.pep:*
. cgn2_6/ptodata/2/ptubpaa/US09_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ap (*
8	Score	Query	Query Match Length DB	DB	CI	Description
ł	38	73.1	3472	6	US-10-027-806-4	Sequence 4, Appli
	38	73.1		σ	US-10-034-623-4	
	38	73.1	3472	σ	US-10-027-801-4	Sequence 4, Appli
	34	65.4	947	0	US-10-101-464A-73	73,
	33	63.5	426	6	US-10-214-766-43	Sequence 43, Appl
	33	63.5		σ	US-09-924-340-108	Sequence 108, App
	33	63.5		σ	US-09-992-600A-108	Sequence 108, App
	33	63.5		6	US-09-746-783-184	Sequence 184, App
	33	63.5	478	6	US-10-000-489-108	
	33	63.5		6	US-10-000-986-108	Sequence 108, App
	33	63.5		σ	US-09-820-843A-26	26, A
	32	61.5	10	10	US-09-947-387-66	Sequence 66, Appl
	32	61.5	٠	10	US-09-778-927A-53	Sequence 53, Appl
	32	61.5		6	US-10-024-066-2	Sequence 2, Appli
	35.	61.5		σ	US-10-024-066-4	Sequence 4, Appli
	32	61.5		10	US-09-919-497-54	Sequence 54, Appl
	32	61.5		10	US-09-925-300-1061	Sequence 1061, Ap
	32	61.5	529	10	US-09-923-304-4	Sequence 4, Appli
	32	61.5		6	US-10-101-921-4	Sequence 4. Appli

equence 2, Ap	Sequence 103	e 4, App	equence 8/8, A	ice 876,	equence 5124.	e 20, Ap	equence 171, A	Sequence 334,	uence 6349,	Sequence 10697	equence 5. Appl	Jence 2. Anni	ddu / panonba	sequence 2, App	4404 Ap	se 5136,	se 10439,	Sequence 340,	equence 1, Ap	equence 9, Ap	equence 130,	sence 68, A	equence 85, A	Sequence 68,	e 85,	equence 68.	editence 85.	250000000000000000000000000000000000000	equence 359,	equence 355,	equence 339,	equence 359,	equence 359,	equence 444,	equence 444,	equence 444,	equence 359,	equence 444,	equence 359,	Š	equence 359,	eduence 328,	equence 444,	equence 444,												
US-09-925-73	US-09-815-242	US-10-151-736-4	US-10-092-154-8/	US-09-764-847-87	-969-9#6-60-60 -969-88-60-511	TS-10-117-846-20	US-09-986-480-17	0 US-09-731-872-33	US-09-738-626-634	0 US-09-815-242-1	115-09-975-139-5	115-10-280-403-	2 CO + COO - CO - CO - CO - CO - CO - CO	2-6/4-/06-60-6	US-U9-/38-626-4454	0 US-09-815-242-5136	O US-09-815-242-104	0 US-09-912-020-34	US-09-909-062-	US-09-909-062-9	US-09-909-062-1	US-09-852-797-6	US-09-852-797-8	0 US-09-853-161-6	0 US-09-853-161-8	0 IIS-09-850-659A-6	TIS-00-827-6594-	0.50 200 00 00 00 00 00 00 00 00 00 00 00 0	C-066-266-60-60	US-03-303-30-30-30-30-30-30-30-30-30-30-30	05-08-989-730-30	US-U9-990-444-35	US-08-989-/30-35	US-U9-99U-436-33	CS-TOT-T66-60-S0	CC- / 00- 586-60-60 - 116- / 00- 086-88	118-09-907-653-35	US-10-174-590-44	US-10-176-758-44	US-10-175-737-44	US-09-993-667-35	US-10-173-706-44	US-10-175-738-44	US-10-175-752-44	US-10-176-482-44	US-10-176-757-44	US-10-176-913-44	US-10-180-552-44	US-10-180-557-44	US-09-990-438-35	US-09-990-562	US-09-997-428-35	US-09-1997-666-33	US-10-173-700-44	US-10-174-572-44	ALIGNMENTS
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32	32	32	31	31	3.1	31	31	3.1	31	31	3.5	7.5	7.0	3. 1.	31	31	31	31	30	30	30	30	30	30	0.00	8	9 6	000	000	900	900	30	30	300	000	000	000	300	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	
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ALIGNMENTS

RESULT 1
US-10-027-806-4
Sequence 4, Application US/10027806
Sequence 4, Application US/10027806
Patent No. US20020160476A1
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
TITLE OF INVEWION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002A
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21

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Sequence 4, Application US/10034623

Sequence 4, Application US/10034623

Publication No: US2002019835A1

GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Carista
TTPLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A

CURRENT PELING DATE: 2001-12-21
PRIOR PRIOR PELICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4

LENGTH: 3472
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Publication No. US20030054364A1
GENERAL INFORMATION:
APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP, 002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTERE (OF WINDOWS VEFSION 3.0)
                                                                                                                                                                                                                                                                      Gaps
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020 PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29 NUMBER OF SEQ ID NOS: 123 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
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                                                                                                                                                                                                                   Score 38; DB 9; Length 347
Pred. No. 1.2e+02;
4; Mismatches 1; Indels
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Pred. No. 1.2e+02;
4; Mismatches 1; Indels
                                                                                                                                                ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4
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US-10-027-801-4
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54.58;
                                                                                                                                                                                                                 Query Match 73.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5-
For Conservative
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2294 EDVIPRGISFS 2304
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                                                                                                          LENGTH: 3472
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LENGTH: 3472
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US-10-034-623-4
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Sequence 73, Application US/10101464A

| Publication No. US20030046728A1
| Publication No. US20030046728A1
| GENERAL INFORMATION:
| APPLICANT: Strabala, Timothy
| APPLICANT: Higgins, Colleen W.
| TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
| TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
| TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
| TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
| TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
| FILE REFERENCE: 11000-1102002
| CURRENT APPLICATION NUMBER: 09/203-18
| PRIOR FILING DATE: 1999-01-12
| PRIOR FILING DATE: 1999-01-12
| PRIOR FILING DATE: 1999-01-13
| PRIOR FILING DATE: 1999-11-01
| PRIOR FILING DATE: 2000-01-11
| PRIOR FILING DATE: 2000-01-11
| NUMBER OF SEQ ID NOS: 989
| SOFTWARE: FastSEQ for Windows Version 4.0
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                                                  Gaps
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Publication No. US2003008447341

RENERAL INFORMATION:
APPLICANT: Gocal, Greg

TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS

FILE REFERENCE: CAll38

CURRENT APPLICATION NUMBER: US/10/214,766

CURRENT PILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.2
    Length 3472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 9; Length 426;
Pred. No. 1.2e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 947;
Score 38; DB 9;
Pred. No. 1.2e+02;
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Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1.
                                                4; Mismatches
73.1%;
54.5%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
                                              Conservative
                                                                                            1 EEVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pinus radiata
US-10-101-464A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| |:|||
686 VMPSGISYS 694
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Query Match
Best Local Similarity
Matches 6; Conserv
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US-10-214-766-43
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LENGTH: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-214-766-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 426
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APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fechtel, Kim Fechtel, Kim TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%; Score 33; DB 9; Length 478; 60.0%; Pred. No. 1.4e+02; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/09/746,783 FILING DATE: 21-Dec-2000 CLASSIFICATION: CURROWN>ATTORNEY/AGENT INFORMATION:
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-746-783-184
    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 742-4214
INFORMATION FOR SEQ ID NO: 184:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENCODING THEM
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                                                                                                                                                                                                                                                                                                                                                                                Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
                                                                                                                                                                                                   Sequence 184, Application US/09746783 publication No. US20030044935A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                              McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                       APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 231
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Best Local Similarity 60...
Best Local 6; Conservative
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           6; Conservative
                                                                                                239 EVAPAGASYN 248
                                                      2 EVVPXGMSYS 11
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                  Matches
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Sequence 108, Application US/09924340

PUDIICATION NO. US20030027248A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.032.REG
CURRENT APPLICATION NUMBER: US/09/924,340

CURRENT APPLICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

SEQ ID NOS: 112

SEQ ID NO 108

LEATH: 478

LEATH: 478
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APPLICANT: Benjanin, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.034.DDV
CURRENT ABLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 33; DB 9; Length 478; 60.0%; Pred. No. 1.4e+02; tive 1; Mismatches 3; Indels
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CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR PILING DATE: 2001-08-06
PRIOR PLILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PAPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PILING DATE: 2001-06-15
PRIOR PELING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
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Best Local Similarity 60.0
Matches 6; Conservative
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                                223 EFVIPAGQSY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: JPatent
SEQ ID NO 108
LENGTH: 478
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us-09-909-164-9.rapb

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US-09-820-843A-26

Sequence 26, Application US/09820843A
Sequence 26, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
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CTHER INFORMATION: iron(III) ABC transporter, permease protein

NAME/KEY: misc_feature

CTHER INFORMATION: gi|9654609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 33; DB 9; Length 653; 66.7%; Pred. No. 1.9e+02; tive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/820,843A CURRENT FILING DATE: 2001-03-30 NUMBER OF SEO ID NOS: 118 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR PELLALING NATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR APPLICATION NUMBER: US 09/168,888
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.74
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Vibrio cholerae
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Best Local Similarity
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LENGTH: 653
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| Sequence 108, Application US/20000986
| Publication No. US20030096247A1
| GENERAL INFORMATION:
| APPLICANT: Benjanin, Stephane
| APPLICANT: Tanaka, Hiroaki
| TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/10/000,986
| PRIOR PILING DATE: 2001-11-14
| PRIOR PILING DATE: 2001-08-06
| PRIOR FILING DATE: 2001-08-06
| PRIOR FILING DATE: 2001-08-06
| PRIOR FILING DATE: 2001-08-06
| PRIOR PILING DATE: 2001-08-06
| PRIOR FILING DATE: 2001-06-15
| PRIOR PLING DATE: 2001-06-25
| SOFTWARE: 108-108-112
| LEMEGTH: 478
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FILE REFERENCE: 91.US6.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-15
PRIOR PRICATION NUMBER: US 60/298,698
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR FILING DATE: 1001-06-15
PRIOR FILING DATE: 2001-06-15
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Best Local Similarity 60.0v
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US-10-000-986-108
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RESULT 11

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TYPE: PRT
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Sequence 2, Application US/10024066

Sequence 2, Application US/2020166134A1

GENERAL INFORMATION:
APPLICANT: Field, LOTER J.
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
CURRENT FILING DATE: 1091-12-18

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN Ver. 2.1
                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WORLEN WUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
CURRENT APPLICATION WUMBER: US/09/778,927A
CURRENT FILING DATE: 2000-02-08
FRIOR PAPLICATION NUMBER: IL135341
FRIOR FILING DATE: 2000-02-09
FRIOR FILING DATE: 2000-03-29
NUMBER OF SED ID NOS: 81
SOFTWARE: PATENTING DATE: 2000-03-29
SOFTWARE: PATENTING DATE: 2000-03-29
SED ID NOS: 81
SOFTWARE: PATENTING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 10; Length 254;
pred. No. 1.1e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; LOCATION: (1)..(254); OTHER INFORMATION: Xaa = any amino acid, unknown, or other US-09-778-927A-53
                                   ; Sequence 53, Application US/09778927A
; Patent No. US20020068342A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%;
60.0%;
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Matches 6; Conservative
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RESULT 13
US-09-778-927A-53
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RESULT 15 US-10-024-066-4

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                 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Field, Loren J.

APPLICANT: Pasumarthi, Kishore Babu S.

APPLICANT: Pasumarthi, Kishore Babu S.

TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

FILE REFERENCE: 7037-450

CURRENT APPLICATION NUMBER: 2001-12-18

PRIOR APPLICATION NUMBER: 60/139,942

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 2000-06-19

NUMBER OF SEQ ID NOS: 8

NUMBER OF SEQ ID NOS: 8

SOSTWARE: PATENTIN Ver. 2.1
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Sequence 54, Application US/09919497

Patent No. US2020106662A1

GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
TITLE OF INVENTION: BROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
TITLE OF INVENTION: 2001/723

CURRENT APPLICATION NUMBER: US 60/221,735

PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn version 3.0
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCI/US00/05988
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 9; Length 289;
Pred. No. 1.38+02;
1; Mismatches 3; Indels
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60.0%; Pred. No. 1.3e+02;
tive 1; Mismatches 3;
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Sequence 4, Application US/10024066
Patent No. US20020166134A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%;
60.0%;
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Best Local Similarity 60...
Best Local Similarity 60...
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Matches 6; Conservative
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74 EEVFPLAMNY 83
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US-09-919-497-54
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US-09-919-497-54
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LENGTH: 289
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us-09-909-164-9.rapb

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LENGTH: 691
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: LOCATION: (277)
: O'THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1061
                                                                                                                                                                                                                     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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APPLICANT: JIANG, FENG
TILLE OF SUNCHING RELATED CANCERS
TILLE OF INVENTION: DEPETCTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
FILE REFERENCE: UTSC:658US
CURRENT APPLICATION NUMBER: US/09/923,304
NUMBER OF SEQ ID AATE: 2001-08-06
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 4
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APPLICANT: Ose, Asuka
APPLICANT: Ose, Asuka
APPLICANT: Ose, Asuka
TITLE OF INVENTION: TRANSPORTER GENES OATP-B, C, D, AND E
TITLE OF INVENTION: TRANSPORTER GENES OATP-B, C, D, AND E
TITLE OF INVENTION: UMBER: US/10/101,921
CURRENT RILING DATE: 200-06-28
PRIOR PPLICATION NUMBER: PCT/JP00/06416
PRIOR PILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: JP 11/267835
PRIOR FILING DATE: 1999-09-21
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890 SECTRARE: Patentin Ver. 2.0 SEQ ID NO 1061 LENGTH: 295
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Patent No. US20020081612A1
GENERAL INFORMATION:
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Publication No. US20030022199Al
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity 50.03
Matches 5; Conservative
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                                                                                                                                         ORGANISM: Homo sapiens
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Best Local Similarity (
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ORGANISM: Homo sapiens
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                                                                                                                                                                                 NAME/KEY: SITE
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US-10-101-921-4
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                                                                          61.5%; Score 32; DB 9; Length 691; 62.5%; Pred. No. 3.2e+02; Live 2; Mismatches 1; Indels
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FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/191,078
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ADEOKUN, NATHONI MONISOLA
APPLICANT: AMEROSE, HELEN JEAN
APPLICANT: CRESSWELL, CARL JOHN
APPLICANT: DUDLEY, ADAM JESTON
TITLE OF INVENTION: CHEMICAL COMPOUNDS
FILE REFERENCE: DJF/009901/00282795
CURRENT APPLICATION NUMBER: US/09/925,731
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET. 2.1
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09925731; Patent No. US20020090622A1; GENERAL INFORMATION;
                                                 Query Match
Best Local Similarity 62.5%;
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ohlsen, Kari L.
APPLICANT: Yaskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
            ; ORGANISM: Homo sapiens US-10-101-921-4
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188 IVPLGLSY 195
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188 IVPLGLSY 195
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TYPE: PRT
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LOCATION
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APPLICANT: Callaghan, Michelle J.
APPLICANT: Sutherland, Lindfield
APPLICANT: Sutherland, Lindfield
APPLICANT: Watts, Colin K.
TITLE OF INVENTION: NO. US20020192160Alel Human Tumour Suppressor Gene
FILLE REPERENCE: RICE-010CON
CURRENT APPLICATION NUMBER: US/10/151,736
CURRENT APPLICATION NUMBER: US/10/151,736
PRIOR PILLING DATE: 1999-10-21
PRIOR PELLING DATE: 1999-10-21
PRIOR FILLING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE RESULED NOS: 17
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                                                                                                                                                                                                                                                                        61.5%; Score 32; DB 10; Length 1377;
45.5%; Pred. No. 6.7e+02;
tive 4; Mismatches 2; Indels C
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILLE REFERENCE: FORDORI
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%; Score 32; DB 9; Length 279
60.0%; Pred. No. 1.4e+03;
tive 2; Mismatches 2; Indels
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-2
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: PSSESEQ for Windows Version 4.0
; SEQ ID NO 10384
; LENGTH: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
US-10-092-154-878
Sequence 878, Application US/10092154
Publication No. US20030054375A1
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/10151736
; Publication No. US20020192160Al
; GENERAL INFORMATION:
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Matches 6; Conservative
                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                        Best Local Similarity 45.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                           US-09-815-242-10384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 878
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-151-736-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-151-736-4
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                   ; LOCATION: (7); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids us-10-092-154-878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
CURRENT APPLICATION ADMEDIATED TEMPORED TO SERVING APPLICATION NUMBER OF SEQ. ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.6%; Score 31; DB 10; Length 53; Best Local Similarity 66.7%; Pred. No. 33; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                            Score 31; DB 9; Length 53;
Pred. No. 33;
1; Mismatches 2; Indels
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APPLICANT: HALKIER, TORDEN
APPLICANT: BAUDITZ, PETER
APPLICANT: HANSEN, PETER
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946, 200-US
CURRENT APPLICATION NUMBER: US/09/948,080
CURRENT FILING DATE: 2001-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 2001-09-06
PRIOR APPLICATION NUMBER: US/08/963,851
PRIOR FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                        ; Sequence 878, Application US/09764847; Patent No. US20020132767A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09948080; Patent No. US20020102702A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
; APPLICANT: VAN DER OSTEN, CLAUS
                                                                                                     Ouery Match 59.6%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
                                                                                                                                                                                                    3 VVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                          US-09-764-847-878
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US-09-948-080-14
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LENGIH: 53
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1 EEVVPXGMSYS 11 |::||:|| 38 EKHIPGGLEYS 48 Q Op

Search completed: June 10, 2003, 14:35:42 Job time: 15.0714 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:31:15; Search time 11.2143 Seconds (without alignments) 94.297 Million cell updates/sec Run on:

US-09-909-164-9 52 Title:

1 EEVVPXGMSYS 11 Perfect score: Sequence: BLOSUM62 Scoring table:

283224 seqs, 96134422 residues Gapop 10.0 , Gapext 0.5 Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical 367K	probable sulfate p	sulfate permease -	V1 protein - tobac	DNA segregation AT		hypothetical prote	zinc finger protei	topoisomerase IV s	DNA-binding protei	hypothetical prote	cell division inhi	probable ABC subst	thetical	-				hypothetical prote	beta-ketoacyl-ACP	hypothetical prote	3-phosphoshikimate	cdc37 protein – fi	iron(III) ABC tran	bacteriocin BCN5 -	ATP-dependent DNA	Q.	grow	DNA-directed RNA p
SOMMANIES	ΠD	T31308	T39116	T40413	A42452	B97355	S57810	T24111	S22293	н82691	A34203	S54619	H69491	C82900	140758	E90544	D69493	C81374	T34536	S75817	T47670	F72281	D82163	T43653	D82352	A30481	AF3286	D87046	26	G82336
	DB	7	7	7	~	~	7	7	7	7	7	~	7	7	~	7	~	7	7	7	7	7	7	N	7	N	C)	~	N	7
	Length	3472	840	877	102	1498	225	425	670	749	2717	156	252	544	94	116	165	253	259	284	298	368	426	466	653	890	1028	1152	1394	1401
dР	Query Match	73.1	71.2	71.2	69.3	69.2	67.3	67.3	67.3	67.3	67.3	65.4	65.4	65.4	63.5	63.5	63.5	63.5	r	63.5	63.5	63.5	63.5	63,5			63.5	Э.	63.5	63.5
	Score	38	37	37	36	36	35	35	35	35	35	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
	Result No.	1	7	٣	4	S	9	7	۵	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hetical protein and protein portion protein cortain protein Grant protein Grant protein Grant protein no	rhsC protein in rh rhsC protein precu RhsC core protein rhsA core protein rhsB protein precu gene 11-1 protein trans regulatory s hypothetical prote probable cobh - My probable purQ prot phosphoribosylform
704456 A38261 B2261 B207333 B207333 B207333 B27323 B47811 I58372 A41984 A41984 A42822 S57922 S57922 S57922 S67730 B42822 B42822 B42822 B42822 B42822 B42822 B42822 B42822 B57925 B6213 B61831 B61831 B61831 B744187 B741	A85570 C64805 C64805 C64805 F91187 E65145 S00485 VKLJS1 A71173 D70764 G70709
	00000000000
1154 1748 1748 1748 1749 1749 1749 1759 1759 1759 1759 1759 1759 1759 175	1397 13997 1411 1948 1134 134 124 124 224
60 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	61.5 61.5 61.5 61.5 61.5 61.5 61.5 59.6 59.6 59.6
	322 322 331 331 311 311
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### ALIGNMENTS

RESULT 1

Tyling 1367K protein - Cenarchaeum symbiosum (Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000 (Species: 11-Jan-2000 #schoper. C.) Debong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V. Bacteriol. 180, 5003-5009, 1998 A;Title: Genomic analysis reveals chromosomal variation in natural populations of A;Title: Genomic analysis reveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations of A;Title: Genomic analysis raveals chromosomal variation in natural populations in natural

0; Gaps Query Match

73.1%; Score 38; DB 2; Length 3472;
Best Local Similarity 54.5%; Pred. No. 59;
Matches 6; Conservative 4; Mismatches 1; Indels

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1 EEVVPXGMSYS 11

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Cispecies: Lycoperation esculentum (control) countrol (Cipate: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000 CiAccession: S57810 Gasser, C.S. Plant Mol. Biol. 28, 691-711, 1995 A;Title: Nature and regulation of pistil-expressed genes in tomato. A;Reference number: S57808; MUID:95375233; PMID:7647301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein R10b12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 "#text_change 15-Oct-1999
C;Accession: T24111
R;Percy, C.
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:9924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
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               A; Cross-references: GB: M81103; NID: 9335283; PIDN: AAA47947.1; PID: 9335284
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Pred. No. 63;
2; Mismatches 2; Indels
                                                           69.2%; Score 36; DB 2; Length 102;
60.0%; Pred. No. 3.5;
.ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 2; Length 225; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA
A;Residues: 1-225 <MIL>
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hypothetical protein precursor (clone TPP11) - tomato
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Best Local Similarity 60.0%;
Matches 6; Conservative
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54.5%;
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Best Local Similarity 54.57
Fig. 6, Conservative
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7 QVVPSGINYS 16
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32 DEVVPNGKTYA 42
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                                                                               Best Local Similarity
Matches 6; Conserv
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                                                           Query Match
                                                                                                                                                                                                                                                    RESULT 5
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V1 protein - tobacco yellow dwarf virus (strain Australia)
C; Species: tobacco yellow dwarf virus
C; Species: tobacco yellow dwarf virus
C; Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C; Accession: A42452
R; Moorlis, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A; Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
A; Reference number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: AL132779; PIDN: CAB60015.1; GSPDB: GN00066; SPDB: SPAC869.05c
A; Experimental source: strain 972h-; cosmid c869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: DNA
A; Residues: 1-877 <LYN>
A; Cross-references: EMBL: AL031261; PIDN: CAA20298.1; GSPDB:GN00067; SPDB: SPBC3H7.02
A; Experimental source: strain 972h-; cosmid c3H7
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                                                                                                                       probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T39116
R; Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, November 1999
A; Reference number: Z21829
A; Accession: T39116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Schizosaccharomyees pombe
C;Date: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 03-bec-1999
C;Accession: T40413
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, August 1998
A;Reference number: 221926
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Pred. No. 21;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sulfate permease - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                              A. Status: preliminary; translated from GB/EMBL/DDBJ
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77.8%;
1:1:1 |:1:1
2294 EDVIPRGISFS 2304
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SPDB:SPAC869.05c
A; Map position: 1
                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-840 <HUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SPDB:SPBC3H7.02
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A; Residues: 1-102 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                   RESULT 2
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chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marti, A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Balmieri Rodrígues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; SE A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.; Sebrence number: A59328
A.; Reference number: A59328
A.; Contents: annotation
                                                                                                                                                                                                                                                                                                                                      A;Gene: XF1353
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Rosidues: 801-1072, N',1074-1168, K',1170-1225, V',1227-1434, N',1436-1607, 'I',1
A;Cross-references: GB:M32019
C;Superfamily: HIV-EP2 enhancer-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X51435; NID:g38017; PIDN:CAA35798.1; PID:g38018
R;Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Biol. 10, 1406-1414, 1990
A;Fitle: A large protein containing zinc finger domains binds to related sequence A;Reference number: A34779; MUID:90205817; PMID:2108316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes Dev. 4, 29-42, 1990
A;Title: A DNA-binding protein containing two widely separated zinc finger motifs
A;Reference number: A34203; MUID:90169514; PMID:2106471
A;Accession: A34203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding protein PRDII-BF1 - human
N;Alternate names: major histocompatibility complex enhancer-binding protein 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X87331; NID:91041652; PIDN:CAA60762.1; PID:9829123 R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; S66879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo saplens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C;Accession: A34203; A34779
R;Fan, C.M.; Maniatis, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 2; Length 749;
Pred: No. 48;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.3%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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A; Residues: 1-2717 <FAN>
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A; Residues: 1-156 <DEH>
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A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carreiro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: S22293; 178656
C;Araboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
A;Filte: IsoSalaion of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: I58280; MUID:91187610; PMID:1901405
A;Reference number: S22293
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C.Sacession: H82691
R.anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A.Fitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A.Reference number: A82515; MUID:20365717; PMID:10910347
A.Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                              A;Cross-references: EMBL:281109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10 A;Experimental source: clone R10D12 C;Genetics:
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A; Residues: 1-670 <MIT>>
A; Residues: 1-670 <MIT>>
A; Cross-references: EMBL:X54250; NID:q57519; PIDN:CAA38151.1; PID:q57520
A; Note: the authors did not translate the codon for residue 1
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription regulation; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
26;
                     submitted to the EMBL Data Library, October 1996 A; Reference number: 219842 A; Accession: T24111 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zinc finger protein AT-BP2 - rat (fragment)
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                                                                                                                                                                                                                                                                                                                                      A)Gene: CESP:R10D12.10
A)Map position: 5
A)Introns: 23/3; 56/3; 113/3; 257/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%;
50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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A;Molecule type: DNA
A;Residues: 1-749 <SIM>
                                                                                                                                                                                                A; Residues: 1-425 <WIL>
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Gaps

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C; Accession: E90644
R; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Mosze Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasm A; Reference number: A99512; MUD:21267165; PMID:11353084
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
C;Accession: D69493
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; I; FKlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Syke
                                                                                                                                                                                                                                                                                                                                                                             Appothetical protein 1 - Campylobacter jejuni (fragment)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Sate: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140758; S47317
R;Hani, E.K.; Chan, V.L.
J. Bacteriol. 177, 2396-2402, 1995
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine A;Reference number: 140758; MUID:95247673; PMID:7730270
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A.Residues: 1-116 <KUR>
A.Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A.Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50s ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mycoplasma pulmonis
C;Date: 24-May_2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: 236940; NID: 9535805; PIDN: CAA85392.1; PID: 9535806
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Pred. No. 17;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 33; DB 2; Length 94; ilarity 55.6%; Pred. No. 13; Conservative 2; Mismatches 2; Indels
                                     Indels
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A;Genetic code: SGC3
C;Superfamily: Escherichia coli ribosomal protein L20
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
                                         Mismatches
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Best Local Similarity 77.00
7; Conservative
                             7; Conservative
                                                                                                                                                                                      135 EEVVPHYLSY 144
                                                                                                            1 EEVVPXGMSY 10
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Best Local Similarity
Lac 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
                                 Matches
                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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                                                                                                                    A;Molecule type: DNA
A;Residues: 1-156 <DEW>
A;Residues: 1-156 <DEW>
A;Cross-references: EMBL: Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cincersolon: H69491
Riklenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson is H69491
Riklenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson is Flaischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
Alvanthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Aritle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-252 ckles
A; Residues: 1-252 ckles
A; Cross-references: GB:AE000970; GB:AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264866
C; Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A; Reference number: A82870
A; Accession: C82900
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-544 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE002133; GB:AF222894; NID:96899339; PIDN:AAF30768.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: C82900 Sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 Sibmitted to GenBank, February 2000 Submitted to GenBank, February 2000 Fe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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65.4%; Score 34; DB 2; Length 252;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 544;
55;
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submitted to the Protein Sequence Database, July 1996 A; Reference number: S66877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                         A; Map position: 15R
C; Superfamily: hypothetical protein YOR013w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: serovar 3; blovar 1
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Best Local Similarity
6; Conserva
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                                                                                   A; Accession: S66879
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hypothetical protein s1r1275 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp. ,
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.6
Matches 5; Conservative
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Les 5; Conserv
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                                                                                                                                                                                            C; Accession: S75817
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Wature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
Smith, H.O.; Woese, C.R.; Venter, J.C. A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69250; MUID: 98049343; PMID: 9389475 A; Accession: D60493
A; Accession: D60493
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                     A;Molecule type: DNA
A;Residues: 1-165 <KLE>
A;Cross-references: GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89307.1; PID:g264859
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73246.1; PID:g696842
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C81374
hypothetical protein Cj0990c [imported] - Campylobacter jejuni (strain NCTC 11168)
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C;Species: Homo sapiens (man)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34539
E;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, October 1999
A;Reference number: 221540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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Pred. No. 25;
1; Mismatches 3; Indels
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60.0%; Pred. No. 40;
tive 1; Mismatches 3; Indels
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A;Residues: 1-259 <POUD>
A;Cross-references: EMBL:AL122063
A;Exporsimental source: adult testis; clone DKFZp434C031
C;Genetics:
A;Note: DKFZp434C031.1
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Pred. No. 39;
2; Mismatches
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55.6%;
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60.0%;
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Best Local Similarity 60.0
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Matches 6; Conserv
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A; Residues: 1-253 <PAR>
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A; Status: preliminary
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Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajim
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecho
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D90913; GB:AB001339; NID:q1653348; PIDN:BAA18276.1; PID:d
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein TM1216 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72281
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.;
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N'Alternate names: protein T26I12.190
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
C;Accession: T47670
S;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, February 2000
A;Reference number: 224471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 25/3
A;Note: T26112.190
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                              A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75817
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-284 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 20
T47670
beta-ketoacyl-ACP reductase-like protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-298 <MON>
A;Cross-references: EMBL:AL132954
A;Experimental source: cultivar Columbia; BAC clone T26I12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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ilarity 55.6%;
Conservative
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Gaps

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iron(III) ABC transporter, permease protein VC0203 [imported] - Vibrio cholerae (st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellé L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004110; GB:AE003852; NID:99654600; PIDN:AAF93379.1; GSPDB:
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decretiocin BCNS - Clostridium perfringens plasmid pIP404
C; Species: Clostridium perfringens
C; Date: 31-Mar-1992 #sequence_revision 3i-Mar-1992 #text_change 24-Nov-1999
C; Accession: A30481; S03779
C; Accession: A108-1196, 1986
C; Accession: B108-1196, 1986
A; Title: Characterization of a bacteriocinogenic plasmid from Clostridium perfringe A; Reference number: JT0354; MUID:87057020; PMID:2877971
A; Accession: A30481
A; Molecule type: DNA
A; Residues: 1-890 cGAR>
A; Cenetics: A; Cenetics: GB:M32882; GB:J03309; NID:g150738; PIDN:AAA98249.1; PID:g1507395
C; Genetics: A; Gene: bon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: D82352
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0
                                A)Cross references: EMBL:ALO49769; PIDN:CAB42371.2; GSPDB:GN00067 A)Experimental source: strain 972h-; cosmid c986 R;Westwood, P.K.; Preston, N.C.; Fantes, P.A. Submitted to the EMBL Data Library, March 1999 A;Description: Schizosaccharomyces pombe cdc37 gene.

A)Reference number: 222603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 653;
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Pred. No. 1.1e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-466 <WE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 2;
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: AJ132377; PIDN: CAB38758.1
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50.0%;
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300 EEVVPSGIT 308
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A; Gene: cdc37; SPAC9B6.10
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Matches 5; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-653 <HEI>
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Matches 6; Conserv
              A; Residues: 1-466 < WOO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-phosphoshikimate 1-carboxyvinyltransferase VC1732 [imported] - Vibrio cholerae (strain C) Species: Vibrio cholerae (C) Date: 18-402000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C) Accession: D82163
RHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; RHeidelberg, J.F.; Eisen, J.A.; Nemathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Residues: 1-426 <HEIS
                                                                            A; Molecule type: DNA
A; Residues: 1-368 <ARN>
A; Cross-references: GB:AE001778; GB:AE000512; NID:g4981757; PIDN:AAD36291.1; PID:g498176
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Cuperfamily: NADH dehydrogenase (ubiquinone) 49K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004251; GB:AE003852; NID:99656248; PIDN:AAF94882.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carboy
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C;Species: Schizosaccharomyces pombe
C;Date: 21-3an-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43653; T40791; T43654.
R;Westwood, P.K.; Preston, N.C.; Fantes, P.A.
Submitted to the EMBL Data Library, March 1999
A;Description: Schizosaccharomyces pombe cdc37 cDNA.
A;Reference number: Z22602
A;Accession: T43653
A;Status: precliminary; translated from GB/EMBL/DDBJ
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69;
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A.Cross-references: EMBL:AJ132376; PIDN:CAB38757.1
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.submitted to the EMBL Data Library, May 1999
A;Reference number: Z21875
A;Accession: T40791
A; Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                             Score 33; DB 2;
Pred. No. 59;
3; Mismatches
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1; Mismatches
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55.6%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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Matches 5; Conservative
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                                                       A; Status: preliminary
                                A; Accession: F72281
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Gaps

A,Genome: plasmid C,Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5 C;Keywords: bacteriocin

0; Gaps Query Match 63.5%; Score 33; DB 2; Length 890; Best Local Similarity 66.7%; Pred. No. 1.5e+02; Matches 6; Conservative 1; Mismatches 2; Indels

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2 EVVPXGMSY 10 |||| | | :| 170 EVVPGGFTY 178 δy

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Search completed: June 10, 2003, 13:49:13 Job time: 11.2143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 10, 2003, 13:25:04 ; Search time 4.5 Seconds (without alignments) 101.387 Million cell updates/sec Run on:

1 EEVVPXGMSYS 11 US-09-909-164-9 52 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

SwissProt_40:* Database: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	986	074377 schizosacch		Q04351 clostridium	P15822 homo sapien	P23622 neurospora			_		schiz	Q9nzm5 homo sapien	clost		vibri	Q14766 homo sapien		rattn		mus m	brachyda	xenobns	gallus g	xenobns	gallu	homo sa	,	2 mus m	m		pomou ;	Q9y616 homo sapien	human
ID	CARB_FUSNN	SULH_SCHPO	Y11K_TYDVA	Y1A9_CLOAB	ZEP1_HUMAN	CY14_NEUCR	A10C_HUMAN	RL20_MYCPU	Y990_CAMJE	AROA_VIBCH	CC37_SCHPO	GSR2_HUMAN	BCN5_CLOPE	LTBS_HUMAN	RPOC_VIBCH	LTBL_HUMAN	LTB1_RAT	CGD2_RAT	CGD2_HUMAN	CGD2_MOUSE	CGD1_BRARE	CGD1_XENLA	CGD2_CHICK	CGD2_XENLA	CGD1_CHICK	CGD3_HUMAN	CGD1_HUMAN	CGD1_MOUSE	CGD1_RAT	TOLB_HAEIN	ENP3_HUMAN	OAT6_HUMAN	PRTP_HSV6U
DB	-	-	7	-	Н	П	7	П	Н		-1	7	7	IJ	Н	1	щ	H	Н	Н	-	~4	٦	٦	Н	Н	-	Н	-	П	П	Н	Н
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% Query Match	73.1	71.2	69.2	69.2	67.3	65.4	65.4	63.5															•	•	٠		•	61.5			61.5	61.5	•
Score	38	37	36	36	35	34	34	33	33	33	33	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
Result No.	-	7	e	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P32784 saccharomyc 662671 rattus norv P28931 tomato aspe P16916 escherichia P16918 escherichia P16918 escherichia P16917 escherichia P16917 escherichia P16917 homo sapien P17280 himpanzee (10676 mycobacteri O59619 pyrococcus O5956 mycobacteri P71841 mycobacteri P71841 mycobacteri O5756 mycobacteri O5756 mycobacteri O59160 arabidopsis (58149 methanococc P10941 cryphonectri P80210 saccharomyc O9420 rattus norv O9489 mus musculu P97564 rattus norv O9489 schizosacch	P00577 escherichia P16919 escherichia 09u2q0 caenorhabdi 1919102 xenopus lae 028825 archaeoglob 09uHf0 homo sapien 066903 aquifex aeo 09rgy0 lactobacil 026270 methanobact 092pil rhizobium m P57489 buchhanococ 0921e3 helicobacte P56006 helicobacte P2833 rattus norv P87033 ustilago ma P26391 salmonella
759 9259 1113393 12949 124197 124197 1252 1252 1252 1252 1252 1252 1252 125	
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.0000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.	559.6 559.6 577.7 577.7 577.7 577.7 577.7 577.7 577.7
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### ALIGNMENTS

[1]

SEQUENCE FROM N.A.

SERVINA-ATCC 25586;

MEDLINE-21886394; PubMed=11889109;

MEDLINE-21886394; PubMed=11889109;

MEDLINE-21886394; PubMed=11889109;

MEDLINE-21886394; PubMed=11889109;

Maptacharyya A., Anderson I., Ivanova N., Gardner W., Grechkin G., Zhu L.,

Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Walunda T., Pusch G., Haselkorn R.,

Fonstein M., Kyrpides N., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";

J. Bacteriol. 184.22005-2018(2002).

J. Bacteriol. 184.22005-2018(2002).

J. Bacteriol. 184.22005-2018(2002). 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422. PRT; 1058 AA. Fusobacterium nucleatum (subsp. nucleatum). Bacteria; Fusobacteria; Fusobacterium. NCBI_TaxID=76856; STANDARD; CARB_FUSNN Q8RG86; RESULT 1
CARB_FUSNN DDT AC OOC OO SEE THE SEE THE

MEDLINE=21848401; PubMed=11859360;

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                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE010554; AAL94625.1; ALT_INIT.

In therPro; IPR005449; CPase_L_D2.

In therPro; IPR005449; CPase_L_D2.

In therPro; IPR005449; CPase_L_D3.

In therPro; IPR005460; CPase_L_D3.

In therPro; IPR003480; CPase_L_Chaln; 2.

In therPro; IPR00389; CPase_L_Chaln; 2.

In pfam; PF02787; CPSase_L_D3; 1.

In Pfam; PF02787; CPSase_L_D3; 1.

In Pfam; PF02787; CPSase_L_D3; 2.

In Pfam; PF02787; CPSase_L_D3; 2.

In Pfam; PF02787; CPSase_L_D3; 2.

In Prositie; PR00866; CPSase_1; 2.

In PROSITE; PS00866; CPSASE_1; 2.

In PROSITE; PS00866; CPSASE_1; 2.

In Prositie; PS00866; C
                                              -I- PATHWAY: Arginine biosynthesis:
-I- PATHWAY: Pyrimidine biosynthesis; first step.
-I- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
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phosphate + L-glutamate + carbamoyl phosphate.
COFACTOR: Binds three manganese ions (By similarity).
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
20-JUDable sulfate permease C3H7.02.
                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE CARB FAMILY.
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3; Mismatches
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60.0%;
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NCBL_TaxID=4896;
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Best Local Similarity
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RA MODOLV, GW1111am R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA MEDLINE-LIOSAGUL, FRA MEDLINE-LIOSAGUL, BAREN S., BASHAM D., BOWMAN S., Chillingworth T., Churcher C. M., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C. M., RA GOLLINS M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamilan N., Harris D., Hidalgo J., Hodgson G. R. Holrcyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Junes K., O'Neil S., Mungall K., Murphy L., Niblett D., Odell C., Alverford K., Rutter S., Saunders D., Seeger K., Sharp S., E., Rutherford K., Rutter S., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Swelton J., Langer I., Whitehead S., Woodward J., Volckært G., Aert R., Robben J., Grymonprez B., Weltjens I., Volckært G., Aert R., Robben J., Grymonprez B., Weltjens I., Volckært G., Aert R., Robben J., Grymonprez B., Weltjens I., Panger M., Schaefer M., Meeller S., Gloux K., Hurst S.M., Eger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt K., Purnelle S., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Gairzon A., Thode G., Barretti L., Lowe T., McCombie W.R., Paulsen I., Potsshkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe.";
R. Rather 415:811-881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
-!- SIMILARITY: CONTAINS 1 STAS DOMAIN.
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Pred. No. 8.3;
1; Mismatches 1; Indels
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InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF00916; Sulfate_transp. 1.
Pfam; PF01740; STAS; 1.
PROSITE; PS01130; SLC264; 1.
PROSITE; PS50801; STAS; 1.
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Matches 7; Conservative
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484
518
543
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877 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Noelling J., Breton G., Onelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; G. Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                               Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component of
thobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonous plants.";
virology 187:633-642(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                             (strain Australia) (TYDV).
                                                                                                                                                                                                             Tobacco yellow dwarf virus (strain Australia) (TYDV
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                     01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                  MEDLINE=92188538; PubMed=1546458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002621; Gemini_mov.
Pfam; PF01708; Gemini_mov; 1.
                                                                                                                      01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein CAC3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.2%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                       STANDARD;
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7 QVVPSGINYS 16
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148 VVPQGMSYA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                NCBI_TaxID=31599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y1A9_CLOAB
                                                                                     Y11K_TYDVA
P31619;
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                                                                      Y11K_TYDVA
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01-APR-1990 (Rel. 14, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
2inc finger protein 40 (Human immunodeficlency virus type I enhancer-
binding protein 1) (HIV-EPI) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                                                                                   small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-:- SIMILARITY: BELONGS TO THE FTSK/SPOILIE FAMILY.
-:- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-90169514; PubMed=2106471;
Fan C.M., Maniatis T.;
Fan Anv-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92232684; PubMed=1567844; Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E., Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                     Sauer U., Duerre P.; "Sequence and molecular characterization of a DNA region encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "High-resolution solution structure of the double Cys2His2 zinc
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ATP (POTENTIAL).
168968 MW; FF42037A335A9649 CRC64;
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MEDLINE-91064333; PubMed-2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; ATP-binding; Complete proteome. NP BIND 675 682 ATP (POTENTIAL). SEQUENCE 1498 AA; 168968 MW; FF42037A335A9649 CRC:
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SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-93273706; PubMed-8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X65276; CAA46379.1; ALT_FRAME.
Interpro; IPR002543; FtsK_SpoillE.
Pfam; PF01580; FtsK_SpoillE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007866; AAK81629.1; -.
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60.0%;
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P15822;
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A10C_HUMAN
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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Gaps
                                                                                                                                                                                                                                                                                                   SMARITE PROMOSS; AME_CARS, TROCETTE STRUCTER PROMOSS; ZINC_FINGER_C2H2_1; 4.

PROSITE: PSSO1028; ZINC_FINGER_C2H2_2; 4.

Transcription regulation; Zinc_finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; 3D-structure.

DOMAIN 406 456 2INC_FINGERS.

ZINC_FING 406 428 C2H2-TYPE.

ZN_FING 434 456 C2H2-TYPE.

DOMAIN 803 806 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.3%; Score 35; DB 1; Length 2717; 66.7%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          C2HC-TYPE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CY14_NEUCR STANDARD; PRT; 788 AA P23622; 01-NOV-1991 (Rel. 20, Created) 01-NOV-1995 (Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 70;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 ZINC FINGERS
                                                                                                             ZINC-FINGER IN-BETWEEN.
-!- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                      nterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                     EMBL; X51435; CAA35798.1; -.
                                                                                                                                                                                                                                                                            Pfam; PF00096; zf-C2H2; 5.
PRINTS; PR00048; ZINCFINGER.
SMART; SM00355; znF_C2H2; 4.
                                                                                                                                                                                                                                                 TRANSFAC; T00497; -.
Genew; HGNC:4920; HIVEP1.
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                                                                                                                                                                                                                      PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
TRANSFAC; T00497; -.
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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DOMAIN
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ZN_FING
STRAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.
-i- MISCELLANEOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.
-i- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE REVISIONS.
MEDLINE=94188926; PubMed=8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
permease II and a putative human tumour suppressor.";
Trends Biochem. Sci. 19:19-19(1994).
-i- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.
                                                                                                                                                                                                                                    **Retter J.S., Jarvi G., Fu Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4FC604B6079BCE77 CRC64;
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                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBL_TaxID=5141;
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     41, Last annotation update)
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2; Mismatches
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POTENTIAL.
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                                                                                                                                                                                                                  MEDLINE-91129256; PubMed-1825178;
                                                                                                                                                                                                                                                                                                                    Neurospora crassa.";
Blochemistry 30:1780-1787(1991).
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060312; Q96914;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87864 MW;
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Sulfate permease II.
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                                                                          Neurospora crassa.
                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISEASE: Defects in ATP10C may be a cause of Angelman syndrome (AS), also known as 'happy puppet syndrome'.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).

-1- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein (By similarity). TISSUE SPECIFICITY: Wide expression, with highest levels in kidney, followed by lung, brain, prostate, testis, ovary, and
                                                                                                                                                                             MEDLINE-21225279; PubMed-11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
                                                                                                                                                                                                                         "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Potential phospholipid-transporting ATPase VC (EC 3.6.3.1) (ATPVC)
(Aminophospholipid translocase VC).
ATPLOC OR ATPVC OR KIAA0566.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-21313119; PubMed-11353404;
Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ArPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505(2001).
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 337-1499 FROM N.A.
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                                                                                 Homo sapiens (Human)
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=9606;
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"The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";

Nucleic Acids Res. 29:2145-2153(2001).

Nucleic Acids Res. 29:2145-2153(2001).

Nucleic Acids Res. 29:2145-2153(2001).

FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL SUBUNIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS OF THAT SUBUNIT (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE L20P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                           Transmembrane; Phosphorylation; Magnesium; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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Pred. No. 62;
0; Mismatches 3; Indels
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D4996A4D0635A68D CRC64;
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EXTRACELLULAR (POTENTIAL).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
RPLT OR MYPU_2610.
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                  InterPro; IPR001757; ATPASe_E1-E2.
InterPro; IPR001454; Hlgnase/hydrlase.
Pfam; PF00702; Hydrolase; 1.
PRNUS; PR00119; CATATPASE.
PROSITE; PS00154; ATPASE_E1_E2; 1.
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                                                                                         Multigene family.
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388
1499
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Q98QV0;
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Length 253;

EMBL; 236940; CAA85392.1; -. Hypothetical protein; Complete proteome. SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;

Query Match

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MEDLINE-20150912; PubMed=10688204;
MEDLINE-20150912; PubMed=10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
The genome sequence of the food-borne pathogen Campylobacter jejuni
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
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bengoylglycine amidohydrolase (Hippuricase) gene in Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 33; DB 1; Length 116; 77.8%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                   EMBL; AL445563; CAC13434.1; -.
MypuList; MYPU_2610; -.
InferPro; IRPOU1081; Ribosomal_L20.
Pfam; PF00453; Ribosomal_L20; 1.
PRINTS; PR00062; RIBOSOMALL20; 1.
PRODOM; PD002389; Ribosomal_L20; 1.
IIGREAMS; TIGR01032; rplr_bact; 1.
PROSITE; PS00937; RIBOSOMAL_L20; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
SEQUENCE 116 AA; 13565 MW; C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y990_CAMJE STANDARD; PRT; 253 AA. P45489; 09PNV0; 01-NOV-1995 (Rel. 32, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein Cj0990c.
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MEDLINE-95247673; PubMed=7730270;
Hani E.K., Chan V.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL139076; CAB73246.1; -
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Best Local Similarity 7/...
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STRAINEL TOT NIGS61 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; VC1732; ...

InterPro; IPR001986; BPSP_syntase.

Pfan: PF00275; EPSP_syntase; 1.

Probom: PF001867; EPSP_syntase; 1.

PROSITE; PS00104; EPSP_SYNTHASE_1; 1.

PROSITE; PS00805; EPSP_SYNTHASE_2; 1.

Aromatic amino acid biosynthesis; Transferase; Complete proteome. SEQUENCE 426 As; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 27;
1; Mismatches 3; Indels
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sixth step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
63.5%; Score 33; DB 1; 55.6%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                           426 AA.
                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004251; AAF94882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%;
60.0%;
                                 55.6%;
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Best Local Similarity 60.00,
                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 EFVIPAGOSY 232
                                                                                                                                                                                          185 DIFPSGMSY 193
                                                                                                                              2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMSY 10
                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR VC1732
                                                                                                                                                                                                                                                                                                                                                       AROA_VIBCH
Q9KRB0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cholerae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                      AROA_VIBCH
                                                               Matches
                                                                                                                                                                                                                                                                                     RESULT 10
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RA WOOD V., GAILILIAM R., RAJANGTAIRSONON,
RA WOOD V., GAILILIAM R., RAJANGTAIRSONON,
RA SQUUROS J., PERAT N., HRAZIES J., BARER S., BASSAMA D., BOWARD S.,
BROOKS K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA COLLINA M., CONNOR R., Croin N., Davis P., Feltwell T., Fraser A.,
RA COLLINA M., CONNOR R., Croin N., Harris D., Hiddalgo J., Jagels K.,
A HOLYOYG S., HORNEDY T., HOWART S., McDonald S., McLean J.,
RA MOOREY P., Moule S., Pearson D., Quail M.A., Rabbinowitsch E.,
A JIWER K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E.,
A Ritheford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Slamnonds M., Squares R., Squares S., Stevens K.,
A Taylor K., Taylor R.G., Aert R., Robben J., Girmonpres B.,
RA Taylor K., Taylor R.G., Aert R., Robben J., Girmonpres B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Euchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Euchs M., Reider H., Wambutt R., Purnelle B.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
R. Goffeau A., Callue E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Lucas M., Rochet M., Galllandin C., Pallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Rapa R.R., Cruado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Rature 415:871-880(2002)
C. - FURNIT: Forms a complex with Hsp90 Interacts with a number of
Kinases, resulting in stabilization and promotion of their
RAM Ramses, resulting in stabilization and promotion of their
RAM Ramses (By similarity).
C. - SIMILARITY: BELONGS TO THE COCT FRINITALING C.
- SIMILARITY: BELONGS TO THE COCT FRANCE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                               15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
HSp90 co-chaperone Cdc37 (HSp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDC37 OR SPAC9B6.10.
                                                                                                                                                                                                                                                                                                                                                                                                             Westwood P.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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EMBL, AJ132376; CAB38757.1; -.
EMBL, AL049769; CAB42371.2; -.
Chaperone; Cell division; Cell cycle.
SEQUENCE 466 AA; 52554 MW; 647238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21848401; PubMed=11859360;
                                                                                              15-JUN-2002 (Rel. 41, Created)
                                                STANDARD;
                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                           CC37_SCHPO
094740;
RESULT 11
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647238B34CABB3C5 CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Unclear.
TISSUE SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
SIMILARITY: BELONGS TO THE GLISCR2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE-20175430; PubMed-10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.; Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
                                       ö
                                                                                                                                                                                                              GSR2_HUMAN STANDARD; PRT; 478 AA.
09NZM5; Q9NPP1; Q9NPR4; Q9UF12; Q9BTC6; Q9HAX6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OUT 2002 (Rel. 41, Last annotation update)
15-UN 2002 (Rel. 41, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
DB 1; Length 466; 30;
                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                       2; Mismatches
63.5%; Score 33;
50.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF182076; AAF62873.1; -. EMBL; BC004229; AAH04229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 218-477 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC004229; AAH04229.1;
EMBL; BC006311; AAH06311.1;
                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 64:44-50(2000).
                                                                                                     : :| |||||
98 DSAIPGGMSY 107
                                                                              1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
  Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                        GLTSCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region
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REIQ -> VLTVSCRGAPCPVMTPSILLPVPPRGYGRHHGCP
WAGPVGPMPRG (IN REF. 5).
EGNILRDRFKSFQRRNMIEPRERAKFKXKVKLVEKRAFR
                                                                                                                                             G -> R (IN REF. 3).
RRKEQLWEKLAKQGELPREVRRAQARLINPSATRAKPGPOD
                                                                                                                                                                     TVERP -> SGRŠSYGRSWPSRAŠSPGGAQGPSPVAQPFCN
KGPNPAPGHRIAA (IN REF. 3).
SDNPLDRPLVGQDEFFIE -> LNNPDKPVVWPGCLFPG
                                                                                                                                                                                                                                             PEGNILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAF
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                            IQL -> RGQHSFETGSRAFRGGI (IN REF. 3)
7F18923E348CB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garnier T., Cole S.T.;
Complete nucleotide sequence and genetic organization of the
bacteriocinogenic plasmid, pIP404, from Clostridium perfringens.";
Plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garnier T., Cole S.T.; "Studies of UV\text{-inducible} promoters from Clostridium perfringens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garnier T., Cole S.T.; "Characterization of a bacteriocinogenic plasmid from Clostridium perfringens and molecular genetic analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium perfringens.
Plasmid pIP404.
Bacteria; Firmicutes, Clostridia, Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                   GGS -> HEG (IN REF. 2; AAH04229).
G -> R (IN REF. 3).
                                                                                                                                                                                                                     A -> S (IN REF. 2; AAH04229).
D -> H (IN REF. 3).
                                                                                                                                                                                                                                                                                                                              DB 1; Length 478;
                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                         FTIG=VAR_011486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                             63.5%; Score 33; 60.0%; Pred. No. 3
                                                                                                                                                                                                           (IN REF.
                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacteriocin-encoding gene.";
J. Bacteriol. 168:1189-1196(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88336297; PubMed=2901768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87057020; PubMed=2877971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89039249; PubMed=2460717;
           AF296124; AAG30413.1;
AL359335; CAB94786.1; -.
AL359336; CAB94787.1; -.
AL122063; CAB59242.1; -.
                                                                                              Nuclear protein; Polymorphism
                                                                                                                                                                                                                                                                                                    478 AA; 54417 MW;
                                              EMBL; AL122063; CAB59242.1;
SWISS-2DPAGE; Q9NZM5; HUMAN.
BC010095; AAH10095.1;
                                                                      HGNC:4333; GLTSCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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9
191
                                                                                                                                                                                                                                                                                                                                                                                                 239 EVAPAGASYN 248
                                                                                                                                                                                                                  235
417
477
                                                                                                                                                                                                                                                                               478
                                                                                                             389
                                                                                                                                                                                                                                                                                                                                                                         2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriocin BCN5
                                                                                                             389
                                                                                                                                                          146
                                                                                                                                                                                            198
                                                                                                                                                                                                                               417
                                                                                                                                                                                                                                                                             434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1502;
                                                                                 MIM; 605691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CPN50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CPN50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CPN50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCN5_CLOPE
P08696;
                                                                                                                                             CONFLICT
                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                          /ARIANT
                                                                       Genew;
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BCN5_CLOPE
                       EMBL;
                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 15 precursor (Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                            63.5%; Score 33; DB 1; Length 890; 66.7%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                             96699 MW; F4E5E8971C31C6C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: The N-terminus is blocked.
SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
vivo and in vitro.";
Mol. Microbiol. 2:607-614(1988).
-!- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-!- INDUCTION: BY UV IRRADIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1394 AA.
                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                 HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Fibroblast, and Platelet;
MEDLINE=90275601; PubMed=2350783;
                                                                                                                                                                                                                                                InterPro; IPR003646; SH3_bac.
SMART; SM00287; SH3b; 3.
Antlbiotic; Bacteriocin; Plasmid.
DOMAIN
B15 869 HYDR
                                                                                                                                                                                                EMBL; M14481; AAA98248.1; -.
EMBL; M32882; AAA98249.1; -.
                                                                                                                                                                                                                                                                                                                                                         Local Similarity 66.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            170 EVVPGGFTY 178
                                                                                                                                                                                                                                                                                                                                                                                                       2 EVVPXGMSY 10
                                                                                                                                                                                                                                  PIR; A30481; A30481.
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                                                                                                                                                                                                                                                                                                             890 AA;
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P22064;
                                                                                                                                                                                                                                                                                                               SEQUENCE
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MIM; 150390; --

R InterPro; IPR000152; Asx.hydroxyl.

R InterPro; IPR000152; Asx.hydroxyl.

InterPro; IPR001881; EGF-like.

InterPro; IPR001881; EGF_Ca.

R InterPro; IPR002212; Fibril-assoc.

R Pfam; PF00008; EGF; 15.

R SMART; SM000179; EGF_CA; 13.

R SMART; SM00001; EGF_Like; 4.

R PROSITE; PS0010010; ASX_HYDROXYL; 13.

R PROSITE; PS01187; EGF_L; 1.

R PROSITE; PS01187; EGF_CA; 15.

R R PROSITE; PS01187; EGF_CA; 15.

R Glycoprotein; Alternative Splicing.

I 20.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 15.
EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
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EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
REPEAT C.
                                                                                                                                                                                                                                              LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1S. EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
          EMBL; M34057; AAA61160.1;
                              HSSP; P00750; 1TPG.
GlycoSuiteDB; P22064; -.
Genew; HGNC:6714; LTBP1.
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Nature 406:477-483(2000).

-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

of DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

SUBSTRATES (By similarity).

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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STRAIN=E1 TOR Ni6961 / Serotype 01;
STRAIN=E20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Brmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).
RPOC OR VC0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MW; DFFCA81A40B2C7D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC.)
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BY SIMILARITY.
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%;
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Matches 5; Conservative
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399 KEICPGGMGYT 409
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Q9KV29;
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CARBOHYD
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RPOC_VIBCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TESURENCE OF 347-1595 FROM N.A.

REQUENCE OF 347-1595 FROM N.A.

TISSUE-Fibrobiast, and Platelet;

MEDLINE-90275601; PubMed-2350783;

A MAYAZONO K., Claesson-Welsh L., Heldin C.-H.;

MAYAZONO K., Claesson-Welsh L., Heldin C.-H.;

TGF-beta l with multiple repeat sequences.";

Cell 61:1051-1061(1990);

Cell 61:1051-1061(1990)

COMPOSED OF THE TGF-BETAI MOLECULE NONCOVALENTLY ASSOCIATED WITH

CELL FIFEBERAL PREDENCENCE OF A DIMER OF THE N-TERMINAL PROPERTIDE

OF THE TGF-BETAI PREDURSOR AND A THIRD COMPONENT DENOTED TGF-

BETAAL-BP. TGF-BETAI-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETAI.

CITCHERNATIVE PRODUCTS: 2 isoforms; a short form (AC P22064) and a long form (shown here); are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN (By similarity).
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Efficient association of an amino-terminally extended form of human latent transforming growth factor-beta binding protein with the extracellular matrix.";
J. Biol. Chem. 270:31294-31297(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1L precursor (Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%; Score 33; DB 1; Length 1401; 50.0%; Pred. No. 93; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olofsson A., Ichijo H., Moren A., ten Dijke P., Miyazono K., Heldin C.-H.;
                                                                                                                                                                                                                                                                                                                   Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                  1401 AA; 155021 MW; DFDB0F2B5514504F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96125117; Pubmed-8537398;
                                                                                                                                                                                                                                                                         Tick; vcuss,
Interpro; IPR000722; RNA_pol_A.
Interpro; IPR002879; RNA_pol_A2.
                                                                                                                                                                                                                             EMBL; AE004121; AAF93502.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-346 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 50.0 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                   Q9КWU6; 1HQM.
                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 1401 AA
                                                                                                                                                                                                                                                                   VC0329
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Q14766;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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LTBL_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                            RGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
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BGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LATENT TRANSFORMING GROWTH FACTOR BETA
BINDING PROTEIN 1L.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
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-!- TISSUE SPECIFICITY: The long isoform is found in fibroblasts.
-!- PIM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
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SIMILARITY.
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                                                                                                                                                                                                                                                                 M34057; AAA61160.1; ALT_INIT. P08709; 1BF9.
                                                                                                                                                                                                                                                                                                                      InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR001281; EGF_Ca.
InterPro; IPR002212; Fibril-assoc.
Pfam; PF00008; EGF; 15.
                                                                                                                                                                                                                                              EMBL; L48925; AAA96327.1;
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PROSITE; PS00002; EGF_1; 2.
PROSITE; PS01186; EGF_2; 10.
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PROSITE; PS01187; EGF_CA; 15.
Growth factor binding; Repeat; EGF_like domain; Hydroxylation; Signal.
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BINDING PROTEIN 1.
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Interpro; IPR001561; EGF-11ke.
Interpro; IPR001881; EGF-Ca.
Interpro; IPR002212; Fibril-assoc.
Pfam; PF00008; EGF; 16.
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           Proc. Natl. Acad. Sci. U.S.A. 87:8835-8839(1990).

-!- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS

-!- COMPOSED OF THE TGF-BETA1 MOLECULE NONCOVALENTLY ASSOCIATED WITH
A MASKING PROTEIN CONSISTING OF A DISULFIDE-BONDED COMPLEX OF A
DIMER OF THE N-TERMINAL PROPERTIDE OF THE TGF-BETA1 PRECURSOR AND
A THIRD COMPONENT DENOTED TGF-BETA1-BP (OR MP LARGE SUBUNIT).

TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1 precursor (Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-1) (Transforming growth factor beta-1 masking protein, large subunit). LTBP1.
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MEDLINE-91062373; PubMed=2247454;
Tsuji T., Okada F., Yamaguchi K., Nakamura T.;
"Molecular cloning of the large subunit of transforming growth factor type beta masking protein and expression of the mRNA in various rattissues.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Oncogene 8:1661-1666(1993).
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                                                                                      SEQUENCE FROM N.A.
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                         cyclin D2.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
Francke U., Jolicoeur P.;
"The Vin-1 gene, identified by provirus insertional mutagenesis,
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45.5%; Pred. No. 1.1e+02;
.ive 3; Mismatches 3; Indels
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01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
61/S specific cyclin D2 (Vin-1 proto-oncogene).
CCND2 OR VIN-1.
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5; Conservative
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718 KEICPGGMGYT, 728
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MEDLINE-93275661; 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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or send an email ...

DR EMBL; 106308; BAA01010.1; -..

DR EMBL; D16308; BAA03815.1; -..

DR InterPro; IPR00436; Cyclin.

DR Pfam; PF02984; cyclin_C; 1.

DR Pfo30292; CycLIN; 1.

DR PG03TE; PS00292; CYCLIN; 1.

DR Pfam; PF02984; cyclin_C; 1.

DR Pfam; PF02984; cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_Cyclin_C
                                                                                                        G1/S transition by prolactin in rat Nb2 cells.";
Gene 147:249-252(1994).
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
MEDLINE=95011623; PubMed=7926809;
Hosokawa Y., Onga T., Nakashima K.;
"Induction of D2 and D3 cyclin-encoding genes during promotion of the
G1/S transition by prolactin in rat Nb2 cells.";
                                                                                                                                                                                                 MEDLINE-93205384; PubMed-8455931;
Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;
"Cyclins Di and D2 are differentially expressed in human B-lymphoid cell lines.";
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xiong Y., Menninger J., Beach D., Ward D.C., "Molecular cloning and chromosomal mapping of CCND genes encoding human D-type cyclins."; Genomics 13:575-584(1992).
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1 EEVVPXGMSY 10
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Matches 6; Conserv
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NCBI_TaxID-7955;
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=10090;
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CGD1_BRARE
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                                                                                                                                                                                                                                                                                                                                                                expression of human cyclin D genes.";
Genomics 13:565-574(1992).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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                                                                                                                                                                                                                                                                                              Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
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                                                                             Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                        Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
CONFLICT 166 167 KL -> NV (IN REF. 5).
T -> H (IN REF. 5).
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01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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InterPro; IPR004367; Cyclin_Cterm.
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EMBL; M88080, AAA51928.1; JOINED.
EMBL; M88081, AAA51928.1; JOINED.
EMBL; M88082; AAA51928.1; JOINED.
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EMBE; D13639; BAA02802.1; -.
EMBL; BC010958; AAH10958.1; -.
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Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 1.
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    Oncogene 8:1049-1054(1993)
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Best Local Similarity bu..
Local 6; Conservative
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PIR; S26580; S26580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 AA;
                                                                                                                                                      ISSUE-Bone marrow;
                                              SEQUENCE FROM N.A.
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               rissue-Placenta;
                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 123833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGD2_MOUSE
ID CGD2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                      Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P30280;
      SOLUTION OF A PROPERTIES OF STREET O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
-:- SUBUNT: INTERACTION.
-:- SUBUNT: INTERACT WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
A SERINE/THREONINE KINASE HOLOGNZYME COMPLEX.
IMPARTS SUBSTRAFT SPECIFICITY TO THE COMPLEX.
-:- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-91235305; Pubmed=1827757; Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.; free cell cycle.";
G1/S-specific cyclin D2.

CCND2 OR CYL-2.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                "Cloning of a D-type cyclin from murine erythroleukemia cells.";
Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                             MEDLINE-92196134; PubMed-1372445;
Kiyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%; Score 32; DB 1; Length 289; 60.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M83749; AAA37519.1; -.

PIR; B400135; B40035.

PIR; B400135; B40035.

PIR; B41984; AA41984.

MGD; MGI:88314; Ccnd2.

RICHEPPO; IPR004366; Cyclin.

RICHEPPO; IPR004366; Cyclin.

RICHEPPO; IPR004366; Cyclin.

PÉAM; PF00134; cyclin. 1.

R PKART; SMORS; CYCLIN. 1.

R SAART; SMO385; CYCLINS; 1.

R PROSITE; PS00292; CYCLINS; 1.

R CYCLIN; Cell cycle; Cell division; Multigene family.

SEQUENCE 289 AA; 32897 WW; 58F322771DDIDA3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 40, Last annotation update)
GL/S-specific cyclin Dl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 AA
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                                                                                     Blochim. Blophys. Acta 1264:257-260(1995).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                        -!- SUBUNT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBUNT: INVERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERING-THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                  Yarden A., Salomon D., Geiger B.,
"Zebrafish cyclin D1 is differentially expressed during early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.5%; Score 32; DB 1; Length 291; 60.0%; Pred. No. 29; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPRRO0430, ...
Interpro; IPRRO0430, ...
Pfam; PPRO134; cyclin, 1.
Pfam; PPRO2984; cyclin, c; 1.
SWART; SW00385; CYCLIN; 1.
PROSITE; PRO0292; CYCLIN; 1.
Cyclin; Cell cycle; Cell division.
Cyclin; Cell cycle; Cell division.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
G1/S.specific cyclin D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 291 AA.
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InterPro; IPR004367; Cyclin_Cterm.
SEQUENCE FROM N.A.
MEDLINE-96138542; PubMed-8547308;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; X87581; CAA60885.1; -ZFIN; ZDB-GENE-980526-176; cycd1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                             (START) TRANSITION.
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                                                                         embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
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P50755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96144302; PubMed-8566807; MEDLINE=96144302; Nidd V.J.; Aidd V.J.; Arenet J., Kidd V.J.; Midd V.J.; Structure and gene expression of avian cyclin D2."; Gene 167:341-342(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (START) TRANSITION.
-1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                   Query Match 61.5%; Score 32; DB 1; Length 291; Best Local Similarity 60.0%; Pred. No. 29; Matches 6; Conservative 1; Mismatches 3; Indels
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                                                            Pfam; PF00134; cyclin; 1.
Pfam; PF0294; cyclin_C; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE: PS00292; CYCLIN; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Cycle; Cell division; Multigene family.
E 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
1-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2001 (Rel. 40, Last annotation update)
GI/S-specific cyclin D2.
        EMBL; X89475; CAA61664.1; -
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004366; Cyclin.
InterPro; IPR004366; Cyclin.
Pfam: PF00134; Cyclln; 1.
Pfam: PF02984; Cyclln; 1.
SWART; SM00385; CYCLIN; 1.
PROSITE: PS00292; CYCLINS; 1.
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Best Local Similarity 60.00
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                     1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                       73 EEVFPLAMNY 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                         CGD2_CHICK
P49706;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (START) TRANSITION.
-!- SUBDUTT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOGNIYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN PAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                        "Xenopus cyclin D2: cloning and expression in oocytes and during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
CYCLIN; Cell division; Multigene family.
SEQUENCE 291 Aa; 32959 WW; 9A290F04F1531E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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                              291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X83503; CAA58493.1; -.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin.Cterm.
Pfam; PF00134; Cyclin.; 1.
Pfam; PF02984; Cyclin.C; 1.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97380591; Pubmed-9237366;
Taieb F., Jessus C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                              early_development.";
Biol. Cell 88:99-111(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G1/S-specific cyclin D1.
                                  STANDARD;
                                                                                                             G1/S-specific cyclin D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMSY 10
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                                                                                                                                                                                                         Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                      NCBI_TaxID=8355;
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15-JUL-1999
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P55169;
                              CGD2_XENLA
P53782;
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              CGD2_XENLA
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RESULT 24
                                                $$ $\frac{1}{2}$$
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                                                                     Li H., Lahti J.M., Kidd V.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CEK4 AND CDK6 PROTEIN
(START) TRANSITION. INTERACTS WITH THE CDK4 AND CDK6 PROTEIN
KINASES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSTIE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 292 Aa; 33263 MW; 7B543029DB45A67D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR004366; Cyclin.
Interpro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                           EMBL; U40844; AAA83271.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00134; cyclin; 1.
Pfam, PF02984; cyclin, 1.
SMART; SM0385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%;
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Matches 6; Conservative
                                                        SEQUENCE FROM N.A.
            NCBI_TaxID=9031;
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Gallus
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Search completed: June 10, 2003, 13:40:20 Job time : 5.5 secs

1 EEVVPXGMSY 10 ||| | |:| 75 EEVFPLAMNY 84

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:30:25; Search time 25.7857 Seconds (without alignments) 87.898 Million cell updates/sec Run on:

US-09-909-164-9 52 1 EEVVPXGMSYS 11 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched: 671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_invertebrate:*
sp_mammal:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_human:* SPTREMBL_21:* sp_mhc:* 9: 110: 112: 113: 114: 115: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	098fxl rhizobium l 08rg86 fusobacteri 074056 cenarchaeum 09ury8 schizosacch 08r126 mus musculu 08v118 mus musculu 040129 lycopersico 09xvk4 caenorhabdi 04373 homo sapien 09bha5 plasmodium 09bh83 plasmodium 09bh83 plasmodium 09bh83 plasmodium 01487 rattus norv 09qm6 xylella fas 014122 homo sapien 012479 saccharomyc
ID	098FX1 08RG86 074056 0974056 0974058 097126 08V126 08V129 040129 095VW4 095VW4 095PW5 095PW6 01487 01487 01487 097182
DB	110 111 111 110 110 111 110 110 110
% Query Match Length DB ID	387 1063 3472 3472 3472 484 484 425 583 583 583 670 749 1902 1156
% Query Match	73.1.1.2.7.3.1.1.2.6.9.2.2.6.9.2.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3.1.3
Score	
Result No.	100 88 4 33 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

028342 archaeoglob 096mul homo sapien 092mde rhizobium m 098bps rhizobium l 090qd2 ureaplasma 09urr4 penicillium 08x105 ralstonia s 085914 homo sapien 08tx62 methanopyru 095x94 mus musculu 028330 archaeoglob	ctococc usobact ynechoc rabidop 011-bor 011-bor 011-bor 011-bor 011-bor	hermotoga- cosphila mo sapien us muscul mo sapien ibrio cho cosophila corcoptina erroptina erroptina erroptina mo sapien nus muscul us muscul	
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# ALIGNMENTS

	PRT; 387 AA.		eated)	18, Last sequence update)	st annotation update)		
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	PRELIMINARY		٠		ēļ.	drolase.	
LT 1 X1	Q98FX1	Q98FX1;	01-OCT-2001	01-0CT-2001	01-OCT-2001	Hippurate hydrolase	MLR3583.
RESULT 1 Q98FX1	Ω	AC	DŢ	DŢ	DI	DE	GN

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Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y., Swanson R.V.;
                                 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JNN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 367.1 kDa protein.
                                                                                                                                                      Archaea; Crenarchaeota; Cenarchaeum.
                                                                                                                                                                                                                                                                                                MEDLINE=98422450; PubMed=9748430;
                                                                                                                                 Cenarchaeum symbiosum.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=46770;
                                                                                                                                                                                                                                                                        STRAIN=B
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Q8R126
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REBL, Appoistor S., Sato S., Sat
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MEDLINE-21886394; PubMed-11889109;
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Battacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Earsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Genome sequence and analysis of the oral bacterium Fusobacterium fucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).

EMBL, AEOLOS54; AALA4625.1;
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                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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Pred. No. 29;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 16; Length 387; Pred. No. 9.8;
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SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
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Bacteria, Fusobacteria, Fusobacterium.
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      Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 074056 PRELIMINARY, PRT; : 074056, 01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                    MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.08;
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hes 6; Conserv
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                                                                                                                                                SEQUENCE FROM N.A.
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"Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
J. Bacteriol. 180:5003-5009(1998).
-!- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
Interpro: IPRO00515; BAD_transp.
Interpro: IPRO00515; BAD_transp.
Interpro: IPRO01680; WD40.
                                                                                                                                                                                                                                                                                                                                    Gaps
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EMBL; AL132779; CAB60105.1; -.
InterPro; IPR002645; STRAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PP07140; STRAS.1.
Pfam; PP07160; STRAS.1.
TIGREAMS; TIGR00815; Sulfate_transp; 1.
SEQUENCE 840 AA; 93317 MW; ED4833E162B69077 CRC64;
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                                                                                                                                                                                                                                                                                          Length 3472;
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                                                                                                                                                              SMART; SM00320; WD40; 2.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
Hypothetical protein; Repeat; WD repeat.
SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable sulfate permease.
                                                                                                                                                                                                                                                                                     Score 38; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840 AA.
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1; Mismatches
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Best Local Similarity '
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tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               Q9XVK4;
                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                  Q9XVK4
                                                                                                                                                                                                                         Matches
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.2 kba profein precursor.
Lycopersicon esculentum (Tomato).
Lycopersicon esculentum (Tomato).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                       01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 54.5 kDa protein (Fragment).
Hypotheticals (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 33;
                                                                                                                                                                                                                        69.2%; Score 36; DB 11; Length 471; 60.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017637; AAH17637.1; -.
MGD; MGI:2138595; AWS36441.
SEQUENCE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                             Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0258HJ0; AAH258HJ0.1; -.
Hypothetical protein.
                                                                                                                                                                                                    471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 225 AA.
                                                                                                                                                                                                                                                                                                                                                              484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                    2; Mismatches
               -JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%;
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Best Local Similarity 60.0.
First Conservative
Conservative
                                                                                                                                                                                                                                          Local Similarity 60.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                    226 EVIPAGASYN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
                                                                                                                                                                                                                                                                             2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                             NCBI_TaxID=10090;
                                                                                                                                   TISSUE=LIVER;
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     AW536441.
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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE=95375233; PubMed=7647301;
MEDLINE=95375233; PubMed=7647301;
Milligan S.B., Gasser C.S.;
Nature and regulation of pistil-expressed genes in tomato.";
Plant Mol. Biol. 28:691-711(1995).
EMBL: U20592: AAA80497.1; -
InterPro; IPR002160; Kunitz_legume.
Propom; PP000197; Kunitz_legume; 1.
                                                                                                                                                                                                                                                                                                                   Score 35; DB 10; Length 225;
Pred. No. 24;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 48; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                    SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 AA.
                                                                                                                                                                                     SMART; SM00452; STI; 1.
PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018("998).
EMBL: 281109; CAB03241.1; -.
InterPro; IPRO0719; Euk_pkinase.
Pfam; PRO0069; Pkinase; 1.
Probom; PD000001; Euk_pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                     UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                             Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                67.3%;
54.5%;
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nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMSYS 11
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32 DEVVPNGKTYA 42
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                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum choline transporter (PfSCT1) gene.";
Plasmodium falciparum choline transporter (PfSCT1) gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY007372; -AAK14816.1;
EMBL; AY007375; AAK14816.1;
InterPro; IPR002123; AAV1/Hransferase.
Pfam; PF01553; Acyltransferase; 1.
SEQUENCE 583 AA; 66917 MW; 2B2BFAE3B395E049 CRC64;
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                                                                                                                                                                                                           DB 4; Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ben Mamoun C., Gluzman I.Y., Goldberg D.E.; Figh gene."; "Plasmodium falciparum choline transporter (PfSCT1) gene."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%; Score 35; DB 5; Length 583; 55.6%; Pred. No. 67;
                                                                                                                                                                                                                                      1; Indels
                                                                                                                     Tubby B.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Z98050; CAB10847.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                         SEQUENCE 556 AA; 59059 MW; ECB00E4033FB2528 CRC64;
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                        Score 35; DB
Pred. No. 64;
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01-JUN-2001 (TrEMBLrel, 17, Last sen
                                                                                                                                                                                                                                                                                                                                                       PRT;
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            DNA binding protein (Fragment).
                                                                                                                                                                                                       67.38;
66.78;
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Best Local Similarity 55.00,
Labes 5; Conservative
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nes 6; Conservative
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                                                                                                                                                                                                                                                                                    244 VVPAGLTYS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
                                                                                                                                                                                                                                                          3 VVPXGMSYS 11
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                                                                                                        SEQUENCE FROM N.A.
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                                                                                 NCBI_TaxID=9606;
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                            DJ451B15
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09BHA5
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WEDDLINE-91187610; Pubmed=1901405;

MITCHELLOUGE C., Traboni C., Cortese R.;

Tisolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-antitrypsin promoter and to the major histocompatibility complex class I enhancer. The ALPHA1-ANTITRYPSIN PROMOTER, TO THE KAPPA INTOCOMPLIANT GENE ENHANCER, AND TO THE MAJOR ATTHE TRAPER INTOCOMPATIBILITY COMPLEX CLASS I ENHANCER; THE ALPHA1-ANTITRYPSIN EXPRESSION IT MAY ACT RESULAND.

AS A NEGATIVE REGULATOR BY INTERFERING AT THE ALPHA1-ANTITRYPSIN COLOR WITH ANOTHER NUCLEAR PROFEIN, CALLED LF-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                           Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: HIGHLY SIMILAR TO AT-BP1 AND TO THE PRDII-BF1 FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X54250; CAA38151.1; -...
HSSP; P15822; 1BB0.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; Zf_C2H2; 2.
SNART; SM00355; Znf_C2H2; 2.
PROSITE; PS50028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Zinc_finger; Nuclear protein; DNA-binding; Transcription regulation; Matal-binding; Multigene family.
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                                                                                                                                                                                                                                                                                                       U1-MAR-2002 (TrEMBLrel. 01, Last sequence update)
DNA-binding protein AT-BP2 (ALPHA1-antitrypsin promoter binding
Fattus norvegicus (Rat).
Eukaryota: Marran.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: ACIDIC AMINO ACID REGION MAY BE INVOLVED IN TRANSCRIPTIONAL ACTIVATION.
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0
                                                                                                    67.3%; Score 35; DB 5; Length 583; 55.6%; Pred. No. 67; 1; Indels ative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 11; Length 670; 66.7%; Pred. No. 78;
EMBL; AY007374; AAK14818.1; -.
EMBL; AY007373; AAK14817.1; -.
InterPro; IPRO123; Acyltransferase.
Pfam; PF0155; Acyltransferase; 1.
SEQUENCE 583 AA; 66918 MW; 4DF83D7530527474 CRC64;
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C(2)H(2) CLASS.
C(2)H(2) CLASS.
; CDD2324152590C17 CRC64;
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                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                Local Similarity 55.6
hes 5; Conservative
                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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160
74
                                                                                                                                                                 3 VVPXGMSYS 11
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82 1
670 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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les 6; Conserv
                                                                                                    Query Match
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ZN_FING
SEQUENCE
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DOMAIN
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RESULT 13

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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ANDELINE-20365717; Pubbed=10910347;

ANDELINE-20365717; Pubbed=10910347;

RA Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M., Anaces M.H.C., Arraya J.E., Bala G.S., Bapteste C.S., Barros M.R.S., Barros M.R.B.S., Barros M.R.B.S., Barros M.R.P., Camargo L.E.A., Carraro D.M., Carrer H., R. Benno M.R.P., Candroo C., Costa M.C.R., Costa N.C.R., Carrer H., R. Farda S.S., Ferreira V.C.A., Ferro J.A., R. Farda S.S., Franco M.C., Fronme M., Furlan L.R., Anderia M.B., Gondman G.H., Goldman M.L., Kemper E.L., Kitajima J.P., R. Garnier M., Goldman G.H., Goldman M.L., Kemper E.L., Kitajima J.P., R. Hopelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., R. Hopelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., R. Hopelsel J.D., Junqueira M.L., Lopes C.R., Machado J.A., R. Marchado M.A., Madeira A.M.B.N., Madeira H.M.F., Marisukuma A.Y., Marcins B.A.L., Martins E.A.L., Marsukuma A.Y., Mandins B.A.L., Martins E.A., Marsukuma A.Y., Moon D.H., Misca E.C., Nunces L.R., Oliveira M.A., Ade Oliveira M.C., de Oliveira R.C., Pereira H.A. Jr., Pesquero J.B., Ade Silveira M.C., de SarG., Santelli R.V., Sawasaki H.E., ade Silveira M.P., Terenzi M.F., Silveira M.A., Ade Silveira M.P., Terenzi M.F., Silveira S.N., Teruffi D., Tsai S.M., Tsubako M.H., Rago M.A., Zater M., Maddanis J., Setubal J.C., Sattelli S.N., Pettore A.L., R. Ago M.A., Zato M.A., Verjovski-Almeida S., Vettore A.L., R. Thogome S. Sato M. M., P. M., P. Terenzi M.F., Pettore M.L., Sawasaki H.E., R. Ago M.A., Zato M.A., Zater M., Wedidanis J., Setubal J.C., Sattellia S., Vettore A.L., R. M., R. Ago M.A., Zato M
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Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
NAR-binding protein (Nbp-1) (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35; DB 16; Length 749; 77.8%; Pred. No. 88;
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                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TEMBLrel. 21, Last annotation update)
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0; Mismatches
                               749 AA
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HSSP; P09097; 1AB4.
INTERPRO; IPR002205; DNA_topoisoIV.
Pfan; PF00521; DNA_topoisoIV; 1.
ProDom; PD000742; DNA_topoisoIV; 1.
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IIGRFAMs; TIGR01062; parC_Gneg; 1.
                               PRT;
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                                                                                                                                                                                                                     Topoisomerase IV subunit.
                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                Xylella fastidiosa.
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                                                                       09PDM6;
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09PDM6
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MEDLINE-94019318; PubMed-8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee Y.S., Shimizu J., Yoda K., Yamasaki M.; "Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevislae."; Biosci. Biotechnol. Biochem. 58:391-395(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYC2 encodes a factor involved in mitochondrial import of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                        SEQUENCE FROM N.A.
MEDLINE=90205817; PubMed=2108316;
MEDLINE=90205817; PubMed=2108316;
MEDLINE=90205817; PubMed=2108316;
Malarge protein containing zinc finger domains binds to related sequence elements in the enhancers of the class I major histocompatibility complex and kappa immunoglobulin genes.";
MACL Cell. Biol. 10:1406-1414(1990).
MEMBL; M32019; AAA17534.1;
HSSP; P15822; 1BBO.
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                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 4; Length 1902;
66.7%; Pred. No. 2.4e+02;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                SEQUENCE 1902 AA; 207457 MW; 35BBF0D961E6ED20 CRC64;
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 156 AA.
                                                                                                                                                                                   InterPro; IPR000822; znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
SMART; SM00355; znp_C2H2; 2.
PROSITE; PS00028; znC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Metal-binding; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Cell. Biol. 13:6442-6451(1993).
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                                                                                                                                                                                                                                                                                                                                     Query Match 67.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                     3 VVPXGMSYS 11
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          NCBI_TaxID=9606;
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PubMed-11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus,
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MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                           65.4%; Score 34; DB 3; Length 156;
66.7%; Pred. No. 27;
Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 17; Length 219;
Pred. No. 38;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of an aerobic thermoacidophilic Crenarcheach, Sulfolobus tokodail strain?.";
DNA Res. 8:123-140(2001).
EMBL; AP000985; BAB66348.1; -.
InterPro; IPR004788; RpiA.
InterPro; PD005813; RpiA.
Isomerase; Hypothetical protein; Complete proteome.
SEQUENCE 219 AA; 24541 MW; A4E9A3F2C4006D90 CRC64;
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EMBL; Z74920; CAA99201.1; -.
EMBL; X87331; CAA60762.1; -.
SGD; S0005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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Archaeoglobaccae; Archaeoglobus.
                                                                                                                                                                                                                                                                                             Last sequence update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cell division inhibitor (MIND-2).
                                                                                                                                                                                                                                                   219 AA
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                                                                                                         Conservative
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                                                                                                                                      2 EVVPXGMSY 10
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131 EVVPVGVAY 139
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                                                                                                                                                                                                                                                                                                                                                    Sulfolobus tokodaii
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=111955;
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6
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Retchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richadson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Tashiro H. Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Tushiro H. Yamazaki M., Komiyama M., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishi S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Waqatsuma M.,
Murakawa K., Kanebori K., Takahashi-Fujii A., Oshima A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ31891 fis, clone NT2RP7003304, weakly similar to YceA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.4%; Score 34; DB 17; Length 252; 75.0%; Pred. No. 44; 1; Indels tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%; Score 34; DB 4; Length 290; 66.7%; Pred. No. 52; 1:ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000707; ATPase_ParA.
Pfam; PF00991; ParA; 1.
Hypothetical protein; Cell division; Complete proteome.
SEQUENCE 252 AA; 27130 MW; A401DC1F93E8C538 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK056453; BAB71188.1; -...
InterPro; IPR001763; Rhodanese-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00581; Rhodanese; 1.
SEQUENCE 290 AA; 32972 MW; 41FB7FB0217C1421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 AA.
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01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000970; AAB89318.1; -. TIGR; AF1937; -.
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Best Local Similarity 60.,.,
Fine 6; Conservative
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Best Local Similarity 75.0°
Matches 6; Conservative
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EEIVPMGIS 43
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                                                                                                                                                                                                                                                                                                                  Venter J.C.;
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Q96MU1
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Q92MD6
   ACCOUNT OF THE SECTION OF THE SECTIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Backer A., Boutry M., Cadleu E., Dreamo S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
Analysis of the Chromosome sequence of the legume symbiont
Sinorhizoblum mellioti strain 1021.",
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL, ALS9191; CAC47269.1;
InterPro; IPR002933; Peptidase_M20.
Pfam; PF01546; Peptidase_M20; 1.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative HIPPURATE Mydrolase protein (EC 3.5.1.32).
HIPO1 OR R02690 OR SMC00682.
Rhizoblum melliloti (Sinorhizoblum melliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizoblum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            65.4%; Score 34; DB 16; Length 387; 50.0%; Pred. No. 70;
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                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase, Complete proteome.
SEOUENCE 387 AA; 41074 MW; 342763088907A6E3 CRC64;
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Last annotation update)
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01-00T-2001 (TrEMBLrel. 18, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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STRAIN-MAFF303099;
MEDLINE-21082930; PubMed=11214968;
                                                                                                                                                                                      MEDLINE=21396507; PubMed=11481430;
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                                                                                                                      NCBI_TaxID=382;
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Schuurs T.A., Newbert R.W., Turner G., Konings W.N., Driessen A.J.M.; Schuurs T.A., Newbert R.W., Turner G., Konings W.N., Driessen A.J.M.; Sulfate Transport in Penicillium chrysogenum: Cloning and Characterization of the surfa and sutB Genes."; J. Bacteriol. 181:7228-7234(1999).

EMBL; AF163994; AR14539.1;
InterPro; IPR001902; Sulfate_transp.
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=5076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=SEROYAR 3;
MEDLINE-20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
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                                                                                                                                                                                                                                                                                                                                                   Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae, Ureaplasma.
NCBI_TaxID=134821;
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PROSITE; PS01130; SULFATE_TRANSP; UNKNOWN_1.
PROSITE; PS01130; SULFATE_TRANSP; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 AA; 61291 MW; CF8756202A389C00 CRC64;
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01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                   01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative ABC substrate-binding protein-iron.
ABCSBP-5 OR UU359.
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Pfam; PF00916; Sulfate_transp; 1.
                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 urealyticum.";
Nature 407:757-762(2000).
EMBL; AE002133; AAF30768.1; -.
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Matches 6; Conservative
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||:|| | :|
445 EELVPVGKAY 454
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Matches 7; Conserv
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Query Match
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                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
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EMBL;
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Matches
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative aminophospholipid translocase (Aminophospholipid-transporting
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Artiguenave Chandlar M., Billault A., Brottler P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claddel-Renard C., Cunnac S., Demange N., Siguler P., Thebault P., Whalen M., Wincker P., Levy M., Schiex T., "Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21225279; PubMed=11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S., Oshimura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.4%; Score 34; DB 16; Length 1049; 75.0%; Pred. No. 2.1e+02; .ive 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1049 AA; 111769 MW; CB59674B670089CE CRC64;
                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable multidrug efflux system transmembrane protein.
MEXD OR RSP0312 OR RS05457.
                                                                                                                                                                                                                                                                              Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                               PRT; 1049 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1499 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL646078; CA017463.1; -
InterPro; IPR001036; Acrflvin_res.
InterPro; IPR004764; HAE1.
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-GMI1000;
MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00873; ACR_tran; I.
PRINTS; PR00702; ACRIFLAVINRP.
TIGRRAMS; TIGR00915; 2A0602; I.
PROSITE; PS50156; SSD; I.
Plaamid; Complete proteome.
SEQUENCE 1049 AA; 111769 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.00,
                                                                                                                                           PRELIMINARY;
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                        3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 MPAGMSYS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VPXGMSYS 11
                                                                                                                                                                                                                                                                                                   Plasmid megaplasmid,
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Ralstonia.
NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (nterPro
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ATP10C.
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                                                                                                 RESULT 23
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Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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MEDLINE=21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I.; Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malyh A.G., Koonin E.V., Kozyavkin S.A.;
The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
EMBL, AE010372; AAM02077.1;
Complete proteome.
                   SEQUENCE FROM N.A.
MEDLINE-21313119; PubMed-11353404;
Herzing L.B.K., Kim S.J., Cook E.H. Jr., Ledbetter D.H.;
The human aminophospholipid-transporting Arpase gene ArploC maps adjacent to UBESA adjacent similar imprinted expression.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00702; Hydrolass; 1.
PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 1499 AA; 167687 MW; D4996A4D0635A68D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 34; DB 4; 72.7%; Pred. No. 3e+02;
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IPR001454; Hlgnase/hydrlase.
                                                                                                                                                                                                                                      EMBL; AY029487; AAK33100.1; JOINED.
EMBL; AY029488; AAK33100.1; JOINED.
EMBL; AY029489; AAK33100.1; JOINED.
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AY029502; AAK33100.1; JOINED.
AY029503; AAK33100.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001757; ATPase_E1-E2.
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                                                                                                                                                              Am. J. Hum. Genet. 68:1501-1
EMBL; AB051358; BAB47392.1;
EMBL; AY029504; AAK33100.1;
Nat. Genet. 28:19-20(2001).
                                                                                                                                                                                                                                                                                                                               AY029491; AAK33100.1;
AY029492; AAK33100.1;
                                                                                                                                                                                                                                                                                                                                                                                                       AAK33100.1;
AAK33100.1;
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                                                                                                                                                                                                                                                                                                                                                                           AAK33100.
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0; 0; Gaps 3; Indels Best Local Similarity 60.0%; Pred. No. 40; Matches 6; Conservative 1; Mismatches

1 EEVVPXGMSY 10 ||:|| | | 75 EELVPQGAGY 84

Dp

Search completed: June 10, 2003, 13:46:32 Job time: 25.7857 secs

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(without alignments)
46.744 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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52
1 EEVVPXGMSYS 11
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| SIDS2/gcgdata/geneseq/genesegp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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| SIDS2/gcgdata/geneseqp-embl/AA1992.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1995.DAT:*/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1996.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2001.DAT:*/SIDS2/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Hepatitis C virus										
	QI	ABB80521	ABB80522	ABB80525	ABB80526	ABB80559	ABB80563	ABB80564	ABB80565	ABB80566	ABB80567	
	DB	23	23	23	23	23	23	23	23	23	23	
	Query Match Length DB	11	11	11	11	11	11	11	11	11	11	
æ	Query Match	96.2	96.2	96.2	96.2	96.2	96.2	96.2	96.2	96.2	96.2	
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11 12 13 14 14 16 16 17 19 20 21 22 23	77777777777777777777777777777777777777	68 69 71 73 74

ALIGNMENTS

ABB80521 ID ABBE RESULT 1

ABB80521 standard; peptide; 11 AA.

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/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Norvaly1 carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.2%; Score 50; DB 23; Length 11 100.0%; Pred. No. 0.0011; ive 0; Mismatches 0; Indels
                                                                 'note= "N-terminal acetyl"
                                                                                                                                                              /note= "C-terminal amide"
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                                                                                                                                     /note= "D-form residue"
                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             Brunck TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                         19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                    21-JUL-2000; 2000US-220101P.
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les 11; Conservative
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                                                                                                                                                                                                                                                                                              (CORV-) CORVAS INT INC.
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                                                                                                                       Misc-difference 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AA;
                                                                                                                                                                                     WO200208251-A2.
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               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating addisorders associated with hepatitis C virus.
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                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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                                                                                                                                                                                                                                                         /note= "C-terminal amide"
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                 residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                        Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB80522 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                               21-JUL-2000; 2000US-220101P.
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                                       08-OCT-2002 (first entry)
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                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus protease
                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                         Modified-site
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                                                                                                                                  Synthetic
                                                                                                           virucide
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31-JAN-2002
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      31-JAN-2002
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residue 7"
                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
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                         /note= "C-terminal amide"
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          /note= "D-form residue"
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100.08; Pie
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                                                                               19-JUL-2001; 2001WO-US23169
                                                                                               21-JUL-2000; 2000US-220101P
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                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSYS 11
                                                                                                                 (CORV-) CORVAS INT INC
                                                                                                                                  Levy OE,
                                                                                                                                                   WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                     Similarity
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   Misc-difference 8
                                                                                                                                                                                                                                                                                            11 AA;
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                                                                                                                                                                                     virus protease
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                                            WO200208251-A2
                    Modified-site
                                                                                                                                  Lim-wilby M,
                                                              31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-terminal acetyl"
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19-JUL-2001; 2001WO-US23169.
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Matches 11; Conservative
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                                                                                                                                                              Lim-wilby M, Levy OE,
                                                                                                         (CORV-) CORVAS INT INC
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                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                   Lim-wilby M, Levy OE, Brunck TK;
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                               (CORV-) CORVAS INT INC.
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                                                                                                                                      WPI; 2002-361643/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AA;
                                                                                                                                                                                                                                                      virus protease
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Modified-site
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Leucyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                        Gaps
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Claim 17; Page 65; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 65; 69pp; English.
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Matches 11; Conservative
                                                                                                                                                                                                                                                                  1 EEVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORV-) CORVAS INT INC
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                                                                                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus protease
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                                                                                                                                                                   Seguence
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/note= "2-aminoisobutyryl carbonyl residue forming a keto-amide linkage with residue 7"
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                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46
                                                                                                                                                                                                                                                    /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                         Location/Qualiflers
                            ABB80566 standard; peptide; 11 AA.
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                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus protease
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                                                            ABB80566;
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 RESULT 9
ABB80566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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  with residue 7"
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                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                     Gaps
                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.
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Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels
                       Score 50; DB 23; Length 11;
Pred. No. 0.0011;
0: Mismatches 0; Indels
                                       100.0%; Pred. No. U.v.
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                           ABB80565 standard; peptide; 11 AA.
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                          96.28;
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                                                          Conservative
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                                                                                     1 EEVVPXGMSYS 11
                                                                                                       1 EEVVPXGMSYS 11
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                                          Similarity
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11 AA;
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                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                           ABB80565;
   Sequence
                            Query Match
                                               Local
                                                            Matches
                                                                                                                                                                   RESULT 8
                                                                                                                                                                                   ABB80565
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Brunck TK;

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                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                           96.2%; Score 50; DB 23; Length 11; 100.0%; Pred. No. 0.0011; Live 0; Mismatches 0; Indels
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Claim 17; Page 65; 69pp; English.
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les 11; Conservative
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-Ketoamide peptide analogues. The peptides have invention are alpha-Ketoamide peptide analogues. The peptides have a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active incredient is useful for treating disorders associated with hepatitis C virus.
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/note= "Alpha-propynyl-glycinyl-carbonyl residue forming
a keto-amide linkage with residue 7*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Norvaly1 carbonyl forming keto-amide linkage with residue 7" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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100.0%; Pred. No. 0.0011;
0; Indels
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                                                                  /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "D-form residue"
                                                                                                                                                                                                               Lim-wilby M, Levy OE, Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80524 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                              Claim 17; Page 65; 69pp; English.
                                                                                                                                       19-JUL-2001; 2001WO-US23169
                                                                                                                                                               21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                      (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMSYS 11
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                                                                                                                                                                                                                                        WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AA;
                                                                                        WO200208251-A2
                                                                                                                                                                                                                                                                                         virus protease
                Modified-site
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                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                         "(s,s)allothreonyl carbonyl residue forming a keto-amide linkage with residue 7"
                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48
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                                                                                                                /note= "N-terminal acetyl"
                                                                                                                                                                          /note= "C-terminal amide"
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                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              Brunck TK;
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                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                      Lim-wilby M, Levy OE,
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                                                                                                Modified-site
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Modified-site
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                                                              Synthetic
                                        virucide
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Best Local (
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/note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
                                                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9
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                                                                                                                                                                                                                                                                                                                                 Score 46; DB 23; Length 11;
pred. No. 0.0075;
0; Mismatches 1; Indels
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Brunck TK;
                                                                                                                                    Claim 17; Page 64; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                        88.5%;
90.9%;
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Matches 10; Conservative
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 Lim-wilby M, Levy OE,
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                                   WPI; 2002-361643/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 9
                                                                                                                                                                                                                                                                                                           11 AA;
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                                                                                                      virus protease
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                                                                                                                                                                                                                                                                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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                                                                                                                                                     Brunck TK
                                                                                                                                                                                                                                                                                      Claim 17; Page 64; 69pp; English.
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                                                19-JUL-2001; 2001WO-US23169.
                                                                                  21-JUL-2000; 2000US-220101P.
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Matches 10; Conservative
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                                                                                                                                                     Lim-wilby M, Levy OE,
                                                                                                                    (CORV-) CORVAS INT INC.
                                                                                                                                                                                       WPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AA;
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                                                                                                                                                                                                                                                         virus protease
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                     31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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RESULT 13 ABB80528

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Length 11; 1; Indels

Score 46; DB 23; Pred. No. 0.0075; 0; Mismatches

88.5%; 90.9%;

11 AA;

1 EEVVPXGMSYS 11

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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                       Local Similarity 90.9
nes 10; Conservative
                                                                                                   Sequence
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                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invention are alpha-ketoamide peptide analogues. The peptides have a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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                                                                                                                                                                                           88.5%; Score 46; DB 23; Length 11; 90.9%; Pred. No. 0.0075; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         ABB80561 standard; peptide; 11 AA.
                         Claim 17; Page 64; 69pp; English.
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Best Local Similarity 90.99
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                                                                                                                                                                11 AA;
 virus protease
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"Norvaly1 carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
                                                                                                                                                                                                                                                        /note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                               note= "Oxymethionine"
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                                                           ABB80562 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brunck TK;
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1 EEVVPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-361643/39.
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                                                                                                                                                                                                      Synthetic.
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1 EEVVPXGMHYS 11
1 EEVVPXGMSYS 11
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                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                            Gaps
    is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
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Best Local Similarity 90.9%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 1; Indels
                                       Score 46; DB 23; Length 11;
Pred. No. 0.0075;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                          /note= "N-terminal acetyl"
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                                                                                                                                               ABB80523 standard; peptide; 11 AA.
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                                           88.5%;
                                                    90.98;
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                                    Lim-wilby M, Levy OE,
                                                                                1 EEVVPXGMSYS 11
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                                                                                                  1 EEVVPXGMDYS 11
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                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-terminal acetyl"
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   AA.
ABB80527 standard; peptide; 11
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Matches 10; Conservative
                                                                                                                  (first entry)
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/note= "Norvalyl carbonyl forming keto-amide linkage with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                 /note= "N-terminal acetyl"
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                                                                                                                             /note= "D-form residue"
                                           Location/Qualifiers
                                                                                                         residue 7"
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Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                              Misc-difference 9
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                                                                                                                                                                          WO200208251-A2.
                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                          virus protease
                                                                           Modified-site
                                                                                                                                      Modified-site
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                                                                                                                                                                                                     31-JAN-2002.
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                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-Ketoamide peptide analogues. The peptides have invention are alpha-Ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #15.
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Pred. No. 0.012;
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                                                                                                                                                                            /note= "N-terminal acetyl"
                                                                                                                                                                                                                           11
/note= "C-terminal amide"
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                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                   residue 7"
                                                                                                                                                                                                                                                                                                                                                                                         Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80536 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                            19-JUL-2001; 2001WO-US23169.
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90.9%;
                                    08-OCT-2002 (first entry)
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Best Local Similarity 90.5.
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                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-361643/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus protease
                                                                                                                                                            Modified-site
                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                        Modifled-site
                                                                                                                                                                                                                                                                                   31-JAN-2002
                                                                                                                         Synthetic
             ABB80535;
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Gaps

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(CORV-) CORVAS INT INC
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                                                                                                                                                           virus protease
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         31-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
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"Norvaly1 carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                             hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                86.5%; Score 45; DB 23; Length 11; 90.9%; Pred. No. 0.012; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                   /note= "C-terminal amide"
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              /note= "D-form residue"
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                                                                                                                                                                  Brunck TK;
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                                                                                                   19-JUL-2001; 2001WO-US23169.
                                                                                                                        21-JUL-2000; 2000US-220101P.
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                                                                                                                                                                   Lim-wilby M, Levy OE,
                                                                                                                                             (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                              11 AA;
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      Misc-difference 8
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                                                                                                                                                                                                                                   virus protease
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                                                           WO200208251-A2
                            Modified-site
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                                                                                 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
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Pred. No. 0.012;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                             Brunck TK;
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19-JUL-2001; 2001WO-US23169
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Matches 10; Conservative
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                                                                                                                                                               Lim-wilby M, Levy OE,
                                                                                                           (CORV-) CORVAS INT INC
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peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
                                                                                           sequence represents a peptide compound of the invention having
                                                                    Claim 17; Page 65; 69pp; English.
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                                                virus protease
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Modified-site
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                                                                                                                                                                                      Sequence
                                    activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                            virucide.
                         Novel
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                                                                                                                         The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have inventide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                          Gaps
                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40
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                                                                                                                                                                                                                                             Score 45; DB 23; Length 11; Pred. No. 0.012;
                                                                                                                                                                                                                                                                     1; Indels
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                 Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                   ABB80560 standard; peptide; 11 AA.
                                                                                                   Claim 17; Page 65; 69pp; English.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                    1 EEVVPXGMHYS 11
              Levy OE,
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                                  WPI; 2002-361643/39.
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                                                                                                                                                                                                                    11 AA;
                                                                               virus protease
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             Lim-wilby M,
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                                                                                                                                                                                                                      Seguence
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                               DB 23; Length 11;
                                                                                                                                                                             Indels
                                                                                                                                                                           1;
                                                                                                                                           Score 45; DB 23;
Pred. No. 0.012;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                         ABB80544 standard; peptide; 11 AA.
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                                                                                                                                           86.5%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                    Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                    1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                 1 EEVVPXGMHYS 11
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                                                                                                           11 AA;
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RESULT 1
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Sequence 236, App
Sequence 236, App
Patent No. 5177197
Patent No. 5177197
Service 236, App
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Appli
Appli
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Sequence 4, 1
Sequence 4, 1
                                                         June 10, 2003, 13:31:45; Search time 9.64286 Seconds (without alignments) 33.564 Million cell updates/sec
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Sequence 7
Sequence 2
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Sequence
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-637-759B-236
US-08-871-355A-236
US-09-201-945-236
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US-08-464-517-22
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US-08-463-772-6
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US-08-460-744-4
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                                                                                                                                                                       262574 seqs, 29422922 residues
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Listing first 75 summaries
                                          OM protein - protein search, using sw model
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Gapop 10.0', Gapext 0.5
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Maximum DB seq length: 200000000
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52
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Match Length DB
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Sequence 6, Appli Sequence 23, Appl Sequence 6, Appli Sequence 23, Appl Sequence 23, Appl Sequence 8, Appli Sequence 8, Appli	Sequence 19, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli
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## ALIGNMENTS

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RESULT 1
US-09-228-986-73
; Sequence 73, Application US/09228986
; Sequence 73, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; TITLE OF INVENTION NUMBER: US/09/228,986
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT PILING DATE: 1999-01-12
; SEQ ID NO 73
; SEQ ID NO 73
; SEQ ID NO 73
; TYPE: PRT
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-73
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                                                    65.4%; Score 34; DB 4; Length 947; 66.7%; Pred. No. 1e+02; Vative 2; Mismatches 1; Indels
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63.5%; Score 33; DB 2; Length 45;
Best Local Similarity 60.0%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 3: The Allocal Standard Conservative 15 Mismatches 3: The Allocal Conservative 15 Mismatches 15 Mi
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY 1996
CLLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
ATORNEY/AGENT INFORMATION:
NAME: PADAE, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
THE FERENCE/DOCKET NUMBER: RPMS 101
THE FERENCE/DOCKET NUMBER: RPMS 101
THE FERENCE/MONTAGENT IN 075-MATON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 236, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
TTLLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 236, Application US/08871355A
Patent No. 6015669
CENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-055/MS-DOS
Query Match
Best Local Similarity 66.7%;
'-hag 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236
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LENGTH: 45 amino acids
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STRANDEDNESS: Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-637-759B-236
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Gaps
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                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTER: USAS ASSOCIATED TO COUNTER TEACHER FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
RERERNEN-ZPOCKET NUMBER: RPMS 101 CON
TELECOMMUNICATION INFORMATION:
TELEFRAN: (404) 873-8794
INFOREMERA: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                            PCT/GB95/02875
                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-201-945-236
; Sequence 236, Application US/09201945
; Patent No. 6342215
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APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                               COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                               Georgia
                                                                                                                                                                                                                                                              FILING DATE: 09
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 6; Conserv
                                                             Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: C.
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-871-355A-236
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APPLICANT: Zhang, the "Library and the "Library applications" is a minimal applicant. The "Library applicant" is a minimal applicant. Cai, Sui Xiong APPLICANT: Cai, Sui Xiong APPLICANT: Cai, Sui Xiong APPLICANT: Day and "Library applicant" of her Enzymes and the Use Thereof FILE REFERENCE: 1735,003001

CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: US 60/093,642

EARLIER APPLICATION NUMBER: US 60/093,642

EARLIER FILING DATE: 21-JUL-1998

NUMBER OF SEQ ID NOS: 139

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:Synthetic; OTHER INFORMATION: Peptide US-09-357-952-66
                                                                                                                                            APPLICANT: KANZAKI, TETSUTO, OLOESSON, ANDERS; MOREN, ANITA;
APPLICANT: KANZAKI, TETSUTO, OLOESSON, ANDERS; MOREN, ANITA;
WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
LENA; HELDIN, CARL-HERRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATE:
REPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.5; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 33; DB 6; Length 139
45.5%; Pred. No. 2.6e+02;
Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 66, Application US/09521650
; Patent No. 6335429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 66, Application US/09357952
Patent No. 6248904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.vv
Best Local 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 KEICPGGMGYT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPXGMSY 10
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                                     399 KEICPGGMGYT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSYS 11
1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                          ; Patent No. 5177197
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1394
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                                                                                                                                                                                                                                                                                                                                                                                             5177197-30
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WERNSTEDT, CHRISTER; HELLMAN, ULE; MIYAZONO, KOHEI; CLAESSON-WELSH,
LENA, HELDIN, CAEL-HERRIK
TILLE OF INVENTION: ISOLATED NUCLECTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATE:

PELLING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, LENA; HELDIN, CARL-HENRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 6; Length 410;
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 6; Length 65; Pred. No. 7.8; 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 33; DB 4; Length 45; 60.0%; Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 5.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                      RPMS 101
                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATGAREY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,284
REPREROCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%;
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity 45.2.
Best Local 5; Conservative
                                                                                                                                                                                                                                                 45 amino acids
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMSY 10
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                        FILING DATE:
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APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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Sequence 4, Application US/08460694
Fatent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/5R0 QD002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: 35,423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-5321
TELEFAX: 713-777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 32; DB 60.0%; Pred. No. 21; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      E: Dr. Benjamin A. Adler
8011 Candle Lane
                                                                                                                                                                         Sequence 23, Application US/08580988A Patent No. 5856161 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         January 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                   1 EEVVPXGMSY 10
                                                                        1 DDIVPCSMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION:
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                                                                                                                                     RESULT 11
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APPLICANT: Weber, Eckard
APPLICANT: Weber, Eckard
APPLICANT: Cai, Suin Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Exemply and a suin Air Application of Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735.0290002
CURRENT PAPLICATION NUMBER: US/09/168,888
EARLIER FILING DATE: 1997-10-10
EARLIER PRING DATE: 1997-10-10
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PatentIn Ver. 2.0
                                                             APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
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Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/521,650
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 09/168,888
EARLIER PILING DATE: 1998-10-09
EARLIER PILING DATE: 1998-10-09
EARLIER PILING DATE: 1997-10-10
EARLIER FILING DATE: 1997-03
EARLIER FILING DATE: 1998-03-03
SOUMBER OF SEQ ID NOS: 142
SOUTHARE: PATCHIN VET. 2.0
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Patent No. 6342611
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                            APPLICANT: Keana, John F.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.5
Best Local Similarity 50.0
Matches 5; Conservative
APPLICANT: Cai, Sui Xiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DDIVPCSMSY 10
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LENGIH: 10
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LENGTH: 152 amino acids
                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Arnold, Andrew
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD! Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERRE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
         STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,744
                                                                                                                                                                              1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFTLANA DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCONDALP, Feelpn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFRAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08460744; Patent No. 6107541; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 152 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-460-694-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 EEVFPLAMNY 29
                       STREET: 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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             ADDRESSEE:
                                                                                                      20002
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                                                                                         Score 32; DB 3; Length 152;
Pred. No. 33;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/07667711B
Sequence 4, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-193-977-7; Sequence 7, Application US/08193977; Sequence 7, Application US/08193977; Patent No. 5625031; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 066
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WEBSTER, KEVIN R. APPLICANT: COLEMAN, KEVIN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
STRANDEDNESS: not relevant;
TOPPLOGY: linear
MOLECULE TYPE: peptide
US-08-460-744-4
                                                                                                   61.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 amino acids
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not relevant
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Matches 6; Conservative
                                                                                Query Match
Best Local Similarity 60.v.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-07-667-711B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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RESULT 17
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TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN UNMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/08464517
Patent No. 586940
GENERAL INFORMATION:
APPLICAMT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 32; DB 1; Length 173; 60.0%; Pred. No. 38; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
CLASSIFICATION: 530
                                                                                                   STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COMPUTENY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                  E: REED & ROBINS
635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-193-977-7
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STREET: b...
""V: Boston
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ZIP: 02109
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APPLICANT: BEACH, David H.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 2; Length 189;
Pred. No. 42;
1; Mismatches 3; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 227-7400
TELEFRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-00T-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/08246361A Patent No. 5998582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      61.5%;
60.0%;
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TELEPAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0%
                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-517-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMSY 10
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STRANDEDNESS: sir
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ZIP: 02109
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GENERAL INFORMATION:
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APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD .
STREET: 60 State Street.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 32; DB 3; Length 189; 60.0%; Pred. No. 42; tive 1; Mismatches 3; Indels
                                                                       Query Match
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 21, Application PC/TUS9305000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       ; Sequence 21, Application US/08463772
; Patent No. 6066501
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Best Local Similarity 60.v.
6; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                             MOLECULE TYPE: peptide
                                                                                                                                                             1 EEVVPXGMSY 10
                                                                                                                                                                                                 74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
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                                               US-08-246-361A-21
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                                                                                                                                                                                                                                                         RESULT 18
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INFERTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 32; DB 5; Length 189; 60.0%; Pred. No. 42; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/05000 FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MA-1992
ATORNET/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSHL91-02A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 22, Application US/08464517; Patent No. 5869640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 189 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0.
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TELEPHONE: 61/-00-
TOWNER 616-861-9540
                                                                                   ADDALL STREET: TWO LECTIVE LEXINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein PCT-US93-05000-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                             02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-464-517-22
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236 amino acids

single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-22
                                                      TYPE: amino acid
STRANDEDNESS: sir
                                LENGTH:
                                                                                                                                                                                                                                                                                           δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
61.5%; Score 32; DB 2; Length 236;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/08/246,361A CLASSITCATION NUMBER: US/08/246,361A CLASSITCATION 1, 435
PRIOR APPLICATION NUMBER: US 07/963,308
FILNG APPLICATION NUMBER: US 07/963,308
FILNG APPLICATION NUMBER: US 07/888,178
FILNG APPLICATION NUMBER: US 07/888,178
FILNG APPLICATION NUMBER: US 07/701,514
FILNG NAME: Matthew P. Vincent
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
                                                                                                   APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             MII-004C
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REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-246-361A-22
; Sequence 22, Application US/08246361A
; Patent No. 5998582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                      NAME: Matthew P. Vincent
REGISTRATION NUMBER: 35,709
REFERENCE/DOCKET NUMBER: MII-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TVPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 | 1:1
20 EEVFPLAMNY 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
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61.5%; Score 32; DB 2; Length 236;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 236;
                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.5%; Score 32; DB 60.0%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION AND CONTROL OF CLASSIFICATION ATTAINS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/863,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MI1-004C
TELECHOUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      ; Sequence 22, Application US/08463772 ; Patent No. 6066501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                   1 EEVVPXGMSY 10
                                                                                       |||| | |:|
20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-772-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSY 10
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Best Local Similarity
Local 6; Conserva'
                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                       02109
                                                                                                                                                  RESULT 22
US-08-463-772-22
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                      STATE:
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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US-08-646-517-6
US-08-66-517-6
Sequence 6, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                      Sequence 22, Application PC/TUS9305000
Sequence 22, Application:
GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%; Score 32; DB 5; Length 236; 60.0%; Pred. No. 54;
                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMUNICATION INCOMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19930525
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 236 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0"
Best Local Similarity 60.0"
                                                                                                                                                        ADDALL
STREET: TWC...
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein PCT-US93-05000-22
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
            PCT-US93-05000-22
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RESULT 23
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Sequence 6, Application US/08463772
Sequence 6. Application US/08463772
Sequence 6. Application US/08463772
Sequence 6. Application US/08463772
Sequence 6. Model Color Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2; Length 280;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING BATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAX-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILLING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                 FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELEPONMICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAS: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 61.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-464-517-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 EEVFPLAMNY 84
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| SEQUENCE CHARACTERISTICS:
| LENGTH: 280 amino acids | TOPOLOGY: amino acids | TOPOLOGY: linear | TOPOLOGY:
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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2003, 13:46:50 ; Search time 15 Seconds

(without alignments)

75.710 Million cell updates/sec
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Title: US-09-909-164-10
Perfect score: 52
Sequence: 1 EEVVPXGMSYS 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Gapop LU.U , Gapext U.S Searched: 392085 seqs, 103240269 residues Total number of hits satisfying chosen parameters: 39208

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Published Applications_AA:*

1. /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2. /cgn2_6/ptodata/2/pubpaa/PCT_REW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_REW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USOS_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOO_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 73, Appl	Seguence 43, Appl	Sequence 108, App	Sequence 108, App	Sequence 184, App		Sequence 108, App	ď	Ċ	Sequence 53, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 54, Appl	Sequence 1061, Ap	Sequence 4, Appli	Sequence 4, Appli	
	ΩI	US-10-027-806-4	US-10-034-623-4	US-10-027-801-4	US-10-101-464A-73	US-10-214-766-43	US-09-924-340-108	US-09-992-600A-108	US-09-746-783-184	US-10-000-489-108	US-10-000-986-108	US-09-820-843A-26	.0 US-09-947-387-66	.0 US-09-778-927A-53	US-10-024-066-2	) US-10-024-066-4	.0 US-09-919-497-54	.0 US-09-925-300-1061	0 US-09-923-304-4	US-10-101-921-4	
	Query Match Length DB	3472 9	3472 9	3472 9	947 9	426 9	478 9	478 9	478 9	478 9	478 9	623 9	10 1	254 1	289 9	289 9	289 1	295 1	529 1	691 9	
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## ALIGNMENTS

RESULT 1

US-10-027-806-4

Sequence 4, Application US/10027806

Patent No. US20020160476A1

GENERAL INFORMATION:

APPLICANT: Seamon, Ronald V.

APPLICANT: Feldman, Robert A.

APPLICANT: Schleper, Christa

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM

FILE REFERENCE: DCORP. 002A

FILE REFERENCE: DCORP. 002A

CURRENT APPLICATION NUMBER: US/10/027,806

CURRENT FILING DATE: 2001-12-21

Gaps

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Length 3472;

73.1%; Score 38; DB 9; Length 347 54.5%; Pred. No. 1.2e+02; Live 4; Mismatches 1; Indels

Query Match
Best Local Similarity 54...
For the conservative of Conservative

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Sequence 4, Application US/10034623

Sequence 4, Application US/10034623

Publication No. US20020198365A1

GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa

TITLE OF INVENTION: UCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A

FILE REFERENCE: 2001-12-21

CURRENT FILING DATE: 2001-12-21

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: RastEED for Windows Version 3.0

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APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT FILING DATE: 2001-12-21
PRIOR PPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
SUFFMARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020 PRIOR FILING DATE: 1999-09-29 NUMBER OF SEQ ID NOS: 123 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20030054364A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Cenarchaeum symbiosum
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ORGANISM: Cenarchaeum symbiosum
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; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4
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2294 EDVIPRGISFS 2304
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Matches 6; Conservative
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LENGTH: 3472
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US-10-034-623-4
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.10202
CURRENT APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 60/228,986
PRIOR PILING DATE: 1999-11-01
PRIOR PILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1090-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEO ID NOS: 989
SOFTWARE: FSELSEO for Windows Version 4.0
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Publication No. US20030084473A1
GENERAL INFORMATION:
APPLICANT: Gocal, Greg
TITLE OF INVENTION:
FILE REFERENCE: CA1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.4%; Score 34; DB 9; Length 947; 66.7%; Pred. No. 1.8e+02; tlve 2; Mismatches 1; Indels
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CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,734
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
                                                                                                                                                     Sequence 73, Application US/10101464A; Publication No. US20030046728A1; GENERAL INFORMATION:
                       |:|:| |:|:|
2294 EDVIPRGISFS 2304
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Best Local Similarity 66.79
Watches 6; Conservative
1 EEVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pinus radiata
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Best Local Similarity
Matches 6; Conserv
                                                                                                                            US-10-101-464A-73
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LENGTH: 947
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APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TILLEOF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.032.REG
CURRENT PELLING DATE: 2001-08-06
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PUBLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
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GENERAL INFORMATION:
APPLICANT: Benjain, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US4.DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 9; Length 478; Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
; Mismatches 3; Indels
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                                                                                                                                               Sequence 108, Application US/09924340 Publication No. US20030027248A1 GENERAL INFORMATION:
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Best Local Similarity 60.0.
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223 EFVIPAGQSY 232
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: JPatent
SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-992-600A-108
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                                                                                                     RESULT 6
US-09-924-340-108
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LENGTH: 478
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LaVallie, Edward R.
Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Schen H.
Fechlel, Kim
FILLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-000-489-108
Sequence 108, Application US/10000489
Publication No. US20030092011A1
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%; Score 33; DB 9; 1
60.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <UNKnown>
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-746-783-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Milasincic, Debra J. REGISTRATION NUMBER: 46,931 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 184:
                                                                                                                                                                      US-09-746-783-184
; Sequence 184, Application US/09746783
; Sequence 180, No. US20030044935A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 478 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                          APPLICANT: Jacobs, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                    239 EVAPAGASYN 248
                                           2 EVVPXGMSYS 11
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Sequence 26, Application US/09820843A
Publication No. US20030039953A1
GENERAL INFORMATION:
APPLICANT: COUNCIL of Scientific and Industrial Research
TITLE OF INVERTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PI
TITLE OF INVERTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
LENGTH: 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Reana, John F.W.
APPLICANT: Reana, John F.W.
APPLICANT: Thew, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: 1735,0290005
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KET: misc_feature
OTHER INFORMATION: iron(III) ABC transporter, permease protein
NAME/KEY: misc_feature
OTHER INFORMATION: gi|9654609
US-09-820-843A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:Synthetic; OTHER INFORMATION: Peptide US-09-947-387-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%; Score 33; DB 9; Length 653; 66.7%; Pred. No. 1.9e+02; tive 2; Mismatches 1; Indels
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CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/061,582
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 66, Application US/09947387; Patent No. US20020150885A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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                       US-09-820-843A-26
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LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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Publication No. US20030096247A1

GENERAL INCOMATION:
APPLICANT: Benjain, Stephane
APPLICANT: Tanaka, Hiroaki
TILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91 US9 DIV
CURRENT FILING DATE: 2001-11-14
FRICA REPLICATION NUMBER: US/10/000,986
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-08-06
PRIOR FILING DATE: 2001-01-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PRILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
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Pred. No. 1.4e+02;
1; Mismatches 3; Indels
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                                                             CUKKENT FILLING DATE: ACULTIL-14

PRIOR PELICATION NUMBER: US 09/924,340

PRIOR FILING DATE: 2001-08-06

PRIOR PELICATION WUMBER: PCT/IB01/01715

PRIOR PELICATION WUMBER: PCT/IB01/01715

PRIOR PELICATION WUMBER: US 60/305,456

PRIOR APPLICATION WUMBER: US 60/302,277

PRIOR PELING DATE: 2001-06-29

PRIOR PELING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 108

LENGTHH: 478
FILE REFERENCE: 91.056.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
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60.08;
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Best Local Similarity 60.0°
Matches 6; Conservative
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239 EVAPAGASYN 248
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SOFTWARE: JPatent
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SEQ ID NO 108
LENGTH: 478
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US-10-000-986-108
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Sequence 2, Application US/10024066

Patent No. US20020166134A1

GENERAL INFORMATION:

APPLICANT: Flead, Loren J.

APPLICANT: Feal C. LOREN J.

TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

FILE REFERENCE: 7037-450

CURRENT APPLICATION NUMBER: 02/10/024,066

CURRENT APPLICATION NUMBER: 06/139,942

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-19

NUMBER OF SEO ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEO ID NO 2

LENGTH: 289
                     Sequence 53, Application US/09778927A

Sequence 53, Application US/09778927A

Sequence 53, Application US/09778927A

Sequence 53, Application US20020068342A1

GENERAL INFORMATION:
TITLE INFORMATION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

FILE REPEBENCE: 2786 -0160P

CURRENT FILING DATE: 2001-02-08

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 81

SEQ ID NO 53

LENTH: 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COCATION: (1)..(254)
CTHER INFORMATION: Xaa = any amino acid, unknown, or other US.09-778-927A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 60.0 Matches 6; Conservative
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Best Local Similarity 60.09
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
RESULT 13
US-09-778-927A-53
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US-10-024-066-2
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RESULT 15 US-10-024-066-4

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Sequence 4, Application US/10024066
Patent No. US20020166134A1
GENERAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Field, Loren J.
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
FILE REPERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 2000-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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Patent No. US20020106662A1

GENERAL INFORMATION:
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

FILE REFERENCE: B0801/7225

CURRENT APPLICATION NUMBER: US/09/919,497

CURRENT FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR FILING DATE: 2000-07-31

SOFTWARE: Patentin version 3.0
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Patent No. US20020151881A1

GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 289;
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60.0%; Pred. No. 1.36+02;
u.:omatches 3; Indels
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Best Local Similarity 60...
Best Local 6; Conservative
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CORGANISM: Homo sapiens
US-09-919-497-54
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 17
US-09-925-300-1061
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US-09-919-497-54
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LENGTH: 691

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Gaps

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Length 691; 1; Indels

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Query Match 61.5%; Score 32; DB 9; I Best Local Similarity 62.5%; Pred. No. 3.2e+02; Matches 5; Conservative 2; Mismatches 1;
                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-921-4
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                                                                                                                                                                                   NAME/KEY: SITE

COCATION: (243)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE

LOCATION: (277)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-300-1061
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APPLICANT: KATZ, RUTH
APPLICANT: JIANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
FILE REFERENCE: UTSC:588US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 2.4e+02;
3; Mismatches 2; Indels
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APPLICANT: Nezu, Jun-Ichi
APPLICANT: Suji, Akira
APPLICANT: Tsuji, Akira
ITLE OF INVENTION: TRANSPORTER GENES OATP-B, C, D, AND E
TILE REPERENCE: 05501-104U51
CURRENT FILIMG DATE: 2002-06-28
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 1999-09-21
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1061 LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09923304
Patent No. US20020081612A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10101921
Publication No. US20030022199A1
GENERAL INFORMATION:
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Matches 6; Conservative
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| ||:| ||:
| EVLPTKMSYA 61
                                                                                                                                              ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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LENGTH: 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                            RESULT 20

US-09-925-731-2

Sequence 2, Application US/09925731

Sequence 2, Application US/09925731

Sequence 2, Application US/09925731

GENERAL INFORMATION:
APPLICANT: ADEOKUN, ANTHONI MONISOLA
APPLICANT: ADMENCSE, HELEN JEAN
APPLICANT: DUDLEY, ADAM JESTON
TITLE OF INVENTION: CHEMICAL COMPOUNDS
FILE REFERENCE: DJB/009901/0282795
CURRENT APPLICATION NUMBER: US/09/925,731
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/226,909
PRIOR FILING DATE: 2000-08-23
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CURRENT PELING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
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Patent No. US20020061569A1
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Yamamoto, Robert T.
Xu, H. Howard
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 691
                              188 IVPLGLSY 195
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ORGANISM: Homo sapiens
3 VVPXGMSY 10
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US-09-815-242-10384
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APPLICANT:
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us-09-909-164-10.rapb

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Query Match
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APPLICANT: Callaghan, Michelle J.
APPLICANT: Callaghan, Michelle J.
APPLICANT: Sutherland, Lindfield
APPLICANT: Watts, Colin R
TITLE OF INVENTYON: NO. US20020192160Alel Human Tumour Suppressor Gene
FILE REFERENCE: RICE-010CoN
CURRENT APPLICATION NUMBER: US/10/151,736
CURRENT FILING DATE: 2002-05-15
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1999-10-20
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Pred. No. 6.7e+02;
4; Mismatches 2; Indels (
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 878
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%; Score 32; DB 9; Length 279
60.0%; Pred. No. 1.4e+03;
tive 2; Mismatches 2; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 2799
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-092-154-878
; Sequence 878, Application US/10092154
; Publication No. US20030054375Al
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/10151736; Publication No. US20020192160A1
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Best Local Similarity 45.5%;
Matches 5; Conservative 4
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Matches 6; Conservative
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                                                                                                                                                                                                                        ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                   369 EQLNPAGLSYT 379
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; GENERAL INFORMATION:
                                                                                                                                                                                                                                               US-09-815-242-10384
                                                                                                                                                               SEQ ID NO 10384
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                                                                                                                                                                                ö
NAME/KEY: misc_feature LOCATION: (7) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ROSen et al.
APPLICANT: ROSen et al.
TITLE OF INVENTION Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT APPLICATION AGER : 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PATEGILN VEr. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.6%; Score 31; DB 10; Length 53; 66.7%; Pred. No. 33;
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Sequence 14, Application US/09948080

Patent No. US20020102702A1

GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: HALKIER, TORDEN
APPLICANT: BAUDITZ, PETER KAMP
APPLICANT: BAUDITZ, PETER KAMP
APPLICANT: HANSEN, PETER KAMP
APPLICANT: HANSEN, PETER KAMP
APPLICANT: HANSEN, PETER KAMP
APPLICANT: HONSEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-US
CURRENT FILING DATE: 2001-09-06
PRIOR FULING DATE: 2001-09-06
PRIOR FULING DATE: 1997-11-04
                                                                                                                                 Query Match 59.6%; Score 31; DB 9; Length 53; Best Local Similarity 66.7%; Pred. No. 33; Matches 6; Conservative 1; Mismatches 2; Indels Matches
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1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 24
US-09-764-847-878
US-09-764-847, Application US/09764847
; Sequence 878, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Enterococcus faecalis US-09-948-080-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 39 VVPTAVSYS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                     3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                    39 VVPTAVSYS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
                                                                                                US-10-092-154-878
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LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 878
LENGTH: 53
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1 EEVVPXGMSYS 11 | ::| |: | |: | | 38 EKHIPGGLEYS 48

oy Db

Search completed: June 10, 2003, 14:35:43 Job time : 16.0714 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:31:15; Search time 11.2143 Seconds (without alignments) 94.297 Million cell updates/sec Run on:

US-09-909-164-10 52 1 EEVVPXGMSYS 11 Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 75 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	hypothetical 367K	probable sulfate p	fate perme	V1 protein - tobac	-		_	zinc finger protei		DNA-binding protei				14	_		_	_	hypothetical prote		hypothetical prote	U2	cdc37 protein - fi	iron(III) ABC tran	bacteriocin BCN5 -	ATP-dependent DNA	ш.	gro	DNA-directed RNA p
		1308	116	413	42452	355	810	111	S22293	691	A34203	S54619	491	C82900	758	E90544	493	374	T34536	817	.670	F72281	D82163	1653	D82352	A30481	AF3286	D87046	9	336
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	DB	. ~																										7		CI
	Query Match Length DB	3472	840	877	102	1498	225	425	670	749	2717	156			94	116	165	253	259	284	298	368	426	466	653	890	1028	1152	1394	1401
æ	Query Match	73.1	71.2	71.2	69.3	69.2	67.3	67.3	67.3	67.3	67.3	65.4	L)	65.4	ω.	63.5	Э.	ω,	ω,	ω.	63.5	ω,			•	•	•	63.5	•	63.5
	Score	38	37	37	36	36	35	35	35	35	35	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
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## ALIGNMENTS

	Cenarchae	
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	protein	
	367K	
308	othetical	

RESULT 1

hypothetical 367K protein - Cenarchaeum symbiosum C; Species: Cenarchaeum symbiosum C; Species: Cenarchaeum symbiosum C; Species: Canarchaeum symbiosum C; Date: 11-Jan-2000 #sequence_revision C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V. J. Bacteriol. 180, 5003-5009, 1998
A; Title: Genomic analysis reveals chromosomal variation in natural populations of the A; Reference number: 220994; MUID: 98422450; PMID: 9748430
A; Reference number: 220994; MUID: 98422450; PMID: 9748430

A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-347 < SCHB
A, Cross-references: EMBL.AF083072; NID:q3599393; PID:q3599394; PIDN:AAC62699.1
C, Superfamily: Cenarchaeum symbiosum hypothetical 367K protein

Gaps .. Query Match
Best Local Similarity 54.5%; Pred. No. 59; Length 3472;
Matches 6; Conservative 4; Mismatches 1; Indels

Gaps

ö

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G; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Ascossion: B97355 Brooth, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, R; Brooling, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. Astrille: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA segregation ATPase, FtsK/SpoiliE family, YUKA B. subtilis ortholog [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:915026814; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accession: S57810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24111
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C;Superfamily: plant Kunitz-type proteinase inhibitor
                      A;Cross-references: GB:M81103; NID:9335283; PIDN:AAA47947.1; PID:9335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rivilligan, S.B.; Gasser, C.S. Plant Mol. Biol. 28, 691-711, 1995
A;Title: Nature and regulation of pistil-expressed genes in tomato. A;Reference number: S57808; MUID:95375233; PMID:7647301
                                                                                                Score 36; DB 2; Length 102;
Pred. No. 3.5;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 1498;
Pred. No. 63;
2; Mismatches 2; Indels
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Pred. No. 13;
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A,Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein precursor (clone TPP11) - tomato
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                                                                                                   69.2%;
60.0%;
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60.0%;
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54.5%;
                                                   Query Match
Best Local Similarity 60.vv
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 54...
6, Conservative
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7 QVVPSGINYS 16
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A; Residues: 1-1498 <KUR>
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A; Residues: 1-225 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CAC3709
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B97355
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S57810
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C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Tille: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
A;Reference number: A42452; MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL132779; PIDN:CAB60015.1; GSPDB:GN00066; SPDB:SPAC869.05c
A;Experimental source: strain 972h-; cosmid c869
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Nolecule type: DNA
A:Residues: 1-877 < LIND
A:Residues: BBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02
A:Experimental source: strain 972h-; cosmid c3H7
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                                                                                                                                                                                                    probable sulfate permease - fission yeast (Schizosaccharomyces pombe) (Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 (Shunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. R; Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. A; Reference number: Z21829 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Schizosaccharon, fear, Contropaccharonyces pombe)
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T40413
R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, August 1998
A; Reference number: 221926
A; Reference number: 240413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.2%; Score 37; DB 2; Length 840; 77.8%; Pred. No. 21; 1.1ve 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.2%; Score 37; DB 2; Length 877; 77.8%; Pred. No. 22; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Best Local Similarity 77.88,
-has 7; Conservative
1:|:| |:|:|
2294 EDVIPRGISFS 2304
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Matches 7; Conservative
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A;Gene: SPDB:SPBC3H7.02
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A; Residues: 1-102 <MOR>
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chado, M.A.; Madelra, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martin A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, R.Odriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Saw, A.J. duthors: da Silva, A.C.; de Silva, A.C.; de Silva, A.M.; Silva, Jr., W.A.; de Silva, A.M.; Silva, Jr., W.A.; de Silva, A.M.; Silva, Jr., W.A.; de Silva, A.M.; Contents: annotation
                                                                                                                                                                                                                                                                                                                                          A;Gene: XF1353
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
A; Molecule type: mRNA
A; Status: 1-271 <FAN>
A; Cross-references: EMBL: X51435; NID: 938017; PIDN: CAA35798.1; PID: 938018
A; Cross-references: EMBL: X5. LeClair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Biol. 10, 1406-1414, 1990
A; Title: A large protein containing zinc finger domains binds to related sequence
A; Reference number: A34779; MUID: 90205817; PMID: 2108316
A; Reference number: A34779
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 801-1072, N', 1074-1168, 'K', 1170-1225, 'V', 1227-1434,'N', 1436-1607,'I', 10
A; Cross-references: GB:M32019
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes Dev. 4. 29-42, 1990
A; Title: A DNA-binding protein containing two widely separated zinc finger motifs
A; Reference number: A34203; MUD:90169514; PMID:2106471
A; Accession: A34203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding protein PRDII-BF1 - human N;Alternate names: major histocompatibility complex enhancer-binding protein 1 N;Alternate names: major histocompatibility complex enhancer-binding protein 1 C;Species: Homo sapiens (man) C;Species: Alono sapiens (man) C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999 C;Accession: A34203; A34779 R;Fan, C.M.; Manitis, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein 02612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Species: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Date: 08-Jul-1995
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A;Residues: 1.156 CDEH>
A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
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66.7%; Pred. No. 1.9e+02;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2;
Pred. No. 48;
0; Mismatches
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R;de Haan, M.; Maarze, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%;
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Matches 7; Conservative
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A;Experimental source: strain 9a5c
R;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docenna, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; França, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junquelra, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
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C; Abete: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C; Accession: Ha2691
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MuID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Mitchelmore, C.; Traboni, C.; Cortese, R. Nucleic Acids Res. 19, 11-147, 1991 Nucleic Acids Res. 19, 11-147, 1991 A; Title: Isolation of two conas encoding zinc finger proteins which bind to the alpha 1-A; Reference number: 158280; MUID:91187610; PMID:1901405
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                        submitted to the EMBL Data Library, October 1996
A; Recession: T2411
A; Accession: T2411
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-425 <WIL>
A; Cross: references: EMBL:Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
A; Experimental source: clone R10D12
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: S22293; I78656
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A; Residues: 1-670 <MIT>
A; Cross-references: EMBL:X54250; NID:957519; PIDN:CAA38151.1; PID:957520
A; Note: the authors did not translate the codon for residue 1
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Superfamily: HIV-EP2 enhancer-binding protein
C; Keywords: DNA binding; transcription regulation; zinc finger
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Pred. No. 43;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%; Score 35; DB 2; Length 425; 50.0%; Pred. No. 26; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zinc finger protein AT-BP2 - rat (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 5
A;Introns: 23/3; 56/3; 113/3; 257/2
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Matches 5; Conservative
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hes 6; Conserv
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A; Residues: 1-749 <SIM>
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hypothetical protein 1 - Campylobacter jejuni (fragment)
C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Decies: 16-Aug-1996 #text_change 08-Oct-1999
C; Accession: 140758; S47317
C; Accession: 140758; S47317
C; Accession: 140758; William Characterization of Campylobacter jejuni benzoylglycine ami A; Reference number: 140758; MUID: 95247673; PMID: 7730270
A; Reference number: 140758
A; Actatus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-94 < RES>
A; Residues: 1-94 < RES>
A; Residues: 1-94 < RES>
A; Cross-references: EMBL: 236940; NID: 9535805; PIDN: CAA85392.1; PID: 9535806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
R;Chambaud, I: Heilig, R:; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer,
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma
A;Title: The complete genome sequence of the murine respiratory pathogen A;Reference number: A99512; MUID:21267165; PMID:11353084
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R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Doc S. Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-116 <KUR>
A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50S ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CIIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein AF1949 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec:1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 2; Length 94;
Pred. No. 13;
2; Mismatches 2; Indels
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A,Genetic code: SGC3
C,Superfamily: Escherichia coli ribosomal protein L20
                                             Mismatches
                                             1;
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5; Conservative
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Best Local Similarity 77.00,
                                    7; Conservative
                                                                                                                                                135 EEVVPHYLSY 144
                                                                                             1 EEVVPXGMSY 10
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26 DIFPSGMSY 34
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                                    Matches
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                                                                                 A.Molecule type: DNA
A.Residues: 1-156 <DEW>
A.Residues: 1-156 <DEW>
A.Cross-references: EMBL:274920; NID:91420109; PIDN:CAA99201.1; PID:91420111; MIPS:YOR01
A.Experimental source: strain S288C
C.Genetics:
A.Cross-references: SGD:S0005539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: He6491
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson C; Accession: He6491
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. A.; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A.; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A.; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Accession: H69491
A; Reference number: A69250; MuID:98049343; PMID:9389475
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-252 <KLE>
A; Residues: 1-252 <KLE>
A; Cross-references: GB:AE000970; GB:AE000782; NID:92689293; PIDN:AAB89318.1; PID:9264866
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A; Reference number: A82870
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A;Residues: 1-544 <GLA>
A;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Usaplasma urealyticum C;Species: 18-wq-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: C82900 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 S;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, Pebruary 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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C,Superfamily: hypothetical protein YOR013w
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Pred. No.
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Matches 6; Conservative
                                 A; Reference number: S66877
A; Accession: S66879
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Best Local Similarity
Matches 6; Conserv
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A; Accession: T47670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Cj0990c [imported] - Campylobacter jejunl (strain NCTC 11168) C; Species: Campylobacter jejuni (species: Campylobacter jejuni C; Species: Campylobacter jejuni C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C; Date: 31-Mar-2001 Mrs. Mandaream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel C.W.; Ouall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000 A; Rither The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A; Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-253 <PAR>
A;Cross-raferences: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73246.1; PID:g696842
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69493
                                                                                                                                                                                      A;Cross-references: GB;AE000968; GB:AE000782; NID:92689291; PIDN:AAB89307.1; PID:9264859
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF1949
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                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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R; Poustka, A; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, October 1999
A; Reference number: 221540
A; Recession: T34536
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-259 <POU>A; A; Cross-references: EMBL: AL122063
A; Cross-references: EMBL: AL122063
C; Genetics:
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                                                                                                                                                                                                                                                                            Query Match 63.5%; Score 33; DB 2; Length 165; Best Local Similarity 60.0%; Pred. No. 25; Matches 6; Conservative 1; Mismatches 3; Indels
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Matches 6; Conservative
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Matches 5; Conservative
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                                                                                                                                                                                A, Residues: 1-165 <KLE>
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A; Status: preliminary
                                                                                                                                                          A; Molecule type: DNA
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C81374
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hypothetical protein slr1275 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: 57581
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, R;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Ya DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-284 CKAN>
A;Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18276.1; PID:d1C
A;Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18276.1; PID:d1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T47670.
C;Accession: T47670.
R;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, February 2000
A;Reference number: 224471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Thermotoga maritima
C.Species: Il-Jun-1999 #sequence_revision Il-Jun-1999 #text_change 21-Jul-2000
C.Accession: F722B
R.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; B
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 399, 323-329, 1999
Attitle: Evidence for lateral gene transfer between Archaea and Bacteria from genon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 25/3
A;Note: T26112.190
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-ketoacyl-ACP reductase-like protein - Arabidopsis thaliana
N:Alternate names: protein T26112.190
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein TM1216 - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%; Score 33; DB 2; Length 284; 55.6%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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A;Experimental source: cultivar Columbia; BAC clone T26112
                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1:| |:| ;
208 VIPAGVSYT 216
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iron(III) ABC transporter, permease protein VC0203 [imported] - Vibrio cholerae (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rieidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. dardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller. I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A.Feference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004110; GB:AE003852; NID:99654600; PIDN:AAF93379.1; GSPDB:GI
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A;Accession: A30481
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: D82352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteriocin BCN5 - Clostridium perfringens plasmid pIP404
C;Species: Clostridium perfringens
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Nov-1999
C;Accession: A30481; S03779
R;Garnier, T.; Cole, S.T.
J. Bacteriol. 168, 1189-1196, 1986
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                          A; Residues: 1-466 <WOO>
A; Cross-references: EMBL:AL049769; PIDN:CAB42371.2; GSPDB:GN00067
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                   A: Experimental source: strain 972h; cosmid cybe R: Westwood, P.K.; Preston, N.C.; Fantes, P.A. submitted to the EMBL Data Library, March 1999 A: Description: Schizosaccharomyces pombe cdc37 gene. A: Reference number: 222603 A: Actaus: preliminary; translated from GB/EMBL/DDBJ A: Molecule type: DNA A: Residues: 1-466 <WEZ>A: Cosmid Sources: EMBL: AJ32377; PIDN:CAB38758.1 C; Genetics: cdc37; SPAC9B6.10
                                                                                                                                                                                                                                                                                                                                                                                                                                               63.5%; Score 33; DB
50.0%; Pred. No. 76;
Live 2; Mismatches
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Best Local Similarity 65.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 DSAIPGGMSY 107
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                                                                                                                                                                                                                                                                                                                                                                      A:Map position: 2
A:Introns: 8/2; 17/2; 21/1
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A; Residues: 1-653 <HEI>
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A; Residues: 1-890 <GAR>
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A; Map position: 1
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Matches
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                                                                                                        A;Cross-references: GB:AE001778; GB:AE000512; NID:g4981757; PIDN:AAD36291.1; PID:g498176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-phosphoshikimate 1-carboxyvinyltransferase VC1732 [imported] - Vibrio cholerae (strain C.Species: Vibrio cholerae
C.Species: Vibrio cholerae
C.Species: Vibrio cholerae
C.Species: Navg-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermodaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Neture 406, 477-483, 2000
A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE004251; GB: AE003852; NID: 99656248; PIDN: AAF94882.1; GSPDB: GN00: A; Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbox
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accasion: T43653; T40791; T45654
R;Westwood, P.K.; Preston, N.C.; Fantes, P.A.
a;Ubmitted to the EMBL Data Library, March 1999
A;Beference number: 222602
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                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                             A;Gene: TM1216
C;Superfamily: NADH dehydrogenase (ubiquinone) 49K protein
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72281
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                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: T40791
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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3; Mismatches
                                                                                                                                                                                                                                                                                   Score 33;
                                                                                                                                                                                                                                                                              63.5%;
55.6%;
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Best Local Similarity
6; Conserve
                                                                        A; Molecule type: DNA
A; Residues: 1-368 <ARN>
                                                                                                                                                                                                                                                                                                   Best Local Similarity
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-426 <HEI>
                                                 A; Status: preliminary
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A;Gene: VC1732
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A;Genome: plasmid
C;Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5_
C;Keywords: bacteriocin
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	0;		
	0; Gaps		
	0;		
Query Match 63.5%; Score 33; DB 2; Length 890; meet 7.00al similarity 66.7%; Pred. No. 1.5e+02;			
Query Match 63.5%;	Matches 6; Conservative	Qy 2 EVVPXGMSY 10	Db 170 EVVPGGFTY 178

Search completed: June 10, 2003, 13:49:13 Job time: 11.2143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

US-09-909-164-10 52 1 EEVVPXGMSYS 11

Title:

Perfect score: Sequence: Scoring table:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 75 summaries Post-processing: Minimum Match 0%

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Description	Q8rg86 fusobacteri			~	_	_		_		0					Ф	ω.	<b>a</b>	7	σ			P50755 xenopus lae			gall	homo	homo	_	m	7 ћаето	5355 homo	_	P52384 human herpe
SUMMARIES		OT.	CARB_FUSNN		Y11K_TYDVA	Y1A9_CLOAB	ZEP1_HUMAN	CY14 NEUCR	A10C_HUMAN	RL20_MYCPU	Y990_CAMJE	AROA_VIBCH	CC37_SCHPO	GSR2_HUMAN	BCN5_CLOPE	LTBS_HUMAN	RPOC_VIBCH	LTBL_HUMAN	LTB1_RAT	CGD2_RAT	CGD2_HUMAN	CGD2_MOUSE	CGD1_BRARE	CGD1_XENLA	CGD2_CHICK	CGD2_XENLA	CGD1_CHICK	CGD3_HUMAN	CGD1_HUMAN	CGD1_MOUSE	CGD1_RAT	TOLB HAEIN	ENP3_HUMAN	OAT6_HUMAN	PRTP_HSV6U
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ALIGNMENTS

STRAIN-ATCC 25586;
MEDLINES-12886394; PubMed=11889109;
MEDLINES-12886394; PubMed=11889109;
MEDLINES-12886394; PubMed=11889109;
Magarral V., Anderson I., Ivanova N., Garchkin G., Zhu L.,
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeek R.;
Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2055-2018(202).
-: CATALYIT CATIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422. Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856; PRT; 1058 AA STANDARD; [1] SEQUENCE FROM N.A. FUSNN CARB_FU Q8RG86; CARB_FUSNN

STRAIN-972;

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                                                         -i- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).

-i- SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; re.
Pfam; re.
Pfam; pro2142; MGS; r.
PRINTS; PR00098; CPGASE.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00870; PESASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
ATP-binding; Manganese; Complete proteome.
DOMAIN 1 401 CARBOXPHNES SYNTHETIC DOMAIN.
402 546 CLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MANGAMESE I (BY SIMILARITY)
MANGAMESE I AND 2 (BY SIMILARITY)
MANGAMESE 2 (BY SIMILARITY).
MANGARESE 3 (BY SIMILARITY).
MANGAMESE 3 (BY SIMILARITY).
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MANGAMESE 3 (BY SIMILARITY).
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Phosphate + L-glutamate + carbamoyl phosphate.
COFACTOR: Binds three manganese ions (By similarity).
PATHWAY: Arginine blosynthesis.
PATHWAY: Pyrimidine blosynthesis; first step.
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ATP (POTENTIAL).
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUM-2002 (Rel. 41, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38;
                                                                                                                                                                                                                                                                         EMBL; AE010554; AAL94625.1; ALT_INIT.
                                                                                                                                                                                                                                                                                       InterPro; IPR005483; CPase_L.
InterPro; IPR005483; CPase_L.D2.
InterPro; IPR005480; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR004362; MGS_LIKe.
Pfam; PF00289; CPSase_L.Chain; 2.
Pfam; PF02786; CPSase_L.D2; 2.
Pfam; PF02787; CPSase_L.D3; 1.
Pfam; PF02787; CPSase_L.D3; 1.
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074377;
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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Rajouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown S., Chilliam W., Colnor R., Cronin A., Davis P. Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., McDonald S., McCannal R., McDonald S., Skelton J., Slamonds M., Squares R., Squares S., Stevens K., Taylor R., Taylor R., Taylor R., Arlorg R., Rolle S., Willers S., Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B., Welthens I., Wanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Rabel C., Fuchs M., Fritzc C., Holzer E., Leharch W., McLeller S., Rochet M., Caillard N., Sanchez M., Rochet M., Gaillardin C., Mark Moody R., Hurst S.M., And Schola B., Charach H., Reinhardt R., Ponsburg S.L., Rabaga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Shapkovski G.V., Ussery D., Barrell B.G., Nurse P., Shakovski G.V., Ussery D., Barrell B.G., Nurse P., Stinvarton M., Harris Benter M., Ralle A., Rather A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
--- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
--- SIMILARITY: CONTAINS 1 STAS DOMAIN.
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InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF00916; Sulfate_transp; 1.
                         MEDLINE=21848401; PubMed=11859360;
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TIGRFAMS; TIGR00815; SulP; 1.
PROSITE; PS01130; SLC26A; 1.
PROSITE; PS50801; STAS; 1.
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77.88;
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Matches 7; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                         MEDLINE-92188538; PubMed-1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiaceae;
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InterPro; IPR002621; Gemini_mov.
Pfam; PF01708; Gemini_mov; 1.
Hypothetical protein.
SEQUENCE 102 AA: 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                    Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                      01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                         102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
                                                                             01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                       EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein CAC3709
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                                                         STANDARD;
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148 VVPQGMSYA 156
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Best Local Similarity
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                                                                                                                                                           NCBI_TaxID=31599;
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                                                      Y11K_TYDVA
P31619;
                                RESULT 3
Y11K_TYDVA
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01-ARR-1990 (Rel. 14, Last sequence update)
16-0CT-2010 (Rel. 40, Last annotation update)
2inc finger protein 40 (Human immunodeficlency virus type I enhancer-
binding protein 1) (HIV-EP1) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
                                                                                Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-! SIMILARITY: BELONGS TO THE FTSK/SPOIIE FAMILY.
-! CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fan C.M., Maniatis T.; "A Maniatis T.; "A bNA binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence."; Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92232684; PubMed-1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
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MEDLINE-91064333; Pubmed-2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; ATP-binding; Complete proteome.
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                               VKM B-1787;
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InterPro; IPR002543; FtsK_SpoillE.
Pfam; PF01580; FtsK_SpoillE; 2.
SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-
MEDLINE=93273706; PubMed=8501044;
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MEDLINE=90169514; Pubmed=2106471;
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us-09-909-164-10.rsp

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15-JUN-2002 (Rel. 41, Last annotation update)
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Gaps
                                                                             SUBCELLULAR LOCATION: Nuclear.
INDUCTION: BY MITOGEN AND PHORBOL ESTER.
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECCONIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                   Genew; HGNC:4920; HIVEP1.

MIM; 194540;
InterPro; IPR000822; Znf_C2H2.

Pram; PR00096; Zf-C2H2; 5.

PRINTS; PR00048; ZINCFINGER.

SMART; SM00355; ZnF_C2H3; 4.

PROSTITE; PS00028; ZINC_FINGER_C2H2_1; 4.

PROSTITE; PSS0157; ZINC_FINGER_C2H2_2; 4.

Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
Nuclear protein; Repeat; 3D-structure.
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66.7%; Pred. No. 70;
ive 2; Mismatches 1; Indels
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C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                           -! - SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                              EMBL; X51435; CAA35798.1; -. PIR; A34203. A34203. PDB; 3ZNF; 15-JAN-92. PDB; 4ZNF; 15-JAN-92. PDB; 1BBO; 31-CT-93. TRANSFAC; T00497; -. Genew; HGNC:4920; HIVEP1.
                                                                                                                 ZINC-FINGER IN-BETWEEN
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Matches 6; Conservative
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2127 213
2717 AA;
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-i- INDUCTION: Highly expressed, but only in cells subject to sulfur limitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.
-i- MISCELLANEOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.
-i- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94188926; PubMed-8140616;
Sandal N.N., Marcker K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
permease II and a putative human tumour suppressor.";
Trends Biochem. Sci. 19:19(1994).
                                                                                                                                                                                           MEDIINE-91129256; PubMed-1825178; Ketter J.S., Jaral G., Fu Y.-H., Marzluf G.A.; "Nucleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in
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                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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InterPro; IPR001902; Sulfate_transp.
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TIGRFAMS; TIGR00815; SulP; 1.
PROSITE; PS01130; SLC26A; 1.
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Sulfate permease II.
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788 AA;
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(Rel. 20, Created) (Rel. 32, Last sequence update)

STANDARD;

CY14_NEUCR P23622; 01-NOV-1991 01-NOV-1995

CY14_NEUCR

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i. DISEASE: Defects in ATP10C may be a cause of Angelman syndrome (AS), also known as 'happy puppet syndrome'.
-i. SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IV.
                                                                                                                                                                                                                                                                                                                                                                                                 "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
                                                                                                                                                            Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(Partential phospholipid-transporting ATPase VC (EC 3.6.3.1) (ATPVC)
(Aminophospholipid translocase VC).
ATPLOC OR ATPVC OR KIAA0566.
                                                                                                                                                                                                                                                                  Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.; "The human aminophospholipid-transporting ArPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression."; Am. J. Hum. Genet. 68:1501-1505(2001).
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                           Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED.
                                                                                                                                                                                                                                                        MEDLINE=21313119; PubMed=11353404;
                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-21225279; PubMed-11326269;
                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 337-1499 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB051358; BAB47392.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kidney, rozz.
                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                            Oshimura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; A
Genew;
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EMBL;
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EMBL;
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EMBL;
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EMBL;
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Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL
SUBUNIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS
OF THAT SUBUNIT (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L20P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galisson F.,
                InterPro; IPR001757; ATPase_E1-E2.
InterPro; IPR001454; H1gnase_hydrlase.
Pfan, PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chambaud I., Hellig R., Ferris S., Barbe V., Samson D., Gali:
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 1499;
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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D4996A4D0635A68D CRC64;
                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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                                                                                                                                                                                                                                       POTENTIAL. CYTOPLASMIC (POTENTIAL).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
55-JUN-2002 (Rel. 41, Last annotation update)
RPLT OR MYPU_2610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 EEVVPRGGSVS 479
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1222
1228
1249
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les 8; Conserv
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                                                                                 Hydrolase; Transı
Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                             388
1499
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1250
1268
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          105830; -
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Q98QV0;
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TRANSMEM
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                                                                                                                                           RANSMEM
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Gaps

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Length 253;

63.5%; Score 33; DB 1; 55.6%; Pred. No. 16; iive 2; Mismatches

5; Conservative

Matches

Query Match Best Local Similarity 2 EVVPXGMSY 10

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EMBL; 236940; CAA85392.1; -. Hypothetical protein; Complete proteome. SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;

> NW KW SO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20150912; PubMed=10688204; Retley J.M., Churcher C., Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quall M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 160-253 FROM N.A.
STRAIN-ATCC 43431 / TGH 9011;
MEDLINE-95247673; PubMed-7730270;
Hani E.K., Chan V.L.;
"Expression and characterization of Campylobacter Jejuni benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 1; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                       Mypulist; MYPU_2610; -.
InterPro; IPR001081; Ribosomal_L20.
InterPro; IPR001081; Ribosomal_L20.
InterPro; IPR001081; Ribosomal_L20.
IPRUNTS; PR00062; RIBOSOMALL20.
ITGREAMS; TGR01033; PDIT_bact; 1.
PROSITAMS; PR00037; RIBOSOMAL_L20; 1.
Ribosomal process, RINA-binding; Complete protecome.
SEQUENCE 116 AA; 13565 MW; C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y990_CAMJE STANDARD; PRT; 253 AA. P45489; O9PNVO; 01-NOV-1995 (Rel. 32, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Hypothetical protein Cj0990c.
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 177:2396-2402(1995).
                                                                                                                                                                       EMBL; AL445563; CAC13434.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL139076; CAB73246.1; -
                                                                                                                                                                                                                                                                                                                                                                                               63.58;
                                                                                                                                                                                                                                                                                                                                                                                                             77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDINE-20406833; PubMed=10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.F., Read T.D., Tetterlin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tetterlin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-Rel)
ROA OR VGI732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406 477-483(2000).
-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00275; EPSP_Syntase; 1.
ProDom; PD001867; EPSP_Syntase; 1.
PROSITE; PS000085; EPSP_SINTHASE_2; 1.
PROSITE; PS00085; EPSP_SINTHASE_2; 1.
Aromatic amino acid blosynthesis; Transferase; Complete proteome. SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBUNIT: Monomer (By similarity).
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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60.0%;
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Matches 6; Conservative
                                                                                                STANDARD;
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223 EFVIPAGOSY 232
185 DIFPSGMSY 193
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                                                                                                                                                                                                                                                     Vibrio cholerae
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                                                                                            AROA_VIBCH
Q9KRB0;
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                                                                          AROA_VIBCH
                                                            RESULT 10
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RA WOOD V., GWilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Raywood V., GWilliam K., Rajandream M.A., Eusham D., Bowman S., Squros.J., Peat N., Hayles J., Basker S., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Cannor R., Cronin A., Davis P., Feltwell T., Fraser A., Golles A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA James K., Jones M., Leather S., McDonald S., McLean J., Ray Jones L., Jones M., Leather S., McDonald S., McLean J., RA Junes K., Jones M., Leather S., McDonald S., McLean J., RA Juner K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rubrerford K., Rutter S., Saunders D., Seeger K., Stavens K., Stannods M., Squares R., Squares S., Stevens K., Stannods M., Squares R., Squares S., Stevens K., Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckeart G., Aert R., Robben J., Grymoppez B., Weltjens I., Volckeart G., Aert R., Robben J., Grymoppez B., Weltjens I., Danger I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Reper P., Zimmermann W., Wedler H., Wambutt R., Hurnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Active M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Allors M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Active Moore R., Hurst S., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shakovski G.V., Ussery D., Barrell B., Nather W., Shakovski G.V., Ussery D., Barrell B., Nather W., Shakovski G.V., Warrell B., Nather M., Schaller B., Marte W., Shakovski G.V., Warrell B., Nather M., Shakovski G.V., Warrell B., Nather M., Shakovski G.V., Warrell B., Nather M., Shakovski G.V., Wasery D., Barrell B., Nather W., Shakovski G.V., Wasery D., Barrell B., Nather W., Shakovski G.V., Wasery D., Barrell B., Nather M., Shakovski G.V., Wasery D., Barrell B., Nather W., Shakovski G.V., Wasery D., Barrell B., Nather W., Washowski G.V., Wasery D., Barrell B., Nather M., Washowski G.V., Wasery 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: With Hsp90 it forms a complex that binds to several kinases, resulting in stabilization and promotion of their activity (By similarity).
SUBUNIT: Forms a complex with Hsp90. Interacts with a number of
                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-Bp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
CDC37 OR SPAC9B6.10.
                                                                                                                                                                                                                                                                                                                                                                                                                Westwood P.K., Preston N.C., Fantes P.A.;
"Schizosaccharomyces pombe cdc37 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ132377; CAB38758.1; -.
EMBL, AJ132376; CAB38757.1; -.
EMBL, AL049769; CAB42371.2; -.
Chaperone; Call division: Cell cycle.
SEQUENCE 466 AA; 52554 MW; 647238B34CABB3C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinases (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE CDC37 FAMILY.
                                                                                                                                                                                                                                                                  Eukaryota, Fungl, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                          466 AA.
                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21848401; PubMed=11859360;
                                            STANDARD;
                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896;
                                            CC37_SCHPO
094740;
                     CC37_SCHPO
RESULT 11
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MEDLINE-99214318; PubMed-10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP2 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U., Portier B.P., Ucki K., Billings S., Ramaswamy S., Mohrenweiser H.W., Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                       GSR2_BUMAN STANDARD; PRT; 478 AA.
G9NZM5; Q9NPP1; Q9NF12; Q9BTC6; Q9HAX6;
16-OCT-2001 (Rel. 40, Created)
15-OCT-2001 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (P60).
                      DB 1; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECTION OF 12-478 FROM N.A. Andrew N., Sumoy L.; Andrew N., Estivill X., Escarceller M., Sumoy L.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. MEDLINE-20175430; PubMed=10708517;
                         Score 33; DB Pred. No. 30; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF182076; AAF62873.1; -. EMBL; BC004229; AAH04229.1; -. EMBL; BC006311; AAH06311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 218-477 FROM N.A.
                            63.5%;
50.0%;
Query Match
Best Local Similarity 50.v.
Best Local 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 64:44-50(2000).
                                                                                                                                                                                                             98 DSAIPGGMSY 107
                                                                                                                                                   1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Muscle;
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                                                                                                                                  GGS -> HEG (IN REF. 2; AAH04229).
G -> R (IN REF. 3).
RRKEQLWEKLAKQGELPREVRRAQARLINPSATRAKPGPQD
                                                                                                                                                                                                                                                      REIQ -> VLTVSCRGAPCPVMTPSLLAVPPRGTGRHHGCP
WAGPVGPMPRG (IN REF. 5).
EGNILRDFKFSCPRNNIEDPREAKFRKXKVKIVJEKRFF
EIQL -> REQUESTETGSAFRGGI (IN REF. 3).
7F18923E348CB52B CRC64;
                                                                                                                                                                                                                   A -> S (IN'REF. 2; AAH04229).
D -> H (IN REF. 3).
PEGNILRDRFKSFQRRNMIEPRERAKFKRYKVKLVEKRAF
                                                                                                                                                                         TVERP -> SGRSSYGRSWPSRASSPGGAQGPSPVAQPFCN
                                                                                                                                                                                  KGPNPAPGHRIAA (IN REF. 3).
SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWPGCLFPG
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; Plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garnier T., Cole S.T.; "Studies of UV-inducible promoters from Clostridium perfringens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garnier T., Cole S.T.; "Characterization of a bacteriocinogenic plasmid from Clostridium perfringens and molecular genetic analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid p1P404
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 478;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                        /FTIG-VAR_011486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                          (IN REF. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteriocin-encoding gene.";
J. Bacteriol. 168:1189-1196(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CPN50;
MEDLINE=87057020; PubMed=2877971;
EMBL; BC010095; AAH10095.1; --
EMBL; AF296124; AAG30413.1; --
EMBL; AL359335; CAB94786.1; --
EMBL; AL359335; CAB94787.1; --
EMBL; AL122063; CAB59242.1; --
SWISS-2DPAGE; Q9NZM5; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88336297; PubMed=2901768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CPN50;
MEDLINE=89039249; PubMed=2460717;
                                                                                MIM; 605691; -. Nuclear protein; Polymorphism.
                                                                                                                                                                                                                                                                                                   478 AA; 54417 MW;
                                                                                                                                                                                                                                                                                                                           63.5%;
                                                                      Genew; HGNC:4333; GLTSCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium perfringens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                239 EVAPAGASYN 248
                                                                                                                                                                                                                                                                            478
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                                                                                                                                                           191
                                                                                                                                                                                                                               417
                                                                                                                                                                                                                                                                                                                                                                        2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garnier T., Cole S.T.;
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriocin BCN5.
                                                                                                                                            9
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                                                                                                                                                                                                                    235
417
433
                                                                                                                                                                                                                                                                            434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CPN50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCN5_CLOPE
P08696;
                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                               CONFLICT
                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                             BCN5_CLOPE
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOSED OF THE TGF-BETAL MOLECULE NONCOVALENTLY ASSOCIATED WITH A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPERTIDE OF THE TGF-BETAL BRECURSOR AND A THIRD COMPONENT DENOMED TGF-BETAL-BP. TGF-BETAL-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETAL.-I- ALTERNATIVE PRODUCTS: 2 isoforms; a short form (shown here) and a long form (AC Q14766); are produced by alternative splicing.

-I- PTM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Fibroblast, and Platelet;
MEDLINE-90275601; PubMed-2350783,
Kanzaki T., Olofsson A., Moren A., Wernstedt C., Hellman U.,
Miyazono K., Claesson-Welsh L., Heldin C.-H.;
"TGF-beta 1 binding protein: a component of the large latent complex
of TGF-beta 1 with multiple repeat sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1S precursor (Transforming growth factor beta binding protein 1) (TGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 33; DB 1; Length 890; 66.7%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 890 AA; 96699 MW; F4E5E8971C31C6C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: The N-terminus is blocked.
-!- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
               MOI. Microbiol. 2:607-614(1988).
-!- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-!- INDUCTION: BY UV IRRADIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   HYDROPHOBIC.
                                                                                                                                                                                                                                                                                                                                                       SMART; SM00287; SH3b; 3.
Antibiotic; Bacteriocin; Plasmid.
DOMAIN 815 869 HYDR
                                                                                                                                                                                                                                                                                                                 PIR; A30481; A30481.
InterPro; IPR003646; SH3_bac.
                                                                                                                                                                                                                                                                          EMBL; M14481; AAA98248.1; -. EMBL; M32882; AAA98249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 66.7
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 EVVPGGFTY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
    vivo and in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTBS_HUMAN
P22064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTBP1
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DR InterPro; IPRU01861; EGF-like.

DR InterPro; IPR002212; Fibril-assoc.

DR Pfam; PF00008; EGF; 15.

DR Pfam; PF00008; EGF; 15.

DR PMART; SM00179; EGF_CA; 13.

DR SMART; SM00001; EGF_CA; 13.

DR PROSITE; PS00010; EGF_1; 2.

DR PROSITE; PS01186; EGF_2; 11.

DR PROSITE; PS01186; EGF_2; 11.

R Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal; II.

M Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-LIKE 14, CALCIOM DINDING (FOIENTIAL).

EGF-LIKE 14, CALCIOM-BINDING (FOIENTIAL).

EGF-LIKE 16, CALCIOM-BINDING (POTENTIAL).

ENTILARITY.

ENTILARITY.
                                                                                                                                                                                                                                                                            REPEAT A.

EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                 POTENTIAL.
LATENT TRANSFORMING GROWTH FACTOR BETA
BINDING PROTEIN 1S.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
                                                                        InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
     EMBL; M34057; AAA61160.1; -
PIR; A35626; A35626.
HSSP; P00750; JTPG.
GlycoSultebB; P22064; -
Genew; HGNC:6714; LTBP1.
MIM; 150390; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1001
1084
1139
1262
1180
1334
1379
849
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Nature 406:477-483(2000).

-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

-i- FUNCTION: DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

SUBSTRATES (By similarity).

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETARIFE I TOT NIG961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Ralzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase RPOC OR VC0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 1;
Pred. No. 93;
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BY SIMILARITY.
HYDROXYLATION.
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Best Local Similarity 45...
5; Conservative
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399 KEICPGGMGYT 409
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 Vibrio cholerae.
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ID RPOC_VIBCH
AC Q9KV29;
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SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE

{RNA}(N).

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A Kanzaki T., Olofsson A., Woren A., Wernstedt C., Hellman U.,

A Kanzaki T., Olofsson A., Woren A., Wernstedt C., Hellman U.,

A Myazono K., Claesson-Welsh L., Heldin C.-H.;

T "TGF-beta 1 binding protein: a component of the large latent complex of fer-beta 1 with multiple repeat sequences.";

Cell 61:1051-1061(1990).

C -1- SUBGNIT: THE LARGE LATENT COMFLEX OF TGF-BETA1 FROM PLATELETS IS

COMPOSED OF THE TGF-BETA1 MOLECULE NONCOVALENTLY ASSOCIATED WITH

COMPOSED OF THE TGF-BETA1 PRECURSOR AND A THIRD COMPONENT DENOTED TGF-

OF THE TGF-BETA1 PRECURSOR AND A THIRD COMPONENT DENOTED TGF-

BETA1-BP. TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.

C -1- ALTERNATIVE PRODUCTS: 2 isoforms; a short form (AC P22064) and a

Long form (shown here); are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN (By similarity).
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Efficient association of an amino-terminally extended form of human latent transforming growth factor-beta binding protein with the extracellular matrix.";
J. Biol. Chem. 270:31294-31297(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1L precursor (Transforming growth factor beta-1 binding protein 1) (IGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.5%; Score 33; DB 1; Length 1401; 50.0%; Pred. No. 93; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olofsson A., Ichijo H., Moren A., ten Dijke P., Miyazono K.,
Heldin C.-H.;
                                                                                                                                                                                                                                                                                                                                   Pfam; PF00623; RNA_pol_A; Pfam; PF01854; RNA_pol_A; 2.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                    1401 AA; 155021 MW; DFDB0F2B5514504F CRC64;
                                                                                                                                                                                                                                                                                           InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
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                                                                                                                                                                                                                                       EMBL; AE004121; AAF93502.1;
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nes 5; Conservative
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SEQUENCE 1401 AA
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Q14766;
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                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                           SMART; SM00181; EGF; 1.
PROSITE; PS00010; ASX_HYDROXYL; 13.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 11.
PROSITE; PS01187; EGF_A; 15.
Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal; Glycoprotein; Alternative splicing.
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EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 15.
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CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                             BINDING PROTEIN 1L. EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
TISSUE SPECIFICITY: The long isoform is found in fibroblasts.
PTM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES (BY SIMILARITY).
SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                     LATENT TRANSFORMING GROWTH FACTOR BETA
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                                                                                                                                 EMBL; L48925; AAA96327.1; -.
EMBL; M34057; AAA61160.1; ALT_INIT.
HSSP; P08709; 1BF9.
MIM; 150390; -.
                                                                                                                                                                         InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002212; Fibril-assoc.
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Pfam; PF00683; TB; 4.
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                                                                                                                                                                                                                    EMBL; M55431; AAA42235.1; -

BERL; M55431; AAA42235.1; -

BIRSP; P16109; IPSE.

R InterPro; IPR000152; Asx_hydroxyl.

R InterPro; IPR000151; EGF-Like.

R InterPro; IPR0002121; Fibril-assoc.

R InterPro; IPR00179; EGF-Like.

R InterPro; IPR00179; EGF-Like.

R Efam; PF00008; EGF; 16.

R SMART; SM000179; EGF-Like; 5.

R SMART; SM00010; ASX_HYDROXYL; 13.

R PROSITE; PS00010; ASX_HYDROXYL; 13.

R PROSITE; PS01186; EGF-2; 10.

R PROSITE; PS01186; EGF-2; 10.

R PROSITE; PS01187; EGF-Like. 2.

R PROSITE; PS01187; EGF-Like. 3.

R PROSITE; PS01187; EGF-Like. 3.

R PROSITE; PS01187; EGF-CA; 15.

R GONTH factor binding; Repeat; EGF-like domain; Hydroxylation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-LIKE 1.

EGF-LIKE 2.

INTERNAL REPEAT 1.

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

INTERNAL REPEAT 2.

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
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EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
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LATENT TRANSFORMING GROWTH FACTOR BETA
BINDING PROTEIN 1.
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-!- SIMILARITY: CONTAINS 18 EGF-LIKE DOMAINS.
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       [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-91062373; PubMed-2247454;
Tsuji T., Okada F., Yamaguchi K., Nakamura T.;
"Molecular cloning of the large subunit of transforming growth factor type beta masking protein and expression of the mRNA in various rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Nati, Acad. Sci. U.S.A. 87:8835-8839(1990).

-!- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS

COMPOSED OF THE TGF-BETA1 MOLECULE NONCOYALENTLY ASSOCIATED WITH
A MASKING PROTEIN CONSISTING OF A DISULFIDE-BONDED COMPLEX OF A
DIMER OF THE N-TERMINAL PROPERTIDE OF THE TGF-BETA1 PRECURSOR AND
A THIRD COMPONENT DENOTED TGF-BETA1-BP (OR MP LARGE SUBUNIT).

TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUJ-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1 precursor
(Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-
1) (Transforming growth factor beta-1 masking protein, large subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBL_TaxID=10116;
  BY SIMILARITY.
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Pred. No. 1.1e+02;
3; Mismatches 3; Indels
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1240 N-LI
1; 173229 MW;
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01-JUL-1993 (Rel. 26, Last sequ
15-JUN-2002 (Rel. 41, Last anno
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45.5%;
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nes 5; Conservative
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ID LTB1_RAT
AC Q00918;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       MEDLINE-95011623; PubMed-7926809; Hosokawa Y., Onga T., Nakashina K.; Nakashina K.; Onga T., Nakashina K.; Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S transition by prolactin in rat Nb2 cells."; Gene 147:249-252(1994).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S (START) TRANSITION.
                                                                                                                                                                                  -!- SUBGUIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLDENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93205384; PubMed-8455931; Palmero I., Peters G.; Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.; "Cyclins D1 and D2 are differentially expressed in human B-lymphoid cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xiong Y., Menninger J., Beach D., Ward D.C.; "Molecular cloning and chromosomal mapping of CCND genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1; Length 288;
Pred. No. 29;
1; Mismatches 3; Indels
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InterPro; IPR004367; Cyclin_Cterm.
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                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L09752; AAA41010.1; -. EMBL; D16308; BAA03815.1; -.
                        Oncogene 8:1661-1666(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human D-type cyclins.";
Genomics 13:575-584(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                      SEQUENCE FROM N.A.
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              the cyclin D2.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
Francke U., Jolicoeur P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1; Length 1712;
Pred. No. 1.1e+02;
3; Mismatches 3; Indels
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N-LINKED (GLCNAC. .)
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01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
61/S-specific cyclin D2 (Vin-1 proto-oncogene).
CCND2 OR VIN-1.
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718 KEICPGGMGYT 728
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es 5; Conserv
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Matches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1-SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THERONINE KINASE HOLDENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S (START) TRANSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.; "Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the cell cycle."; cell 65:701-713(1991).
                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of a D-type cyclin from murine erythroleukemia cells.";
Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
                                                                                                                                                                                                                                                                                         MEDLINE-92196134; PubMed-1372445;
Kiyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 32; DB 1; Length 289;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 40, Last annotation update)
61/S-specific cyclin Dl.
CYCD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 AA.
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M83749; AAA37519.1; --
EMBL; M86182; AAA37503.1; --
PIR; B40035; B40035.
PIR; A41984; A41984.
MGD; MGI:88314; CCnd2.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin.
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MEDLINE-91235305; PubMed=1827757;
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G1/S-specific cyclin D2.
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Best Local Similarity
'... 6; Conserv?
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                              NCBL_TaxID=10090;
                                                 CCND2 OR CYL-2.
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Q90459;
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            NXX OCC OS OF THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -. SUBMIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-. SIMILARITY: BELONGS TO THE CYCLIN PAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression of human cyclin D genes.";
Genomics 13:565-574(1992).
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic organization, chromosomal localization, and independent
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InterPro; IPR00436/; ...

A pfam; PF00134; cyclin.; 1.

R Pfam; PF02844; cyclin.; 1.

DR PR021TE; P800292; CYCLINS; 1.

DR PR05ITE; P800292; CYCLINS; 1.

Cyclin; Cell cycle; Cell division; Multigene family.

Cyclin; Cell cycle; Cell division; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    Miyajima N.;
Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases.
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(Rel. 25, Last sequence update)
(Rel. 40, Last annotation update)
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EMBL; M88080; AAA51928.1; JOINED.
EMBL; M88081; AAA51928.1; JOINED.
EMBL; M88082; AAA51928.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=92347850; PubMed=1386335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M90813; AAA51926.1; -.
EMBL; X68452; CAA48493.1; -.
EMBL; D13639; BAA02802.1; -.
EMBL; BC010958; AAH10958.1; -.
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                        Oncogene 8:1049-1054(1993).
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PIR; S26580; S26580.
Genew; HGNC:1583; CCND2.
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Best Local Similarity
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                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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01-APR-1993 (
16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                              -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOBNZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                          Blochim. Blophys. Acta 1264:257-260(1995).
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-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                    Yarden A., Salomon D., Geiger B., "Zebrafish cyclin Dl is differentially expressed during early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 32; DB 1; Length 291; 60.0%; Pred. No. 29; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            LATAN, CALL DEARL DOUGLE ALV. CYCLI.
INTERPROS IPR00436; CYCLIN.
INTERPROS IPR00436; CYCLIN.
Pfam; PF00134; CYCLIN; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
CYCLIN; Cell CYCLE CALL division.
SEQUENCE 291 AA; 33067 WW; FA5274CB1B46D5EF CRC64;
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01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
SEQUENCE FROM N.A.
MEDLINE-96138542; PubMed-8547308;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X87581; CAA60885.1; -ZFIN; ZDB-GENE-980526-176; cycdl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G1/S-specific cyclin D1.
                                                                                                                                  (START) TRANSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMSY 10
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                              embryogenesis.
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P50755:
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SUBJUILT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.

SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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                                                                                                                                                                                                                                                                                                                           Length 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, U28980; AAA96955...,
InterPro: IPR004366; Cyclin.
InterPro: IPR004367; Cyclin.
InterPro: IPR004367; Cyclin.
InterPro: IPR004367; Cyclin.
InterPro: IPR0044; Cyclin; Interpro: IPR0284; Cyclin; Interpro: IPR0284; Cyclin; Interpro: IPR0285; Cyclin; Interpro: IPR0217E; PS00292; Cyclin; Interpro: IPR0517E; PS00292; Cyclin; Interpro: IPR0517E; I
               EMBL; X89475; CAA61664.1; -.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin.
Pfam; PF02134; cyclin.c; 1.
Pfam; PF02984; cyclin.c; 1.
SMART; SM00392; CYCLIN; 1.
PROSITE; PS00292; CYCLIN; 1.
PROSITE; PS00292; CYCLIN; 1.
Cyclin; Cell cycle; Cell division; Multigene family, SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;
                                                                                                                                                                                                                                                                                                                  61.5%; Score 32; DB 1; 60.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-001-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
16-001-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                     Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGD2_CHICK
P49706;
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74 EEVFPLAMNY 83

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Gallus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION:
-1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
-1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        early development.";
Biol. Cell 88:99-111(1996).
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Xenopus cyclin D2: cloning and expression in oocytes and during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
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E 291 AA; 32959 MW; 9A290F04F1531E89 CRC64;
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01-077-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                       291 AA
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EMBL; X83503; CAA58493.1; -.
InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97380591; Pubmed=9237366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00134; cyclin; 1.
Pfam; PF0294; cyclin_C; 1.
SMART; SM00385; CYCLIN_1 .
PROSITE; PS00292; CYCLINS; 1.
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Matches 6; Conservative
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                                                              STANDARD;
                                                                                                                                                                                                            G1/S-specific cyclin D2.
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                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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CGD1_CHICK
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RESULT 24
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                                                                                                                                                                  SEQUENCE FACE. .....
Li H., Lahti J. M., Kidd V.J.;
Li H., Lahti J. M., Kidd W.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
-!- FUNCTION: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                     (START) TRANSITION. INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 292 Aa; 33263 MW; 7B543029DB45A67D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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Interpro; IPRO04366; Cyclin.
Interpro; IPRO04367; Cyclin_Cterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                             SECUENCE FROM N.A.
                                    NCBI_TaxID=9031;
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Search completed: June 10, 2003, 13:40:20 Job time: 4.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:30:25; Search time 25.7857 Seconds (without alignments) 87.898 Million cell updates/sec Run on:

US-09-909-164-10 52 1 EEVVPXGMSYS 11 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 671580 seqs, 206047115 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_hivertebrate:*
6: sp_mamal:*
7: sp_mhc:* sp_organelle:* sp_phage:* sp_archeap:* sp_plant:*
sp_rodent:* sp_virus:* 10: 112: 13: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•	Description	098fxl rhizobium l	Q8rg86 fusobacteri	074056 cenarchaeum	Q9ury8 schizosacch	Q8r126 mus musculu	Q8vd18 mus musculu	Q40129 lycopersico	Q9xvk4 caenorhabdi	O43733 homo sapien	Q9bha5 plasmodium	Q9bh83 plasmodium	Q01487 rattus norv	Q9pdm6 xylella fas	Q14122 homo sapien	Q12479 saccharomyc	0971s2 sulfolobus
SUMMARIES																	
SOME	a a	Q98FX1	Q8RG86	074056	Q9URY8	Q8R126	Q8VD18	040129	Q9XVK4	043733	Q9BHA5	09вн83	001487	O9PDM6	014122	012479	097182
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	% Query Match Length DB	387	1063	3472	840	471	484	225	425	556	583	583	670	749	1902	156	219
	& Query Match	73.1	73.1	73.1	71.2	69.5	69.2	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	65.4	65.4
	Score	38	38	38	37	36	36	35	35	35	35	35	35	35	35	34	34
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Q98mul homo sapien Q96mul homo sapien Q96mul homo sapien Q96bp5 rhizobium n Q98pd2 ureaplasma Q98xt05 ralstonia s Q96914 homo sapien Q8xx62 methanopyru Q9xxq4 mus musculu Q8xx63 methanopyru Q9xxq4 mus lactococcus Q8re56 fusobacteri P74187 synechocyst Q9m3C0 arabidopsis Q9q9q9 soil-borne Q9q9q5 soil-borne Q9q9q7 soil-borne Q9q9q7 soil-borne Q9q9q7 soil-borne Q9qq5 soil-borne Q9qxy dorsophila Q9kx87 drosophila Q9kx87 drosophila Q8y111 brucella me Q9cc95 mycobacteri Q9cyp5 sulfolobus	ara clo clo clo sulf rat rat the csch ara ara
028342 096MU1 093MD6 098BP5 099BP5 099BP5 090BP6 090BP6 090BP6 090BP7 090BP6 090BP6 090BP7 090BP7 090BP7 090BP7 090BP7 090BP7 090BP7 090BP8	065531 088349 098349 090000 0900019 090819 090814 099814 0997CD0 047284 032330 095851 090809
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# ALIGNMENTS

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	PRT;		Created)	Last seq	Last ann		
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	PRELIMINARY		(TrEMBLrel.	(TrEMBLrel.	(TrEMBLrel.	drolase.	
RESULT 1 Q98FX1	Q98FX1	Q98FX1;	01-OCT-2001	01-OCT-2001	01-OCT-2001	Hippurate hydrolase	MLR3583.
RESULT Q98FX1	Ω	Y V	DI	DŢ	DI	DE	ВN

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                                                                      STRAINWARF503099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Maneko T., Nakamura T., Sato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishda Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-AUCC 25586;
MEDLINE-21886394; PubMed=11889109;
MEDLINE-21886394; PubMed=11889109;
MEDLINE-21886394; PubMed=11889109;
MEDLINE-21886394; PubMed=11889109;
Maptacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaqa O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586";
J. Bacteriol. 184:2005-2018(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                      73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 9.8;
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                                                                                                                                                                    Mesorhizoblum loti.";

DNA Res. 7:331-338(2000).

EMBL, AP003002; BAB50445.1; ...
Interpro; IRR00293; Peptidase_M20.

Pfam; PF01546; Peptidase_M20; 1.

Hydrolase; Complete proteome.

SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1063 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusobacterium nucleatum (subsp. nucleatum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Fusobacteria; Fusobacterium
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                                                                                                                                                                                                                                                                                Local Similarity 60.0
nes 6; Conservative
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367 DEAIPHGMSY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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195 EIVPNGLNYS 204
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                                                             SEQUENCE FROM N.A
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                                      NCBI_TaxID-381;
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Q8RG86;
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Matches
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                                                                                                                                                                                                                                                                                                          "Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";

of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";

1. Bacteriol. 180:5003-5009(1998).

INTERPROY CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).

EMBL; AF083072; AAC62699.1; -..

INTERPROY IPRO00515; BPD transp.

InterPro; IPR0010680; WD40.

Pfam; PF00400; WD40; 4.

PROSITE; PS00402; WD40.2

PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_I.

Hypothetical protein; Repeat; WD repeat.

SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
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Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ALI32779; CABGOUS-11, -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS: J.
Pfam; PF00916; Sulfate_transp; 1.
TIGRRAMS; TIGR00815; Sulfate_transp; 1.
SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CRC64;
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                                                                                                                                                                                                                                                                 Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y., Swanson R.V.;
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Pred. No. 1e+02;
4; Mismatches 1; Indels
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Pred. No. 37;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaee,
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable sulfate permease.
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                                                                                                          Archaea; Crenarchaeota; Cenarchaeum.
NCBI_TaxID=46770;
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                                                                                                                                                                                                                                         MEDLINE=98422450; PubMed=9748430;
                                                      Hypothetical 367.1 kDa protein.
Cenarchaeum symbiosum.
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77.88;
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2294 EDVIPRGISFS 2304
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Matches 6; Conservative
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|135 VVPQGMSYA 143
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ID Q8R126
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SEQUENCE FROM N.A.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.2 kDa protein precursor.
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OBR126;
01-UON-2002 (TrEMBLrel. 21, Created)
01-UON-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 54.5 kDa protein (Fragment).
Hypothetical source)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straugherg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017637; AAH17637.1; -.
MGD; MGI:2138595; AW536441.
SPONTENCE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 33;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                             69.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 EVIPAGASYN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 EVIPAGASYN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                  IISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8VD18
Q8VD18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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ACTION OF THE STATE OF THE STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percy C.M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z81109; CAB03241.1; -.
InterPro; IPR00719; Buk_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Buk_pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 425 AA: 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN 21 225 UNKNOWN.
SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                      ProDom; Purvect.
SMART: SMO04283: SOYDEAN_KUNITZ; UNKNOWN_1.
Hypothetical protein; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.3%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.3
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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32 DEVVPNGKTYA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R10D12.10 protein.
R10D12.10.
Caenorhabditis elegans.
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hes 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
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EMBL; AY007374; AAK14818.1; -.
EMBL; AY007373; AAK14817.1; -.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SEQUENCE 583 AA; 66918 MW; 4DF83D7530527474 CRC64;

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RESULT 13
       SO BR BR
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                                                                                                                                                                                                                                    Gaps
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pen Manoun C., Gluzman I.Y., Goldberg D.E.;
Plasmodium falciparum choline transporter (PfSCT1) gene.";
Submitted (AUG-2000) to the EMBL/Genbank/DDBJ databases.
EMBL; AY007375, AAK14816.1; -
EMBL; AY007375, AAK17947.1; -
EMBL; PR002133; Acyltransferase.
Pfam; PP01553; ACYltransferase.
SEQUENCE 583 AA; 66917 MW; 2B2BFAB3E395E049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ben Mamoun C., Gluzman I.Y., Goldberg D.E.; "Plasmodium falciparum choline transporter (PfSCT1) gene."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     Score 35; DB 4; Length 556; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.3%; Score 35; DB 5; Length 583; 55.6%; Pred. No. 67; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                 1; Indels
                                                                                                                       Tubby B.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Z98050; CAB10847.1; -.
                                                                                                                                                                          556 AA; 59059 MW; ECB00E4033FB2528 CRC64;
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     583 AA
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                                                                                                                                                                                                                                2; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-070-2001 (TrEMBLrel. 17, Created)
01-070N-2001 (TrEMBLrel. 17, Last seq
01-070N-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                     PRT;
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              DNA binding protein (Fragment).
                                                                                                                                                                                                     67.38;
                                                                                                                                                                                                               Local Similarity 66.7
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 55.6 ses 5; Conservative
                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                        ||| |::||
244 VVPAGLTYS 252
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                                                                                                                                                                                                                                                         3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                   Choline transporter.
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                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-5833;
                         DJ451B15.2
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                Q9BHA5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09вн83;
                                                                                                                                                                                                                                                                                                                                                  Q9BHA5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTIONAL ACTIVATION

1- SINILARITY: HIGHLY SIMILAR TO AT-BP1 AND TO THE PRDII-BF1 FACTOR.

BMBL; X54250; CAA38151.1; --
HSSP; P15822; 1B80.

InterPro; IPR000822; Znf_C2H2.

Ffam; PF00096; Zf-C2H2; -2.

SWART; SM00355; ZnF_C2H2; -2.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.

PROSITE; PS0157; ZINC_FINGER_C2H2_2, 2.

Zinc_finger; Nuclear protein; DNA-binding; Transcription regulation; Metal_binding; Multigene family.
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DNA-binding protein AT-BP2 (ALPHA1-antitrypsin promoter binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- MISCELLANEOUS: ACIDIC AMINO ACID REGION MAY BE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                             Length 583;
                                                                                Indels
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C(2)H(2) CLASS.
CDD2324152590C17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                             DB 5;
                                                                                                                                                                                                                                                                                                              670 AA.
                                                     Pred. No. 67;
3; Mismatches
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ACIDIC.
                          67.3%; Score 35; 55.6%; Pred. No.
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Query Match
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Best Local 5; Conservative
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376 VVPAGLIYS 384
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DOMAIN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

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A Simpson A.J.G., Relaach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arruda P., Bala G.S., Baptista C.S., A Alvarenga R., Alves L.M.C., Arruda J.E., Bala G.S., Baptista C.S., A Alvarenga R., Alves L.M.C., Arruda J.E., Bove J.M., Briones M.R.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., A Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Ra Faca J.S., Ferreira A.J.S., Ferreira V.G.M., Ferreira A.J.S., Ferreira W.C.A., Ferro J.A., Ra Fraga J.S., Ferreira A.J.S., Ferreira W., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ra Krieger J.E., Kuramae E.E., Lajoyet F., Lambais M.R., Leite L.C.C., Ra Krieger J.E., Kuramae E.E., Lajoyet F., Lambais M.R., Leite L.C.C., Ra Lemos E.G.M., Lemos M.V.F., Lopes G.M., Martins E.M.F., Matsukuma A.Y., Marques M.V., Martins E.M.F., Matsukuma A.Y., Marques M.V., Martins E.M.F., Martins E.M.F., Matsukuma A.Y., Marques M.V., Martins E.G., Miyaki C.Y., Monteiro-Vitorello C.B., Monto D.H., Nagal M.A., Nascimento A.L.T.O., Netto L.E.S., Monto D.H., Nagal M.A., Nascimento A.L.T.O., Netto L.E.S., A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Paris A., Maria A. Jr., Noberto P.G., Rodrigues V., de Rosa A.J.M., A de Sluva A.C.R., de Sluva A.M., da Silva F.R., Silva M.A., Verjovski-Almeida S., Vettore A.L., RA de Sluva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., RA de Suuza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., RA Zago M.A., Zatz M., Meidanis J., Setubal J.C., Stuteira W.J., Gesluence of the plant pathogen Xylella fastidiosa F. R. Rebell A.B., Denter D. S., Roberto Of the plant pathogen Xylella fastidiosa F. B. Rebell D. S. Rebellos J., Salva E.B., Santalli S. V. Salva E.B., Santalli 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 35; DB 16; Length 749; 77.8%; Pred. No. 88;
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Last annotation update)
                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                              749 AA.
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01-NOV-1996 (TrEWBLrel. 01, Last sequen
01-MAR-2002 (TrEMBLrel. 20, Last annota
DNA-binding procein (Mbp-1) (Fragment).
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                                                                  Created)
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TIGRFAMS; TIGR01062; parc_Gneg; 1.
                              PRT;
                                                                                                                                                                                                                                                                                               MEDLINE-20365717; PubMed-10910347;
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Best Local Similarity 77.0%
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                                                                                                                          Topoisomerase IV subunit.
                                  PRELIMINARY;
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                                                                                                                                                                Xylella fastidiosa
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
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      PEDGINE FORD AND THE PROBLEM TO THE PROBLEM THE PROBLEM THE PROBLEM THE SEQUENCE OF THE PROBLEM THE PROBLEM THE PROBLEM THE PROBLEM THE PROBLEM TO THE PROBLEM THE PROBLEM TO THE PROBLEM THE PROBLEM TO THE PROBLEM THE PROBLEM TO THE
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Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHSI, which complements a drug-
hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 58:391-395(1994).
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66.7%; Pred. No. 2.4e+02;
ive 2; Mismatches 1; Indels
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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1590 VVPAGLTYS 1598
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Best Local Similarity
SEQUENCE FROM N.A.
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                                                                                     Gaps
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Sulfolobus.
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PubMed-11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
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SEQUENCE FROM N.A.
STRAIN-VC-16, DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                        Score 34; DB 3; Length 156;
Pred. No. 27;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.4%; Score 34; DB 17; Length 219; 66.7%; Pred. No. 38;
                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of an aerobic thermoacidophilic Caraarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001)
EMBL, AP000985; BAB66348.1;
InterPro: IPR004788; RpiA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
EMBL; 274920; CAA99201.1; -.
EMBL; X87331; CAA60762.1; -.
SGD; S0005539; YOR013W.
SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Probon, P0005813; Rp1A; 1.
Isomerase; Hypothetical protein; Complete proteome.
SEQUENCE 219 AA; 24541 MW; A4E9A3F2C4006D90 CRC64;
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Last annotation update)
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01-3AN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                            219 AA.
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Best Local Similarity 66./*,
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                                                                                                2 EVVPXGMSY 10
                                                                                                             Archaeoglobus fulgidus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EVVPXGMSY 10
                                                                                                                                                                                                                                               Sulfolobus tokodaii
                                                                  Local Similarity
                                                                                                                                                                                                                                                                              NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                      Query Match
                                                                                                                                                                                  097152;
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                                                                   Best Loc
Matches
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Ouackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback A., Zhou L., Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Sadow P.W., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ31891 fis, clone NT2RP7003304, weakly similar to YceA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE000970; AABB8318.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Julestro, .....
Pfam; PF00991; ParA; 1.
Hypothetical protein; Cell division; Complete proteome.
SEGUENCE 252 AA; 27130 MW; A401DC1F93E8C538 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK056453; BAB71188.1; -...
InterPro; IPR001763; Rhodanese-like.
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SEQUENCE 290 AA; 32972 MW; 41FB7FB0217C1421 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR000707; ATPase_ParA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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445 EELVPVGKAY 454
     Query Match
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                                                                   RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                MEDLINE-1195507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Codrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Renard C., Thebault P., Vandenbol M., Weidner S., Gallbert F.;
"Analysis of the Chromosome sequence of the legume symbiont
Sinorhizoblum meliloti strain 1021.";
EMBL, AL591791; CAC472691; - ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
putative HIPPURATE hydrolase protein (EC 3.5.1.32).
HIPO1 OR R02690 OR SMC00682.
HIPO1 OR R02690 OR SMC00682.
Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group; Rhizoblaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.4%; Score 34; DB 16; Length 541; 60.0%; Pred. No. 1e+02; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 34; DB 16; Length 387; 50.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Complete proteome.
SEQUENCE 387 AA; 41074 MW; 342763088907A6E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
PROSITE; PS50160; DNA_LIGASE_A3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                   EMBL; AL591791; CAC47269.1; -.
InterPro; IPR002933; Peptidase_M20.
Pfam; PF01546; Peptidase_M20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesorhizoblum loti.";
DNA Res. 7:31-338(200).
BMBL; AP003006; BAB51927.1:
InterPro; IPR000977; DNA_ligase.
Pfam; PF01068; DNA_ligase; 1.
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Best Local Similarity 60.09
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 50.0 hes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable DNA ligase.
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                                                                                                                                                            SEQUENCE FROM N.A.
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Q98BP5
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A STRAIN-0176;

XC STRAIN-0176;

XC MEDLINE-20042342; PubMed-10572125;

RA MEDLINE-20042342; PubMed-10572125;

RA Schuurs T.A., Newbert R.W., Turner G., Konings W.N., Driessen A.J.M.;

RA Schuurs T.A., Newbert I. W., Turner G., Konings W.N., Driessen A.J.M.;

RT Sulfate Transport in Penicillium chrysogenum: Cloning and Characterization of the suth and sutB Genes.";

RT Characterization of the suth and sutB Genes.";

RL J. Bacteriol. 181:7228-7344(1999).

DR InterPro; IPR001545; STAS.

DR InterPro; IPR001902; Sulfate_transp.

DR Pfam: PF01740; STAS: 1.

DR Pfam: PF01740; STAS: 1.

DR Pfam: PF01740; SULFATE_transp; 1.

DR PGRPAMS; TIGR00815; sulfate_transp; 1.

DR PROSITE; PS01130; SULFATE_TRANSP; UNKNOWN_1.

PROSITE: PS01130; SULFATE_TRANSP; UNKNOWN_1.
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Eurotlales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=5076;
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                                                                                                                                                                                                                                                                                                                                          STRAIN=SEROVAR 3;
MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                        Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 34; DB 16; Length 544; 70.0%; Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                             Last sequence update)
Last annotation update)
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66.7%; Pred. No. 1.v.
... 2; Mismatches
                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence upo
01-MAR-2002 (TrEMBLrel. 20, Last annotation of
12 trative ABC substrate-binding protein-iron.
ABCSBP-5 OR UU359.
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544 AA.
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  PRT;
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Nature 407:757-762(2000).
EMBL; AE002133; AAF30768.1; ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 70.0
Matches 7; Conservative
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     PRELIMINARY;
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Best Local Similarity
6; Conservat
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SEQUENCE 544 AA;
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Nat. Genet. 28:19-20(2001).
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EMBL;
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096914, 0. Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; ALG46709, CAD17463.1; --
InterPro; IPR004764; HAEI.
InterPro; IPR004764; HAEI.
InterPro; IPR004764; HAEI.
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MEDLINE-21225279; PubMed=11326269;
MEDLINE-21225279; PubMed=11326269;
Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S., Oshimura M.;
"A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.4%; Score 34; DB 16; Length 1049; 75.0%; Pred. No. 2.1e+02; .ive 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PICTION ACR_tran, 1.
PRINTS; PR00873. ACR_tran, 1.
TIGREAMS; TIGR00915, 2A0602; 1.
PROSITE; PS50156; SSD; 1.
PROSITE; PS50156; SSD; 1.
Plasmid; Complete proteome.
SEQUENCE 1049 AA; 111769 MW; CB59674B670089CE CRC64;
                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
101-Dable multidrug efflux system transmembrane protein.
MEXD OR RSP0312 OR RS05457.
Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                               PRT; 1049 AA.
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MEDLINE-21681879; PubMed-11823852;
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   3 VVPXGMSYS 11
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ATP10C.
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Q8XT05;
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Q8XT05
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Methanopyrus kandleri,
Archaea; Euryarchaeota; Methanopyr1; Methanopyrales; Methanopyraceae;
Methanopyrus.
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EMBL, AE010372; AAM02027.1; -. 99:4644-4649(2002).

SEQUENCE 143 AA: 15734 MM, 408B28AlFBBEDDDB CRC64:
SEQUENCE FROM N.A.
MEDLINE=21313119; PubMed=11353404;
MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.J., Cook E.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ArPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression.";
EMBL; AB051358; BAB47392.1; ---
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PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN_1.
SEQUENCE 1499 AA; 167687 MW; D4996A4D0635A68D CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR001454; Hlgnase/hydrlase.
                                                                                                                                                             , AAK33100.1; -, AAK33100.1; -, AAK33100.1; JOINED.
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MEDLINE=21927647; Pubmed=11930014;
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es 8; Conserv
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DB 17; Length 143;

63.5%; Score 33;

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1 EEVVPXGMSY 10 ||:|| | | | 75 EELVPQGAGY 84

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Search completed: June 10, 2003, 13:46:32 Job time : 25.7857 secs

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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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56
1 EEVVPXGMHYS 11
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Ü	Hepatitis C virus	O	υ	υ	υ	υ	Hepatitis C virus	Hepatitis C virus	Hepatitis C virus	
SUMMARIES			ID	ABB80523	ABB80527	ABB80558	ABB80560	ABB80537	ABB80541	ABB80546	ABB80550	ABB80554	ABB80555	
			e :	23	23	23	23	23	23	23	23	23	23	
			Match Length DB	11	11	11	11	11	11	11	11	11	11	
	æ	Query	Match	96.4	96.4	96.4	96.4	87.5	87.5	85.7	85.7	85.7	85.7	
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ALIGNMENTS

RESULT 1 ABB80523 ID ABB8

ABB80523 standard; peptide; 11 AA.

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Query Match
Best Local Similarity 100.
Matches 11; Conservative
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      virucide.
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                                                                                                                                                         "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
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                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                       "C-terminal amide"
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                                                                                                                    Location/Qualifiers
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100.0%; Pre
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                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                 virus protease
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                     /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                          'note= "N-terminal acetyl"
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Location/Qualifiers
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100.08; Fig.
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/note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                             "Oxymethionine"
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                                                                                                                                                           Lim-wilby M, Levy OE,
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                                                                                                                                         (CORV-) CORVAS INT INC
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Best Local Similarity
Matches 11; Conserv
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"Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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Pred. No. 0.00045;
0; Mismatches 0; Indels
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virus protease
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                                                                           Peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
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90.9%; Pred. No. 0.0043;
1ve 0; Mismatches 1.
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        21-JUL-2000; 2000US-220101P.
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                         (CORV-) CORVAS INT INC
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hepatitis C virus (HCV) protesse inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protesse. A pharmaceutical composition comprising the peptide as an active incredient is useful for treating disorders associated with hepatitis C virus.
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peptide compound having hepatitis C virus protease inhibitory ty useful for treating disorders associated with hepatitis \mathsf{C}
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Pred. No. 0.0043;
0; Mismatches 1
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                                                                                                             Claim 17; Page 65; 69pp; English.
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90.9%;
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Best Local Similarity
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Indels

Pred. No. 0.0067; ); Mismatches 1;

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90.98;

Best Local Similarity

Matches

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30
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                                                                                                  Score 48; DB 23; Length 11;
Pred. No 0.0067;
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                                                                                                    85.78;
90.98;
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                                                                                                                 Local Similarity 90.5
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Length 11;

85.7%; Score 48; DB 23;

Query Match

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                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34.
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pred. No. 0.0067; 
0; Mismatches 1; Indels
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                  (first entry)
10; Conservative
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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11.
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                                                                                                                                                                                                                                                                                                         'note= "N-terminal acetyl"
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                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35.
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Pred. No. 0.0067;
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                            ABB80555 standard; peptide; 11 AA.
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90.9%;
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Matches 10; Conserv
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                                                                                                                                            08-OCT-2002
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                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                     ABB80555;
                                                                                                                                                                                                                                                                               virucide.
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Gaps

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1; Indels

RESULT 11 ABB8053

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                          11 AA;
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                                                                                                                                                                          virus protease
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WO200208251-A2.
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                                                                                                                                                                                                                                                                                                                                                     .10;
                      31-JAN-2002
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                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB80522
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    residue 7"
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                                                                                                                                                                                                                                                                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                   /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                /note= "N-terminal acetyl"
                                                                                           /note= "C-terminal amide"
                                                                      /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                            Brunck TK;
                                                                                                                                                                                                                                                                                                                Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.1%;
90.9%;
                                                                                                                                                                                 21-JUL-2000; 2000US-220101P.
                                                                                                                                                              19-JUL-2001; 2001WO-US23169.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 90.9 nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMHYS 11
                                                                                                                                                                                                                             Lim-wilby M, Levy OE,
                                                                                                                                                                                                       (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                 WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                              11 AA;
                                                               Misc-difference 9
                                                                                                                                                                                                                                                                                            virus protease
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                                                                                                                  WO200208251-A2
         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 23; Length 11; pred. No. 0.026; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "D-form residue"
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                                                                                                                                                                  Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 64; 69pp; English.
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19-JUL-2001; 2001WO-US23169.
                                                       21-JUL-2000; 2000US-220101P
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                                                                                                                                                                     Lim-wilby M, Levy OE,
                                                                                                                  (CORV-) CORVAS INT INC
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Claim 17; Page 64; 69pp; English.
             virus protease
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                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                               ABB80525;
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                        virucide.
                                                                                                                                                                                                                                                      RESULT 16
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                                                                                                                      The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have a medicament to treat useful for treating and in the manufacture of pharmaceutical composition comprising the peptide as an active ingredient is useful for treating addisorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                             peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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0
                                                                                                                                                                                                                                  80.4%; Score 45; DB 23; Length 11; 90.9%; Pred. No. 0.026;
                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "D-form residue"
                        Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               ABB80524 standard; peptide; 11 AA.
                                                                                                    Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brunck TK;
                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.55,
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
 (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                         1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                     Lim-wilby M, Levy OE,
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                                         WPI; 2002-361643/39
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                                                                                                                                                                                                              11 AA;
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                                                                                  virus protease
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                                                                                                                                                                                                             Sequence
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                                                              Novel
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invention are alpha-ketoamide peptide analogues. The peptides have a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
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                                                                                                                                                                     Score 45; DB 23; Length 11; Pred. No. 0.026;
                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               ABB80525 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 64; 69pp; English.
                                                                                                                                                                80.4%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                  1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                               1 EEVVPXGMDYS 11
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                                                                                                                                     11 AA;
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DB 23; Length 11;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis {\tt C}
                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6
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0
                                                                                     Score 45; DB 23; Length 11;
Pred. No. 0.026;
                                                                                                                1; Indels
                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residue 7"
                                                                                                                                                                                                                                            ABB80526 standard; peptide; 11 AA.
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                                                                                     80.4%;
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                  Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                             1 EEVVPXGMSYS 11
                                                                                                                                             1 EEVVPXGMHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 9
                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                            Sequence
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                                                                                        Query Match
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11 AA;

Sequence

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                                    Gaps
                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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                                  1; Indels
          Score 45; DB 23
Pred. No. 0.026;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                            /note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                  ABB80528 standard; peptide; 11 AA.
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            80.4%;
90.9%;
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Ouery Match
Best Local Similarity 90.>
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es 10; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus protease
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                                                                                                                            RESULT 18
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(first entry)
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            08-OCT-2002
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                                                                                                       Synthetic.
                                                                              virucide
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    residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invention are alpha-ketoamide peptide analogues. The peptides have a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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                                                                                                                                                                                                                                                                                                                                             /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
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                           ABB80529 standard; peptide; 11 AA.
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                                                                                 (first entry)
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Best Local Similarity
Matches 10; Conserv
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    RESULT 19
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                   ABB80529
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ABB80559 standard; peptide; 11 AA.

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ABB80559;

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39.
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Pred. No. 0.026;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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us-09-909-164-11.rag

Synthetic virucide

31-JAN-2002

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                        "Norvaly1 carbonyl forming keto-amide linkage with residue 7".
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/note= "N-terminal acetyl"
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                                  /note=
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                                                                   Misc-difference
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                                                                                                                                      /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
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                                                                                                          'note= "N-terminal acetyl"
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Matches 10; Conserva
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Modified-site
                                                                                                                                                                               Misc-difference
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                                                                                                                               Modified-site
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Sequence

Query Match

ŏ g Synthetic

virucide

ABB80562;

RESULT 22

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Gaps

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(CORV-) CORVAS INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-2002
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                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        virucide.
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Matches
                                                                                                                                                                                                                                                                                                                                         RESULT 25
                                                                                                                                                                                                                                                                                                                                                    ABB8056
           g
                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have a rectivity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Leucyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                          Score 45; DB 23; Length 11; Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                      Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80564 standard; peptide; 11 AA.
                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
                                                                     19-JUL-2001; 2001WO-US23169.
                                                                                         21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                         80.4%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                Local Similarity 90.9
les 10; Conservative
                                                                                                                                  Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC.
                                                                                                                                                     WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                    11 AA;
                             WO200208251-A2
                                                                                                                                                                                              virus protease
Modified-site
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norleucyl carbonyl forming keto-amide linkage with residue 7"
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                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.
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                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
Lim-wilby M, Levy OE, Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80565 standard; peptide; 11 AA.
                                                                                                                                  Claim 17; Page 65; 69pp; English.
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                               WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                              11 AA;
                                                                                                        virus protease
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Search completed: June 10, 2003, 13:39:08 Job time : 31.3571 secs

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0; Gaps

80.4%; Score 45; DB 23; Length 11; 90.9%; Pred. No. 0.026; tive 0; Mismatches 1; Indels

Query Match 80.4 Best Local Similarity 90.9 Matches 10; Conservative

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:31:45; Search time 9.64286 Seconds (without alignments) 33.564 Million cell updates/sec Run on:

US-09-909-164-11 56 1 EEVVPXGMHYS 11 Perfect score: Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database :

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 4794, Ap	19. Ar			Sequence 3950, Ap		m	ς,	Sequence 4, Appli	4	4	7	21,	21,	21,	21,	22	Sequence 22, Appl	22,	22,	9	Sequence 6, Appli	4	4	Sequence 6, Appli	23,	,
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SUMMAKLES	ID	US-09-134-001C-4794	US-08-821-119-19	US-08-821-118-2	US-09-724-864-36	US-09-134-001C-3950	-08-5	US-08-879-995A-3	US-09-215-096-3	US-08-460-694-4	US-08-460-744-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	US-08-246-361A-21	US-08-463-772-21	PCT-US93-05000-21	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22	US-08-464-517-6	US-08-463-772-6	US-08-246-361A-4	PCT-US93-05000-4	PCT-US93-05000-6	US-08-464-517-23	
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æ	Query Match Length DB	9.69	60.7	60.7	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1		57.1	
	Score	39	34	34	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	
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30	3.7	57	7	25	S	CT-US93-05000	g	'n	Appl
31	32	57.	1	95	_	US-07-947-120-8	Sequence	8, A	ppli
32	32	57.	1	95		-08-472-8	Se	4	ppli
33	32	57.	1 2	95		-08-460-694	e)	~	ppli
34	32	57	1	95		464-517-1	ce		Appl
35	32	57	1 2	295	~	-08-464-517-2	(I)	0	Appl
36	32	57	1 2	95		361A-1		_	Appl
37	32	57	1 29	95		US-08-246-361A-20	a	20,	Appl
38	32		1 2	95	•	-463-772-1	a	19,	Appl
39	32		1 2	95		S-08-463-772			Appl
40	32	57	1 2	95		-460-744			Appli
41	32	57	1 2	92		- 199	Sequence	2, 4	App11
	32	57	1 2	95		US-08-947-492-8	Sequence		Appli
	32	57	1 2	95		PCT-US93-05000-2			Appli
	32	57	1 2	95		PCT-US93-05000-19		19,	Appl
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46	32	57.	س	60		US-08-464-517-4	Sednence	_	pp11
	32	٠.		60		US-08-463-772-4	Sequence		App11
48	32			15		US-08-663-566A-17	Seguence	'n	Appl
49	32			15		US-08-023-610-17	Seguence	17,	Appl
20	32			15		US-08-288-065A-17	a	17,	Appl
51	32			15		US-08-362-240A-17		17,	Appl
52	32		1 6.	15		PCT-US95-10245-17	Sequence	17,	Appl
53	32			18		US-08-770-761A-3			pp11
54	32			47		-770-761A-	ø		App11
22	32			9		-770-761A	a)		Appli
26	32		1 6(	62		-770-761A-	a)	5, 2	Appli
22	32	•		05		-770-761A		_	ppli
28	32			19		-464-517-7			Appli
29	32			19		-246 - 361			ppli
09	32			19		63-772-7			ppli
61		٠		19		00050-668			pp11
62	31.5			01		-408-	a)	ī	Appl
63	31	٠.		50		S-08-963-851-1	_	14,	Appl
64	37	٠		5.5		so.		м,	7197
92	31		4	10		97-1	Patent No.	517	7197
99	31	٠.	4	47		-08-961-083-		82	, App
67	31	٠.	ഗ	02		-09-342-647-			/pp1i
99	31	٠.	5.	59		-09-240-639-			/ppli
69	31	٠.	9	22		S-08-459-146		2, 2	Appli
70	31		4 . 6.	22		S-08-459-065-			ppli
71	31	٠.	4	30		S-09-342-647-	edneuce	~	Appli
72	31	٠.	4 6	67		S-09-342-647-		ωÌ	Appl
73	31		7	38		S-08-530-010	edneuce	3, 4	Appli
74	31	٠.	7.	38		S-08-530-010-			ppli
75	31	55.	7.	38		30-010-	edneuce		ppli

## ALIGNMENTS

Sequence 4794, Application US/09134001C

Patent No. 638070

GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCG
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

LENGTH: 1037 RESULT 1 US-09-134-001C-4794

TYPE: PRT ORGANISM: Staphylococcus epidermidis

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4 VPXGMHYS 11
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                                                                     ADDRESSEE:
STREET: 40
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LENGIH: 747
                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-821-118-2
                                                                                                                     STATE:
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                                                                                                                                                                           RESULT 2
US-08-821-119-19
US-08-821-119-19
Sequence 19, Application US/08821119
Patent No. 5821104
GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Halkier, Torben
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58211040 No. 5821104th America, Inc.
STREET: 405-14
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                                                                     Gaps
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                                Score 39; DB 4; Length 1037;
Pred. No. 16;
2; Mismatches 2; Indels
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Pred. No. 82;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFFWARE: FRASLEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107.204-US
TELEPHONICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08821118
Patent No. 5989889
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                Query Match 69.6%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 75.0%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REAABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNET/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEC ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
                                                                                                                                    199 KEVVSNGLHYS 209
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                                                                                                  1 EEVVPXGMHYS 11
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US-09-134-001C-4794
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SEE: No. 59898890 No. 5989889disk of No. 5989889th America, Inc.: 405 Lexington Avenue
New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Watson, James D
APPLICANT: Watson, James G.
TITLE OF INVENTION: Polynuclectides and methods for their use.
TITLE OF INVENTION: by the polynuclectides and methods for their use.
TITLE OF INVENTION: by the polynuclectides and methods for their use.
FILE REFERENCE: 11000.105001
CURRENT APPLICATION NUMBER: 105/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 2;
Pred. No. 82;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastEED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-724-864-36
Sequence 36, Application US/09724864
Patent No. 6380362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: LAMDLITS, EILSS J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                          ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.9%;
Best Local Similarity 71.4%;
Matches 5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.7%;
75.0%;
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.7
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
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                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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Gaps
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                                                                                                                                                                                                                                                    Score 32; DB 2; Length 102;
Pred. No. 29;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TILE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOTER: IBM COMPATIBLE
COMPOTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; Score 32; DB 66.7%; Pred. No. 36; Live 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08879995A Patent No. 5985606 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                        57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acids
LENGIH: 102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.1
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                      Query Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
                                                                                                                                                                     internal
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                                                                                                    DESCRIPTION: protein POTHETICAL: no
                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                    24 EEVFPLAMNY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LIBRARY: GenBank
; CLONE: 163590
US-08-879-995A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                 TYPE: amino acid
STRANDEDNESS:
                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Por CITY: Palo Alto
                                                                                                                                                          FRACMENT TYPE: 1 ORIGINAL SOURCE: US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                MOLECULE TYPE:
                                                                                                                           HYPOTHETICAL:
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ZIP: 94304
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCUS
TITLE DE INVENTION: BPIDEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GFC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1988-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-01-14
SPIOR FILING DATE: 1997-08-14
SPIOR FILING DATE: 1997-08-14
SEQ ID NO 3950
LENGTH: 70
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APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: Receptor-I-Sasociated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
TITLE OF INVENTION: For Its Use
TOWNERS OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423 REFERENCE/DOCKET NUMBER: D5721C1P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALK: '.'O'.

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
                                                                                                                             Sequence 3950, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3950
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STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/08580988A Patent No. 5856161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: January CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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36 MPKGFHYS 43
    | |:|||
627 PGGLHYS 633
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                                                                                       RESULT 5
US-09-134-001C-3950
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US-08-580-988A-23
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NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-460-744-4; Sequence 4, Application US/08460744; Patent No. 6107541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-COMPUTED:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                         152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 152 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear .; MOLECULE TYPE: peptide US-08-460-694-4
                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMHY 10
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          CITY: Washington
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                                                                                                       MEDIUM TYPE:
                                                                 20005
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                          STATE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: V
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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                       APPLICANT: Hallman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: RASEC., Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 32; DB 66.7%; Pred. No. 36; Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATCRNEY/AGBNT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION INFORMATION:
TELEFRON: 415-845-0555
TELEFRX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
                                                                                                                                  Sequence 3, Application US/09215096
Patent No. 6008194
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                      1:111 | 1
28 EQVVPGGGH 36
  1 EEVVPXGMH 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linea; IMMEDIATE SOURCE: ; LIBRARY: GenBan; CLONE: 163590 US-09-215-096-3
                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                          94304
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                                                                                                             US-09-215-096-3
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                                                                                               RESULT 8
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APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI CYCLIN and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: US-JUN 1995
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: MCCONathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REGISTRATION NUMBER: 36,279
REGISTRATION NUMBER: 0609.4070002
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
FILLIGATION NUMBER: US/08/460,744
FILLIG DATE: 02-JUN-1995
CLASSIFICATION: 435
NAME: AGENT
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KEVIN G.
PEPTIDE INHIBITORS OF THE P33CDK2 AND P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN PAPILLOMAVIRUS E7 ONCOPROTEIN
                                                                                                                                            Gaps
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                                                                                            Score 32; DB 3; Length 152;
Pred. No. 44;
                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and Its CDNA
TURBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/07667711B Patent No. 6110700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08193977 Patent No. 5625031
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
IENGTH: 152 amino acids
TYPE: amino acid
                                                                                                 Query Match 57.1%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                 TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-460-744-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPXGMHY 10
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APPLICANT: WEBSTER, K
APPLICANT: COLEMAN, K
TITLE OF INVENTION: F
TITLE OF INVENTION: F
                                                                                                                                                                                                                       20 EEVFPLAMNY 29
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US-08-193-977-7
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                                                                                                                                                                                                                                                                                        RESULT 11
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Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 1; Length 173;
Pred. No. 51;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB.1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0016
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
                                                                         CITY: PALO ALTO
STATE: CALIFORNIA
COUTRY: UNITED STATES OF AMERICA
ZIV: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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60.0%;
                                      E: REED & ROBINS
635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 173 amino acids
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Best Local Similarity 60.0.
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MOLECULE TYPE: peptide

US-08-193-977-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMHY 10
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
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                                         ADDRESSEE:
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US-08-246-361A-21
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APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 2; Length 189;
Pred. No. 56;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
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MEDIUM TYPE: FLORPY disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/246,361A
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MX-1991
ATCONEY AGENT INFORMATION:
NAME: MALTHOW P. VINCENT
RECISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
                                NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERNECE/OCKET NUMBER: MIT-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-08-246-361A-21
; Sequence 21, Application US/08246361A
; Patent No. 5998582
                                                                                                                                                                                                                                                                                                                                                                             57.1%;
60.0%;
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-21
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TOPOLOGY: linear
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74 EEVFPLAMNY 83
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Best Local Similarity
Matches 6; Conserva
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Gaps
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APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESSONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 Stative & Leet
  57.1%; Score 32; DB 2; Length 189; 60.0%; Pred. No. 56; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%; Score 32; DB 3; Length 189; 60.0%; Pred. No. 56; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MALTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OFFICE STATES
SEQUENCE: CHARACTERISTICS:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application PC/TUS9305000 GENERAL INFORMATION: APPLICANT: MITOTIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       US-08-463-772-21
; Sequence 21, Application US/08463772
; Patent No. 6066501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 189 amino acids
Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
These 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-463-772-21
                                                                                          1 EEVVPXGMHY 10
                                                                                                                                    74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMHY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02109
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RESULT 18
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Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 5; Length 189;
Pred. No. 56;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Particia
RAGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/464,517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.1%;
60.0%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 189 amino acids
AMINO ACID
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Best Local Similarity 60.00
المالية والمالية والمالية
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MOLECULE TYPE: protein
PCT-US93-05000-21
                                                                                                                                                                                                                   Lexington
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMHY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 15 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JUST SOSTON STATE: MA
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                                                                                                                                                                                                                                                                                                                                       02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                     STATE:
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Sequence 22, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; Score 32; DB 2; Length 236; 60.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-WAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-WAY-1992
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATTHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
RELECOMMUNICATION INFORMATION:
TELEFAN: (617) 227-7400
TELEFAN: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: Amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAX-1991
ATTORNEY/AGENT INFORMATION:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60...
G. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-464-517-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMHY 10
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CITY: Boston
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RESULT 21
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Sequence 22, Application US/08463772
GENERAL INFORMATION:
APPLICART: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                  Score 32; DB 2; Length 236;
Pred. No. 72;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%; Score 32; DB 3; Length 236; 60.0%; Pred. No. 72; tive 1; Mismatches 3; Indels
                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: MII-004C
REFERENCE/DOCKET NUMBER: MII-004C
TELEPAX: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                              57.1%;
60.0%;
                                                                                           Ouery Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0°
Matches 6; Conservative
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                   1 EEVVPXGMHY 10
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20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-463-772-22
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                                                           US-08-246-361A-22
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PCT-US93-05000-22
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                                                                                                                                                                                                                                                       RESULT 19
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                                                         TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 32; DB 5; Length 236; 60.0%; Pred. No. 72; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
Sequence 22, Application PC/TUS9305000 GENERAL INFORMATION: APPLICANT: MITOTIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08464517 Patent No. 5869640
                                                                                                                                                                                                                                    ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 236 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0 Matches 6; Conservative
                                                                                                                                                                        CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 EEVFPLAMNY 29
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                      COUNTRY:
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0; Gaps

3; Indels

DB 3; Length 280;

Score 32; DB Pred. No. 87; 1; Mismatches

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57.1%;
60.0%;
                                                                                                                    Best Local Similarity 60.0
Matches 6; Conservative
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-772-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 EEVFPLAMNY 83
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75 EEVFPLAMNY 84
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PCT-US93-05000-4
                                                                                                                                                                                                                                                                                                       US-08-246-361A-4
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                                                                                                     Query Match
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Patent No. 6066501
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.1%; Score 32; DB 2; Length 280; 60.0%; Pred. No. 87; tive 1; Mismatches 3; Indels
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTATION NUMBER: MI-004C
FELECOMMUNICATION INFORMATION:
TELEFRONE: (617) 227-7400
TELEFRONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
RECISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: MII-004C TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400 TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 280 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-464-517-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'RY: USA 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-463-772-6
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THE OF INVENTION US/08246361A

Sequence A, Application US/08246361A

Sequence A, Application US/08246361A

Sequence A, Application US/08246361A

TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO CORRESPONDENCE: 50
CORRESPONDENCE: 50
CORRESPONDENCE ADDRESS:
CORR
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0
Sequence 4, Application PC/TUS9305000
GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millian Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 32; DB 5; Length 289; 60.0%; Pred. No. 90; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/O7/888,178
FILING DATE: 26 MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFENCE/DOCKET NUMBER: CSHL91-02A
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSHL91-02A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application PC/TUS9305000
GENERAL INFORMATION:
APPLICANT: MITOTIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-05000-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMHY 10
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74 EEVFPLAMNY 83
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Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                        02173
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PCT-US93-05000-6
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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2003, 13:46:50 ; Search time 15 Seconds (without alignments)
75.710 Million cell updates/sec
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75.710 Mi Title: US-09-909-164-11 Perfect score: 56 Sequence: 1 EEVVPXGMHYS 11

Sequence: 1 EEVVPXGMHYS 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database: Publi

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USOE_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USOE_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOZ_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USOZ_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description		9 Sequence 4919,	663			ß	sequence 5	-2 Sequence 2, Appli	Sequence 4,	Sequence 54,	Sequence 26,	-16 Sequence 16, Appl		Sequence 80,	S		1-40832 Sequence 40832, A	Sequence 119,	-171 Sequence 171, App
	· GI	US-10-270-333-126	US-09-738-626-4919	US-09-866-050A-663	US-10-027-806-4	US-10-034-623	US-10-027-801-4	US-09-778-927A-53	US-10-024-066-2	US-10-024-066-4	US-09-919-497-54	US-09-820-843A-26	US-09-252-088-16	US-09-252-088-15	US-10-047-542-80	US-09-870-759-52	US-09-948-080-1	US-09-864-761-40832	US-10-001-857-119	US-09-986-480-171
	DB		6	6	σ	Φ	6	10	6	φ	10	6	6	σ	σ	σ	10	10	σ	σ
	Query Match Length DB	567	622	747	3472	3472	3472	254	289	289	289	653	715	793	662	847	59	73	192	192
dР	Query	58.9	58.9	58.9	58.9	58.9	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	56.2	56.2	55.4	55.4	55.4	55.4
	Score	33	33	33	33	33	33	32	32	32	32	32	32	32	31.5	31.5	31	31	31	31
	Result No.		101	m	4	· C	9	7	- σο	6	10	11	12	13	14	15	16	17	18	19

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2260 22960 22960 23336 23337 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 2010 20	222222
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	000000000000000000000000000000000000000
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## ALIGNMENTS

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RESULT 1

US-10-270-333-126

US-10-270-333-126

Sequence 126, Application US/10270333

Sequence 126, Application US/2030092124A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,

TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS

FILE REFERENCE: CLOO733CON

CURRENT APPLICATION NUMBER: US/10/270,333

CURRENT FILING DATE: 2002-10-15
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                        58.9%; Score 33; DB 9; Length 567; 83.3%; Pred. No. 2.8e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.9%; Score 33; DB 9; Length 622; 50.0%; Pred. No. 3.1e+02; .ive 3; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: 60/168,677
PRIOR FILING DATE: 1999-12-03
PRIOR PRILING DATE: 1999-12-03
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 198
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
LENGTH: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4919, Application US/09738626; Publication No. US20020197605al
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: APPLICANT: ANDO, SEIKO
APPLICANT: APTEISH!, NAKIO
APPLICANT: TOCHIAL, KEIKO
APPLICANT: TOKOI, HARUHIKO
APPLICANT: TOKOI, HARUHIKO
APPLICANT: TOKOI, HARUHIKO
APPLICANT: TOKOI, HARUHIKO
APPLICANT: TOKOI, AKHHRO
APPLICANT: ASENGH, AKHRO
APPLICANT: ASENGH, AKHRO
APPLICANT: ASENGH, AKHRO
APPLICANT: ASENGH, AKHRO
APPLICANT: ABOSH, AKHRO
APPLICANT: ABOSH, AKHRO
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159163
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ TWARRE PALENTIN VEY: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4919
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                 ; ORGANISM: Drosophila
US-10-270-333-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 PSGMHY 407
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 5; Conserv
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Sequence 663, Application US/09866050A Publication No. US20030040471A1 GENERAL INFORMATION: APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew

US-09-866-050A-663

```
Sequence 4, Application US/10027806
Patent No. US20020160476A1
GENERAL INFORMATION.
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: UNCLEIC ACIDS AND PROFEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER PRICATION NUMBER: 09/408,020
NUMBER OF SEQ. ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10034623
Publication No. US20020198355A1
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
SCHIEDER:
CONTINE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 9; Length 747;
Pred. No. 3.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
               APPLICANT: MILEON, Names G.
APPLICANT: MILEON, Names G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c40
CURRENT PAPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SSFUARE: FastSEQ for Windows Version 4.0
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
                                                                                                                                                                                                                                                                                                                                                                                                         58.9%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 71.4 Matches 5; Conservative
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2294 EDVIPRGISFS 2304
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Onrust, Rene
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627 PGCLHYS 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                       US-09-866-050A-663
                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-027-806-4
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Length 254;

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sequence 53, Application US/09778927A

sequence 53, Application US/09778927A

sequence 53, Application US/09778927A

sequence 53, Application US/09778927A

sequence 53, Application US/08068342AI

sequence 53, Application US US/08/08

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Publication No. US20030054364A1
GENERAL INFORMATION:
APPLICANT: Swanson, Robert A.
APPLICANT: Schleger, Christa
APPLICANT: Schleger, Christa
APPLICANT: Schleger, Christa
APPLICANT: Schleger, Christa
APPLICANT: Christa
APPLICANT: Christa
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: ERRLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                Score 33; DB 9; Length 3472;
Pred. No. 2.1e+03;
4; Mismatches 2; Indels
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COTHER INFORMATION: Xaa = any amino acid, unknown, or other US-09-778-927A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 9; 1
Pred. No. 2.1e+03;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Cenarchaeum symbiosum US-10-027-801-4
                                                                                                                    ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.9%;
45.5%;
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Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 45.59
Matches 5; Conservative
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2294 EDVIPRGISFS 2304
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2294 EDVIPRGISFS 2304
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US-09-778-927A-53
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Patent No. US20020166134A1

GENERAL INFORMATION:

APPLICANT: Field, Lishore Babu S.

APPLICANT: Pasumarthi, Kishore Babu S.

TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

FILE REFERENCE: 7037-450

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/139,942

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1900-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WITH ENHANCED PROLIFERATIVE POTENTIAL,
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                                                     Gaps
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APPLICANT: Pasumarthi, Kishore Babu S.
TITLE OF INVENTION: CARDLOMYOCYTES WITH ENHANCED PROLIFERATIVE PO:
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT APPLICATION NUMBER: 60/139,942
PRIOR PILLING DATE: 1999-06-18
PRIOR FILLING DATE: 1999-06-18
PRIOR FILLING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 2.1e+02;
1; Mismatches 3; Indels
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Pred. No. 2.1e+02;
            Score 32; DB 10;
Pred. No. 1.8e+02;
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                                                     1; Mismatches
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Best Local Similarity 60.0%;
Matches 6; Conservative
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60.0%;
                57.1%;
60.0%;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 289
Query Match
Best Local Similarity 60.ue
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                               1 EEVVPXGMHY 10
                                                                                                                                    74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Mus musculus
US-10-024-066-2
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APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905, 0004, CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
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Sequence 15, Application US/09252088

PUBLICATION OF US20030031682A1

APPLICANT: BRODEUR, Bernard R.
APPLICANT: BTOUX, Climent

APPLICANT: BTOUX, MAILINE

APPLICANT: CHARLEBOIS, Isabelle

APPLICANT: HAMEL, Jose

TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS

FILE REFERENCE: 8331-9002

CURRENT FILING DATE: 1999-02-18

CURRENT FILING DATE: 1999-02-18

EARLIER APPLICATION NUMBER: US/60/075,425

EARLIER FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 32; DB 9; Length 793; 75.0%; Pred. No. 6.4e+02; tive 0; Mismatches 2; Indels
                                   APPLICANT: HAMEL, JOSE
APPLICANT: HAMEL, JOSE
APPLICANT: MATTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER PILING DATE: 1999-02-20
NUMBER OF SEQ ID NOS: 444
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Patent No. US20020168367A1
GENERAL INFORMATION:
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; ORGANISM: group B streptococcus
US-09-252-088-16
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                   APPLICANT: CHARLEBOIS, Isabelle
                                                                                                                                                                                                                                                                                                                                                                             57.1%;
ilarity 75.0%;
Conservative
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SEQ ID NO 16
LENGTH: 715
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Best Local Similarity
Matches 6; Conserval
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LENGTH: 793
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Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
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                                                                                                 Sequence 54, Application US/09919497
Patent No. US20020106652A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE PAPLICATION NUMBER: US/09/919,497
CURRENT APPLICATION NUMBER: US 60/221,735
PRIOR APPLICATION NUMBER: US 60/221,735
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 32; DB 10; Length 289; 60.0%; Pred. No. 2.1e+02; Live 1; Mismatches 3; Indels
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Pred. No. 5.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
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Publication No. US20030031682A1
GENERAL INFORMATION:
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SEQ ID NO 26
LENGTH: 653
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Best Local Similarity 75.0%;
Matches 6; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-54
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    74 EEVFPLAMNY
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                                                                                 US-09-919-497-54
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 54
LENGTH: 289
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Query Match 55.4%;
Best Local Similarity 45.5%;
Matches 5; Conservative
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38 EKHIPGGLEYS 48
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US-09-864-761-40832
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LENGTH: 73
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/870,759

CURRENT APPLICATION NUMBER: US 60/208,128

PRIOR FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 166

SOFTWARE: Patentin version 3.1

EBUGTH: 847
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Pred. No. 6.5e+02;
2; Mismatches 2; Indels
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APPLICANT: HALKIER, TORDEN
APPLICANT: BAUDITZ, PETER
APPLICANT: HANDEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-US
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US/08/963,851
PRIOR FILING DATE: 1997_11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 59
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Patent No. US20020102702A1
GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
          PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PAtentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 52, Application US/09870759 Patent No. US20020177551A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Enterococcus faecalis US-09-948-080-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       623 ENVIPDFPEDEGIHYS 638
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                                                                                                                                                                                                                                                                                                                1 EEVVP----XGMHYS 11
                                                                                                                                                                                                                                  Ouery Match 56.2%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-09-870-759-52
                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-047-542-80
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                                                                                                                   SEQ ID NO 80
LENGTH: 662
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                                                                                                                                                             TYPE: PRT
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APPLICANT: 29skind, Judith W.
APPLICANT: 29skind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramancto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
GURRENT FILING DATE: 2001-03-21
FRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 10; Length 26
Pred. No. 2.9e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                         APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John D.
APPLICANT: Yamamotto, Robert T.
APPLICANT: Yamamotto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TILLE OF INVENTION: DEPARTMENT OF ESSENCY
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT APPLICATION NUMBER: 06/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRASEED FOR WINDOWS Version 4.0
                                                                                                                                                                                            ; Sequence 13489, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION; APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13613, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.4%;
Best Local Similarity 60.0%;
Matches 6; Conservative
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari r
                                2 EVVPXGMHYS 11
                                                                             52 ENIPEGLNYS 61
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LENGTH: 260
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CURRENT APPLICATION NUMBER: US/10/001,857
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
RUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
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CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
CTHER INFORMATION: EST_HUMAN HIT: AW027739.1, EVALUE 7.00e-14
US-09-864-761-40832
                                                                                                                   Ouery Match 55.4%; Score 31; DB 10; Length 73; Best Local Similarity 71.4%; Pred. No. 72; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.4%; Score 31; DB 9; Length 192; 57.1%; Pred. No. 2.1e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%; Score 31; DB 9; Length 192; 50.0%; Pred. No. 2.1e+02; tive 3; Mismatches 2; Indels
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TITLE OF INVENTION: 143 Human Secreted Proteins
FILE REFERENCE: PS500P1
CURRENT APPLICATION NUMBER: US/09/986,480
CURRENT PILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: PCT/US00/12788
PRIOR PILING DATE: 2000-05-11
PRIOR PILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
SOFTWARE OF SEQ ID NOS: 456
SOFTWARE PALENTIN Ver. 2.0
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                       Sequence 119, Application US/10001857
Publication No. US20020183500A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 171, Application US/09986480 Publication No. US20030027999A1 GENERAL INFORMATION:
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Best Local Similarity 57.10
-208 4; Conservative
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; ORGANISM: Homo sapien
US-10-001-857-119
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US-09-986-480-171
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145 IIPKGMH 151
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Best Local Similarity
Matches 5; Conserv
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LENGTH: 192
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Gaps

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RESULT 23
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Pred. No. 3.4e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 10; Length 260;
Pred. No. 2.9e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Oblish, Kari L.
APPLICANT: Oblish, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tamanoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/25,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 13613
LENGTH: 260
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10697, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13613
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US-09-815-242-10697
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Similarity 40.0%;
4; Conservative
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Best Local Similarity 60.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | | |:||
188 EEKVGEGVHY 197
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Best Local Similarity
Matches 4; Conserv
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CON 1 ERWYKARHY 10

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RESULT 23 APPLICATION US/09782974C

165-09-794C-86

174TLG OF NUMBER: 09-714.49

174TLG OF NUMBER: 09
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Sequence 2, Application US/10270144

Fublication No. US20030049790A1

Fublication No. US20030049790A1

GENERAL INFORMATION:

APPLICANT: WIL MING-Hui et al

TITLE OF INVENTION:

FILLE REFERENCE: CLOO750CON

CURRENT APPLICATION NUBBER: US/10/270,144

FILLE REFERENCE: CLOO750CON

CURRENT APPLICATION NUBBER: US/10/270,144

FRICH APPLICATION NUBBER: US/205,196

FRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SED ID NO 2

LENGTH: 337

CORANISM: Human

US-10-270-144-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.4%; Score 31; DB 9; Length 337; Best Local Similarity 50.0%; Pred. No. 3.8e+02; Matches 5; Conservative 2; Mismatches 3; Indels
; PRIOR APPLICATION NUMBER: US 60/296,660
; PRIOR FILING DATE: 2001-06-07
; PRIOR PILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Version 3.1
; LENGTH: 337
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Job time: 15.0714 secs
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Best Local Similarity 50.0°
Matches 5; Conservative
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26 DENIPLKMHY 35
                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-775B-2
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OM protein - protein search, using sw model

June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds (without alignments) 94.297 Million céll updates/sec Run on:

US-09-909-164-11 56 1 EEVVPXGMHYS 11 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283224 seqs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	ftsH proteinase ac	rbamoyı-pro		٠,	٠,	hypothetical prote		DNA binding protei	GMP synthetase, su	hypothetical prote	T518.1 protein - A	diphthine synthase	hypothetical prote	3-dehydroquinate s	probable DNA ligas	cell division prot	hypothetical prote		hypothetical prote	ATP-dependent DNA	hypothetical prote	polyamine transpor	conserved hypothet	probable amino aci	amino acid antipor	finger protein (cl	cytochrome-c3 hydr	coenzyme F420-quin	hypothetical prote
ID	A72207	F89892	A4 24 5 2	AEZOOI	\$59046	838143	D82618	T02590	н69194	T24111	G86430	G69117	C75538	B75478	T35025	E69086	C83903	S58132	T28717	AF3286	S54619	E83607	G82253	G71542	н81697	S65811	HQDVLB	A69284	T08564
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Length	308		<b>∓</b> ∂	7	4	7.	-	2				7		Ë	ξ	ř	425	4	4	10	1	Ē	4	4	4	4	S	3	Ŋ
% Query Match	66.1	1.00	04.3	64.3	4	Þ	62.5	62.5	62.5	62.5	62.5	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	58.9	58.9	8	58.9	58.9		8	58.9	58.9
Score	37	37	9 0	36	36	36	32	35	35	35	35	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33
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2 A69663 2 C5061 2 C5061	76845 76845 768265 782235 782836 782633 73675 73675 73675 73675
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## ALIGNMENTS

RESULT 1

fish proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72207
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; FGarrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genom A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72207

A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 ARNN
A;Residues: 1-308 ARNN
A;Cross-references: GB:AE001819; GB:AE000512; NID:g4982396; PIDN:AAD36885.1; PID:g.
A;Experimental source: strain MSB8
C;Genetics:
C;Genetics:
C;Superfamily: erythrocyte band 7 integral membrane protein

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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2001
A;Status: preliminary
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A;Residues: 1-743 <VAN>
A;Cross-references: EMBL:228292; NID:9486536; PIDN:CAA82146.1; PID:9486537; MIPS:YKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: U43703; NID: 91244769; PIDN: AAB68221.1; PID: 91244776; MIPS: Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein YP1139c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: S6946
B;Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, Submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A;Reference number: S69046
A;Accession: S69046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae) C; Species: Saccharomyces cerevisiae C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
                                                                                                                                                                          A,Molecule type: DNA
A;Residues: 1-252 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB77929.1; PID:g17135383; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1563
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62.5%; Pred. No. 25;
iive 2; Mismatches 1; Indels
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R; van Vietr Reedijk, J.C.; Planta, R.J.
submitted to the Protein Sequence Database, March 1994
A; Reference number: §38130
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Query Match

Best Local Similarity 75.0%; Pred. No. 43;

Matches 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: SGD:UME1
A;Cross-references: SGD:S0006060; MIPS:YPL139c
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C;Keywords: transmembrane protein
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Matches 5; Conservative
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Matches 5; Conservative
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                                            8, 205-213, 2001
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A; Residues: 1-460 <HAL>
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                                                                                                                                                                                                                                                                                                                                               C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #text_change 22-Oct-2001
C;Accession: F9892
C; Shiba, T.; Hattori, M.; Ogasawara, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F98982
A;Actaus: Preliminary
A;Molecule type: DNA
A;Residues: 1-1057 < KUR>
A;Cross-references GB:BO00018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2001
C;Accession: AE2001
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W12452
V1 protein - tobacco yellow dwarf virus (strain Australia)
V2 pectes: tobacco yellow dwarf virus
C3 pectes: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C3Accession: A42452
R3Morris, Ba.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A7 Virology 187, 633-642, 1992
A7 Virology 187, 633-642, 1992
A7 Virology 187, 633-642, MUID:92188538; PMID:1546458
                                                                                                                                                                                                                                                                                                                              carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N31!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
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Pred. No. 39;
2; Mismatches 2; Indels
                                    66.1%; Score 37; DB 2; Length 308; 75.0%; Pred. No. 10;
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Pred. No. 5;
3; Mismatches
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60.08;
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60.0%;
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Matches 6; Conservative
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7 QVVPSGINYS 16
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Query Match
Best Local Similarity
6; Conserve
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41 VVPSGIHY 48
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Matches 6; Conserv
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A; Residues: 1-102 <MOR>
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R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A; Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-311 <WTH>
A; Cross-references: GB:AE000850; GB:AE000666; NID:g2621794; PIDN:AAB85215.1; PID:g2
A; Experimental source: strain Delta H
C; Genetics:
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewas ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816 820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K.
                                                                      GMP synthetase, subunit B. - Methanobacterium thermoautotrophicum (strain Delta H)
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                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T24111
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C;Spacies: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
                                                                                                  C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: H69194
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A;Molecule type: DNA
A;Residues: 1-425 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.5%; Score 35; DB 2; 50.0%; Pred. No. 37; tive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, October 1996 A; Reference number: 219842 A; Accession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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335 EQIVPGGLQY 344
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Best Local Similarity
'-hag 5; Conserve
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              A; Accession: H69194
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submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kirager, J.E.; Kuramae, E.E.; Laigi chado, M.A.; Madeira, A.M. B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Roiliques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Silva, A.C.; Salmieri, D.P. A; Authors: da Silva, A.C. R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.C. R.; Salvasak, M.; Tsuhako, M.H.; Vallada, H.; Van Sllvys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A; Reference number: A59328
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A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene responsi A;Reference number: 214671; MUID:95276459; PMID:7756828
A;Accession: T02590
                                                                                                                                                                                                                                                                                           C;Accession: D82618
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Itle: Hopenome Sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Modecule type: DNA
A;Rosiduss: 1-156 SSIN>
A;Cross-references: GB:AE004014; GB:AE003849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GN001
                                                                                                                                                                                               conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
C;Accession: T02590
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A;Experimental source: strain BY4; tissue-type leaf
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Pred. No. 19;
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Pred. No. 13;
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A;Molecule type: mRNA
A;Residues: 1-233 <OHM>
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60.0%;
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                                                       294 VVPCGLHY 301
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Best Local Similarity
5; Conserve
VVPXGMHY 10
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Matches 6; Conserv
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252 EAVAYGMHYA 261
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A; Status: preliminary
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                                                                                A; Gene: DR0271
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A; Gene: DR0777
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                                 C; Genetics:
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.Authors: Salzberg, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Verter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719; PMID:11130712
A.Status: preliminary
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-510 <STO>
A.C. Salzberge: DNA
A.C. 
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C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: 05-Dec-1997
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
K, Gui, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Reference number: A69000; MuiD:98037514; PMID:9371463
A;Reference number: Accession: G69117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C; Accession: C75538
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamatheyan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID:20036896; PMID:10567266
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A; Cross-references: GB:AE000940; GB:AE000666; NID:g2623011; PIDN:AAB86340.1; PID:g262301
A; Experimental source: strain Delta H
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A;Experimental source: strain R1
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60.0%;
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Best Local Similarity 60.0.
6; Conservative
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Best Local Similarity
5; Conservat
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A; Residues: 1-279 <WHI>
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3.dehydroquinate synthase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75478
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R. W.; Shen, M.; Vannathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-350 <WHI>
A;Cross-references: GB:AE001932; GB:AE000513; NID:g6458481; PIDN:AAF10353.1; PID:g64
A;Experimental source: strain R1
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A; Reference number: 221565
A; Reference number: 221565
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-355 CSEE>
A; Cross-references: EMBL:AL079355; PIDN:CAB45581.1; GSPDB:GN00070; SCOEDB:SC4C6.17c
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C;Superfamily: 3-dehydroquinate synthase; 3-dehydroquinate synthase homology
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
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                                     protein DR0271
                                                                                      Length 279;
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A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical
                                                                                   Score 34; DB 2;
Pred. No. 38;
0; Mismatches
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Pred. No. 48;
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                                                                                Query Match 60.7%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Matches 6; Conservative
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A;Cross-references: EMBL:Z50154; NID:g1052827; PID:g1052828
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Matches 5; Conservative
                                                                                                4; Conservative
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                                                Query Match
Best Local Similarity
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A; Gene: CESP:F10D2.3
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Matches
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
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submitted to the EMBL Data Library, July 1995
A;Description: S1s1p, an endoplasmic reticulum component, is involved in the protein tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05746.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                 A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Accession: E69086
                                                                                                                                                                                                                                                                                                               A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule type: DNA A.Molecule type: DNA A.Residues: 1-360 CMTHA A.Residues: 1-360 CMTHA A.Residues: 1-360 CMTHA A.R.COGAS-references: GB:AE000923; GB:AE000666; NID:g2622766; PIDN:AAB86115.1; PID:g262277 A.Experimental source: strain Delta H
                                                                                                                                                R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
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                                                            cell division protein - Methanobacterium thermoautotrophicum (strain Delta H)
                                                                                     C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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C;Species: Yarrowia lipolytica, Candida lipolytica
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Sep-1997
C;Accession: S58132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein BH2027 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: C83903
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Pred. No. 59;
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Pred. No.
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45.5%;
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Best Local Similarity 45.
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-426 <BOI>
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A; Molecule type: DNA
A; Residues: 1-425 <STO>
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                                                                                                                                   C; Accession: E69086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: MTH1642
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R;Delivecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivar, Mazur, W.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; I.; Lattle. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella mel A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-dependent DNA helicase BMEI0275 [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-495 <GRA>
A;Cross-references: EMED:AF022972; PIDN:AAC48234.1; GSPDB:GN00023; CESP:F10D2.3
A;Experimental source: strain Bristol N2; clone F10D2
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A;Residues: 1-1028 <KWR>
A;Cross-references: GB:AbD008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
A;Experimental source: strain 16M
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                               hypothetical protein F10D2.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28717
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Length 426;
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                                                                  Indels
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A;Introns: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rigraves, T.; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, September 1997 A; Description: The sequence of C. elegans cosmid F10D2. A; Reference number: 220515
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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50.0%; Pred. No. 70;
tive 2; Mismatches
60.7%; Score 34; DB 2;
44.4%; Pred. No. 59; .
Live 4; Mismatches
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probable amino acid transporter - Chlamydia trachomatis (serotype D, strain UW3/Cx) (Species: Chlamydia trachomatis (Species: Chlamydia trachomatis (Species: Chlamydia trachomatis (Species: Chlamydia trachomatis (Species: Or 1542 (Species: Chlampia trachomatis (Species: Or 1542 (Species: Or 1542 (Species: Or 1544) (
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A;Cross-references: GB:AE001295; GB:AE001273; NID:g3328617; PIDN:AAC67808.1; PID:g33
A;Experimental source: serotype D, strain UW-3/Cx
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000
C;Accession: H81697
C;Accession: H81697
C; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbo Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39
A;Tetle: Gunner: A81500; MUID:20150255; PMID:10684935
                                               1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82253
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-441 <HEI>A;Residues: 1-441 <HEI>A;CESSTEFERENCES: GB:AE004182; GB:AE003852; NID:g9655461; PIDN:AAF94166.1; GSPDB:CC;Genetics:
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A;Experimental source: strain N1gg (MOPn)
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C;Superfamily: conserved integral membrane protein HP0758
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Pred. No. 98;
2; Mismatches
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C;Superfamily: L-lysine transport protein
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C;Superfamily: L-lysine transport protein
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 62.55
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A; Residues: 1-466 <TET>
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hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
C, Species: Saccharomyces cerevisiae
C, Accession: S54619; S66879
R, Accession: S54619; S66879
R, Accession: S54619; S66879
R, Reference number: S54617
R, Reference number: S54617
R, Reference number: S54617
R, Residues: 1-156 CDEH>
A, Rocession: S54619
A, Rolecule type: DNA
A, Residues: 1-156 CDEH>
R, Accession: S68877
R, Accession: S68878

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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82253
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H
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A;Reference number: A82950; MUID:20437337; PMID:10984043
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C;Superfamily: Escherichia coli spermidine/putrescine-binding protein
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Pred. No. 32;
1; Mismatches 2; Indels
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44.4%; Pred. No. 81;
tive 3; Mismatches 2; Indels
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C; Superfamily: hypothetical protein YOR013w
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66.78;
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Matches 4; Conservative
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A:Molecule type: DNA
A:Residues: 1-367 <STO>
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                                                    0; Gaps
Query Match 58.9%; Score 33; DB 2; Length 466; Best Local Similarity 62.5%; Pred. No. 1e+02; Matches 5; Conservative 2; Mismatches 1; Indels
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4 VPXGMHYS 11 :| ||:|| 453 IPFGMYYS 460 QQ ΩŊ

Search completed: June 10, 2003, 13:49:14 Job time: 12.2143 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 10, 2003, 13:25:04 ; Search time 4.5 Seconds (without alignments) 101.387 Million cell updates/sec Run on:

US-09-909-164-11 56 1 EEVVPXGMHYS 11 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

					SUMMARIES		
Result		% Ouerv					
ON .	Score	Match	Length	DB	£1	Description	
1	38	67.9	1058	Н	CARB_FUSNN		
7	37	66.1	1057	Н	CARB_STAAM		
e	37	66.1	1057	Н	CARB_STAAW		
4	36	64.3	102	П	Y11K_TYDVA		
ъ	36	64.3	460	Н	UME1_YEAST	Q03010 saccharomyc	
9	36		743	Н	YK47_YEAST	_	
7	35	62.5	227	-	IDI1_MESAU	035586 mesocricetu	
80	35	62.5	308	H	GAAB_METTH	O26806 methanobact	
6	34		426	<del>, -1</del>	SLS1_YARLI		
10	33		513	Н	PHSL_DESBA		
11	33		627	Н	MUTL_BACSU		
12	33		1188	Н	KPBA_CAEEL	-	
13	33		1396	Н	VLTF_BPT5	P13390 bacteriopha	
14	32	57.1	126	_	TKNK_BOVIN	P08858 bos taurus	
15	32		267		RR2_CHLVU	_	
16	32		288	-	CGD2_RAT		
17	32		289	-	CGD2_HUMAN		
18	32		289	Н	CGD2_MOUSE	_	
19	32	57.1	291	Н	CGD1_BRARE		
20	32	57.1	291	-	CGD1_XENLA	xenopus	
21	32	57.1	291	-	CGD2_CHICK		
22	32	57.1	291	Н	CGD2_XENLA	xenopu	
23	32	57.1	292	Н	CGD1_CHICK	$\neg$	
24	32	57.1	292	Н	CGD3_HUMAN	homo	
25	32		295		CGD1_HUMAN	P24385 homo sapien	
26	32	57.1	295	1	CGD1_MOUSE	mus 1	
27	32	•	295	٦	CGD1_RAT	P39948 rattus norv	
28	32	•	341	Н	HYPE_AZOVI		
29	32	57.1	353	Н	T2BA_BACAR		
30	32	57.1	759	Н	SCT1_YEAST		
31	32	57.1	877	-	SULH_SCHPO	_	
32	32	57.1	1401	-	- 1	vibri	
33	32	57.1	2717	Н	ZEP1_HUMAN	P15822 homo sapien	

P20273 homo sapien P17280 chimpanzee P97885 rattus norv 058349 methanococc P10941 cryphonectr 028354 archaeoglob P52210 ovis atles P44640 haemophilus 07535 homo sapien P40739 bacillus su P27989 moorella th 049230 brassica ol P49333 arabidopsis P23622 neurospora P49452 mus musculu 009541 caenorhabdi 062190 mus musculu P22064 homo sapien 007436 drosophila 004351 clostridium 01476 homo sapien 000918 rattus norv 0929a8 chlamydia t 096528 arabidopsis 036834 trichophyto 09uhf0 homo sapien P22917 bacteriopha P49855 bacillus su P23988 salmonella 095293 drosophila 024536 citrus tris 09618 rattus rats	
CD22_HUMAN REV_SIVCZ S205_RAT Y939_METJA XHA1_CRYPA XHA1_CRYPA XHA1_CRYPA XHA1_CRYPA XHA1_CRYPA RU3_BACFU ALFB_SHEEP Y325_HAEIN PTBA, BACFU DCMB_MOOTH ETR1_ARATH CY14_NEUCR CENC_MOUSE LTBS_HUMAN KOR_OUSE LTBS_HUMAN LTBS_HUMAN LTBS_HUMAN LTBS_HUMAN LTBS_HUMAN LTBS_HUMAN LTBS_HUMAN LTBS_HUMAN LTBS_HUMAN TRIRU TRIL_CHLTR CAT1_ARATH NU4M_TRIRU	SCOA_HELPY YA52_HAEIN LDHC_HUMAN YVAA_BACSU PIT1_CHICK PIT1_MELGA DHH_HUMAN
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# ALIGNMENTS

The State of the Caracteristics of the oral bacterium Fusobacterium RT Genome sequence and analysis of the oral bacterium fusobacterium fulleature sequence and analysis of the oral bacterium fulleature.

The state of the control of the control of the oral bacterium fusobacterium fusobacterium fulleatum strain ATC 25586.";

The control of the oral bacterium fusobacterium fusobacterium fulleatum strain ATC 25586.";

The control of the oral bacterium fusobacterium fulleatum strain ATC 25586.";

The control of the oral bacterium fulleatum fulle 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422. PRT; 1058 AA. Fusobacterium nucleatum (subsp. nucleatum). Bacteria; Fusobacteria; Fusobacterium. STANDARD; NCBI_TaxID=76856; CARB_FUSNN Q8RG86; 

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RESULT 3
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
phosphate + L-glutamate + carbamoyl phosphate.
COFACTOR: Binds three manganese ions (By similarity).
PATHWAY: Arginine biosynthesis.
PATHWAY: Pyrimidine biosynthesis, first step.
SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                  OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-CARB OR PAYALO3 OR SAN1046.
Staphylococcus aureus (strain MuSO / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria: Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                             Pfam; PF02142; mus, ...
PRINTS; PR00008; CPSASE_1; 2.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Pyrimidine broteome.

ATP-binding; Manganese; Complete proteome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
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                                                                                    similarity)
SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 10;
                                                                                                                                                                                                                  EMBL; AE010554; AAL94625.1; ALT_INIT.
InterPro; IPR005483; CPase_L.
InterPro; IPR005480; CPase_L.D2.
InterPro; IPR005480; CPase_L.D3.
InterPro; IPR005481; CPase_L.D3.
InterPro; IPR004362; MGS_like.
Pfam; PF00786; CPSase_L.Chain; 2.
Pfam; PF00786; CPSase_L.D3; 1.
Pfam; PF007878; CPSase_L.D3; 1.
Pfam; PF007878; CPSase_L.D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.9%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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190 EIVPNGLNYS 199
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SEQUENCE FROM N.A.
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Q99UR5;
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STRAIN-Mu50 / ATCC 700699, and N315;
MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Ranehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                            -I- PATHWAY: Arginine blosynthesis.
-I- PATHWAY: Pyrimidine blosynthesis; first step.
-I- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                          Lancet 357:1225-1240(2001).
-1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.
-1- COFACTOR: Binds three manganese ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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DOMAIN 1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 402 546 OLIGOMERIZATION DOMAIN.

DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

DOMAIN 930 1057 ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR00548; CPase_L.
InterPro; IPR00549; CPase_L.D2.
InterPro; IPR005409; CPase_L.D3.
InterPro; IPR005401; CPase_L.D3.
InterPro; IPR004362; MGS_Like.
Pfan; PF00789; CPSase_L.D2; 2.
Pfan; PF02786; CPSase_L.D2; 2.
Pfan; PF02787; CPSase_L.D3; 1.
Pfan; PF02787; CPSase_L.D3; 1.
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REPEAT
NP_BIND
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                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                          MEDLINE=22040717; PubMed=12044378; MEDLINE=22040717; PubMed=12044378; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Baba T., Tuwam N., Asano K., Naimi T., Kuroda H., Cui L., Yamanoto K., Hiramateu K.; Rimanoto K., Hiramateu K.; Renome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00866; CPSASE 1; 2.
PROSITE: PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                         Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLOSTERIC DOMAIN.
             PRT; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117185 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP004825; BAB94951.1; -.
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             STANDARD;
                                                                                                           CARB OR PYRAB OR MW1086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 EIVSNGLHYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Manganese.
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1057
546
1057
210
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                                                                                                                                                     NCBI_TaxID=196620;
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    acquired MRSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9:
             CARB_STAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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METAL
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CARB_STAAW
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           Db
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102 AA.

STANDARD;

Y11K_TYDVA P31619;

A ID

Y11K_TYDVA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-S288C / AB972;
STRAIN-S288C / AB972;
STRAIN-S288C / AB972;
BUSSEY H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Araujo R., Aparicio A., Burchine B., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis R.W., Dietrich F.S., Dellus H., DiPaolo T., Dubois E., Duesterhoeft A., Dietrich F.S., Dellus H., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebuling U., Heumann K., Hilbert H., Hillier L., Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                     MEDILINE-92188538; PubMed=1546458; MATIS B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses vinfecting monocotyledonous plants."; virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.3%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 2.3; i.ve 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002621; Gemini_mov.
Pfam; PF01708; Gemini_mov; 1.
Hypothetical protein.
SEQUENCE 102 Aa: 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                              Tobacco yellow dwarf virus (strain Australia) (TYDV).
                                                                                                                   ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMEI_YEAST STANDARD; PRT; 460 AA. 003010; P87330; Created) 10.NOV-1997 (Rel. 35, Last sequence update) 115-JUN-2002 (Rel. 41, Last annotation update) Meiosis negative regulator UMEI.
  Created)
Last sequence update)
Last annotation update)
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-JUT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 OVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A42452; A42452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A364A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                       Viruses;
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                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseétsb-sib.ch).
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Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Schramm S., Schrams S., Schrams S., Schrams S., Schrams S., Schroeder M., Sdiou A.M., Tettelin H., Urestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             van Vliet Reedijk J.C., Planta R.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                           -1- FUNCTION: TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION AND SILENCING. WEGATURE REGULATOR OF MEIOSIS.
-1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
-1- SIMILARITY: STRONG, TO YEAST WIMI AND WIM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCPI-METI intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U.3.03; L. BMBL; U.43703; L. BMBL; U43703; L. BMBL; U43703; L. BMSCRAC; T040309; L. DR SGD; S0006060; UMBL. DR InterPro; IPR001680; WD40. DR SMART; SM00320; WD40; 3. DR SMART; SM00320; WD40; 3. DR PROSITE; PS50081; WD_REPEATS_1; FALSE_NEG. DR PROSITE; PS50294; WD_REPEATS_2; REGION; FALSE_NEG. DR Transcription requlation; Meiosis; Repeat; WD repeat. Transcription requiation; Meiosis; Repeat; WD repeat. 233 equiation; Mio. 3. MD 1. 236 4148776049 CRC64; MD 3. MD 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 460;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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62.58;
                                                                                                                                                                        Nature 387:103-105(1997)
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85 IVPLGLHY 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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P36148;
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Matches
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    RAPARA RA
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-GUN-2002 (Rel. 41, Last annotation update)
15-GUN-2002 (Rel. 41, Last annotation update)
15-GUN-2003 (Rel. 41, Last annotation update)
15-GUN-2004 (Rel. 41, Last annotation update)
15-GUN-2004 (Rel. 41, Last annotation update)
16-GUN-2004 (Rel. 41, Last annotation update)
17-GUN-2004 (Rel. 39, Last annotation update)
18-GUN-2004 (Rel. 39, Last annotation update)
19-GUN-2004 (Rel. 39, Last annotation u
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MEDLINE-97373600; PubMed-9228075;
Paton V.G., Shackelford J.E., Krisans S.K.;
"Cloning and subcellular localization of hamster and rat isopentenyl diphosphate dimethylallyl diphosphate isomerase. A PTS1 motif targets the enzyme to percoxisones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 272:18945-18950(1997).
-!- FUNCTION: CATALYZES THE 1.3-ALIXLIC REARRANGEMENT OF THE HOMOALLYLIC SUBSTRATE ISOPENTENTE (IPP) TO ITS HIGHLY ELECTROPHILIC ALLYLIC ISOMEN, DIMETHYLALLYL DIPHOSPHATE (DWAPP).
-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
-!- PATHWAY: ISOPRENOID BIOSYNTHETIC PATHWAY WHOSE END PRODUCTS
INCLUDE DOLICHOLS, VITAMINS A, D, E, AND K, STEROID HORMONES,
CAROTROIDS BILE ACIDS AND CHOLESTEROL.
-!- SUBCELLULAR LOCATION: Peroxisomal.
-!- SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE I FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 743; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00293; NUDIX; 1. Probom; PD004109; IPP_isomerase; 1. Isomerase; Isoprene biosynthesis; Cholesterol biosynthesis; Sterol biosynthesis; Peroxisome; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
84B9946E56B82F15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                           PIR; S38143; S38143.
SGD; S0001775; YKR067W.
InterPro; IPR002123; Acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF003836; AAC53283.1; -.
InterPro; IPR002667; IPP_isomerase.
InterPro; IPR000086; NUDIX_hydrolase.
                                                                                                                                                                                                                                                                                                                                                                   Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            69 85 PO
502 524 PO
539 555 PO
743 AA; 83644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.3%;
75.0%;
                                                                                                                                                  EMBL; Z28292; CAA82146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 75.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
TRANSMEM 31 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 VVPCGLHY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDI1_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                      ö
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: GMP biosynthesis.
-!- SUBUNIT: HETERODIMER COMPOSED OF A GLUTAMINE AMIDOTRANSFERASE SUBUNIT (A) AND A GMP SYNTHASE SUBUNIT (B) (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE GMP SYNTHASE FAMILY.
                                                                                                                                                                                                           GMP synthase [glutamine-hydrolyzing] subunit'B (EC 6.3.5.2) (GMP synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                     .
0
                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00884; quaA_Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 1; Length 308; Pred. No. 12;
                                                 Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMP-BINDING (BY SIMILARITY)
86 BY SIMILARITY.
1148 BY SIMILARITY.
227 MCROBODY TARGETING SIGNAL.
26317 MW; F500A6586385E803 CRC64;
                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; F2DCF6ED202CAEC1 CRC64;
                                                  DB 1;
                                                                                                                                                                               (6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                  Score 35; DB 1
Pred. No. 8.5;
0; Mismatches
                                                                                                                                                             308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000850; AAB85215.1; ALT_INIT.
                                                                                                                                                                                                                                            Methanobacterium thermoautotrophicum.
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                      STRAIN-Delta H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001674; GMP_synt_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.5%;
63.6%;
                                                  62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00958; GMP_synt_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                     Conservative
                                                                                                                                                             STANDARD;
                                                                                                            121 EEVDPNEMHY 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                         1 EEVVPXGMHY 10
                                         Query Match
Best Local Similarity
"-haq 7; Conserve
 86
148
225
227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P04079; 1GPM
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
                                                                                                                                                                                                                                GUAAB OR MTH710.
                                                                                                                                                             GAAB_METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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 ACT_SITE
ACT_SITE
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                    GAAB_METTH
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                                                                                                                                          RESULT 8
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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (EC 1.18.99.1) (NiFeSe hydrogenlyase large chain).
Desulfovibrio boculatus (Desulfomicrobium baculatus).
Bacteria; Proteobacteria; delta subdivision; Desulfomicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACT DIRECTLY WITH TRANSLOCATING POLYPERTIDES TO FACILITATE THEIR TRANSFER AND/OR HELP THEIR FOLDING IN THE ER. IT IS NOT REQUIRED FOR VIABILITY BUT IS ESSENTIAL FOR OPTIMAL GROWTH AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREVENT SECRETION FROM ER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.7%; Score 34; DB 1; Length 426; 44.4%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OACD7EF17540B8E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513 AA.
                                                                                                                                 426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLS1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=88058744; PubMed=3316183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z50154; CAA90516.1; -.
InterPro; IPR000886; ER_target.
PROSITE; PS00014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 AA; 47201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endoplasmic reticulum; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEVATED TEMPERATURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
|||| |:| |
EEVVESGLHES 226
                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                            SLS1 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|:| |:|
52 DQVIPAGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHSL_DESBA
                                                                                                                                 SLS1_YARLI
099158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                    216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHSL_DESBA
                                                                                                          SLS1_YARLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Periplasmic.
-1- MISCELLANEOUS: PERHAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS A TRANSPORT VEHICLE FOR BOTH SUBUNITS.
-1- SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE
                                                                                                                                                                                                                   "The crystal structure of a reduced [NiFeSe] hydrogenase provides an image of the activated catalytic center.";
Structure 7:557-566(1999).
-I- CATALYTIC ACTIVITY: 2 reduced ferredoxin + 2 H(+) = 2 oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Menon N.K., Peck H.D. Jr., le Gall J., Przybyla A.E.; "Cloning and sequencing of the genes encoding the large and small subunits of the periplasmic (NIFeSe) hydrogenase of Desulfovibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001501; N1_hdL.
Pfam; PF00374; NiFeSe_Hases; 1.
PR051TE; PS00507; NI_HGENASE_L_1; 1.
PR0SITE; PS00508; NI_HGENASE_L_2; 1.
Oxidoreductase; Periplasmic; Nickel; Selenium; Selenocysteine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                         Garcin E., Vernede X., Hatchikian E.C., Volbeda A., Frey M.,
Fontecilla-Camps J.C.;
                                                                                                                                                                                                                                                                                                 -1- COFACTOR: ONE NICKEL ION, TWO 4FE-4S CLUSTERS AND ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 1; Length 513;
                                                                                                                                                                                                                                                                                                                                SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                             non N.K., Pect H.D. Jr., le Gall J., Przybyla A.E.,
Bacteriol. 170:4429-4429(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC8285A6F80576FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRON 2.
NICKEL.
IRON 1 AND NICKEL.
IRON 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON 1 AND NICKEL
IRON 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 50;
1; Mismatches
                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
MEDLINE-99306038; PubMed-10378275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NICKEL.
                                                             Bacteriol. 169:5401-5407(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56683 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, A33101; HQDVLD.
PIR, A33101; HQDVLD.
PEANDIO; IPR001501; Ni_hdL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M18271; AAA23375.2; -. PIR; A33101; HQDVLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                 ferredoxin + H(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 PGGLHYS 303
                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PXGMHYS 11
                                                                                                                                                                                                                                                                                                                  SELENOCYSTEINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3D-structure,
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTL_BACSU
P49850;
                                                  paculatus
                                                                                                                Menon N.K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SE_CYS
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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METAL
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MUTL_BACSU
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(Rel. 34, Created) (Rel. 34, Last sequence update) (Rel. 41, Last annotation update)

01-0CT-1996 01-0CT-1996

DI DI

15-JUN-2002

DNA mismatch repair protein mutL.

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A MUDIALE-TOUGHAGUAS; PURDMEGG-21043//;
A MIDIALE-TOUGHAGUAS; PURDMEGG-21043//;
A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Dertero M.G., Bessieres P., Bolotin A., Borchert S.,
Bourise R., Boursier L., Brans A., Braun M., Brigaell S.C., Bron S.,
Bourilet S., Bruschl C.V., Caldwell B., Capuano V., Carter N.M.,
A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Ghim S.Y., Glaser P., Goffeau A., Galiszia A., Galiszon D.,
A Titz C., Fujita M., Fujita Y., Fuma S., Galizzia A., Galieron N.,
A Ghiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Medina N., Mellado P.P., Muzuno M., Moestl D., Noback M.,
A Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Presscan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
A Bettor M., Rivolta C., Rocha E., Rapoport G., Rey M., Reynolds S.,
A Bettor M., Ravolta C., Rocha E., Rapoport G., Rey M., Sadaie Y.,
Schleich A., Tanakoshi H., Takamashi H., Takemaru K.,
A Takeuchi M., Tamakoshi B., Takadashi H., Takamaru K.,
A Taseuchi M., Tamakoshi B., Takadashi H., Pakemaru K.,
A Taseuchi W., Tamakoshi R., Wadler F., Wadler F., Wadler F.,
A Tosator V., Warit R. Wadler F., Wadler F.,
A Tosator R.,
A Tosator R.,
A Tosator R.,
A Taskan R.,
A Waller R.,
A Walle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS PROTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN DNA. IT IS REQUIRED FOR DAM-DEPENDENT METHYL-DIRECTED DNA MISMATCH REPAIR. MAY ACT AS A "MOLECULAR MATCHAKER", A PROTEIN THAT PROMOTES THE FORMATION OF A STABLE COMPLEX BETWEEN TWO OR MORE DNA-BINDING PROTEINS IN AN ATP-DEPENDENT MANNER WITHOUT ITSELF BEING PART OF A FINAL EPFECTOR COMPLEX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Zumstein E., Yoshidaw H.F., Zumstein E., Yoshidaw H., Danchin A.; The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                          Ginetti F., Perego M., Albertini A.M., Galizzi A.;
"Bacillus subtilis mutS mutL operon: identification, nucleotide
                                                      Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P23367; IBKN.
Subtlist; BG11402; mutt.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR004099; DNA_mis_repair.
InterPro; IPR00459; HIS_KIM_sig.
Pfam; PF01119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                              MEDLINE-96349107; PubMed-8760914;
                                                                                                                                                                                                                                                                              sequence and mutagenesis."; Microbiology 142:2021-2029(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00585; mutl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U27343; AAB19236.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                            Bacillus subtilis.
                                                                                                                                       SEQUENCE FROM N.A.
                                                                          NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168;
                                                         Bacteria;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callagham M.,
Parsons J., Percy C., Rifken L., Roppra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable phosphorylase B kinase alpha regulatory chain (Phosphorylase
                                                                          Gaps
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Glycogen metabolism; Calmodulin-binding.
SEQUENCE 1188 AA; 135558 MW; DE9BB875F3603863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 1; Length 1188;
Pred. No. 1.2e+02;
1; Mismatches 4; Indels
                                                Length 627;
                                                                          Indels
             DNA repair; Complete proteome.
SEQUENCE 627 AA; 70431 MW; 068A0509CC265343 CRC64;
                                                58.9%; Score 33; DB 1; 54.5%; Pred. No. 61;
                                                              Pred. No. 61;
1; Mismatches
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.9%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L15188; AAA27954.2; -
                                                             ilarity 54.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep; C14B9.8; CE26870.
                                                                                                                    488 EMIVPLTFHYS 498
                                                                                                                                                                                            STANDARD;
                                                                                                    1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                        kinase alpha subunit)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAINS FAMILY.
                                                              Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wohldman P.;
                                                                                                                                                                                            KPBA_CAEEL
P34335;
                                                   Query Match
                                                                                                                                                                                                                                                                                      C14B9.8.
                                                                                                                                                                                 KPBA_CAEEL
                                                                  Best Loc
Matches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                        Bacteriophage T5.
Viruses; dSDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
NCBI_TaxID=10726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-1- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Kaliman A.V., Kryukov V.M., Bayev A.A.;
"The nucleotide sequence of bacteriophage T5 DNA at the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The nucleotide sequence of the bacteriophage T5 ltf gene."; FEBS Lett. 366:46-48(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.9%; Score 33; DB 1; Length 1396; 50.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                986 986 V -> A (IN REF. 2).
1396 AA; 147989 MW; 18CD2192F65FFFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
                                                                                                                                                                             VLTF_BPT5 STANDARD; PRT; 1396 AA. P13390; O48502; Clarated) Clara-1990 (Rel. 13, Created) Start 1996 (Rel. 33, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) L-shaped tail fiber protein (LTF protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95309401; PubMed=7789514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ001191; CAA04591.1; -. PIR; S01982; S01982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X69460; CAA49220.1; -.
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datches 5; Conservative
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                                 1 EEVVPXGMHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kryukov V.M.;
"The nucleotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAC3 OR NKNB
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P08858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.
                                                                                           MEDLINE-86313713; PubMed=3462746; Kotani H., Hoshimaru M., Nawa H., Nakanishi S.; Kotani H., Hoshimaru M., Nawa H., Nakanishi S.; Structure and gene organization of bovine neuromedin K precursor."; Proc. Natl. Acad. Sci. U.S.A. 83:7074-7078(1986).

-I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION (G-96 PROVIDE AMIDE GROUP).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%; Score 32; DB 1; Length 126; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=IAM C-27 / Tamiya;
MEDLINE=97303241; PubMed=9159184;
Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446EF433498EC059 CRC64;
                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Chloroplast 30S ribosomal protein S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEUROKININ B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; M14347; AAA30723.1; JOINED.
BERL; M14488; AAA30723.1; JOINED.
EMBL; M14349; AAA30723.1; JOINED.
EMBL; M14350; AAA30723.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002040; Tachykinin.
ProDom; PD020370; Neurokinin; I.
PROSITE; PS00267; TACHYKININ; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003635; Neurokinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M14351; AAA30723.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                           Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1:111 | 1
28 EQVVPGGGH 36
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                                                                                 SEQUENCE FROM N.A.
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                       NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RR2_CHLVU
P56351;
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SEQUENCE
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There are no restrictions on it
Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T., Inamura A., Yoshinaga K., Sugiura M.; Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: the existence of genes possibly involved in chloroplast division."; Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
-!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hosokawa Y., Onga T., Nakashima K.; "Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S transition by prolactin in rat Nb2 cells."; Gene 147:249-252(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93275661; PubMed=8502486;
Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
Francke U., Jolicoeur P.;
"The Vin-1 gene, identified by provirus insertional mutagenesis, is
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01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
GL/S.specific cyclin D2 (Vin-1 proto-oncogene)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO1011; rpsB bact; 1.
PROSITE; PS00962; RIBOSOWAL_S2_1; FALSE_NEG.
PROSITE; PS00963; RIBOSOWAL_S2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 40;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                              EMBL; AB001684; BAA57862.1; -.
InterPro; IPR001865; Ribosomal_S2.
Pfam; PF00318; Ribosomal_S2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein; Chloroplast.
SEQUENCE 267 AA; 30699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00395; RIBOSOMALS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%;
40.0%;
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Best Local Similarity 40.v.
4; Conservative
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CGD2_RAT
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                                                                                                                                                                          EMBL; D16308; BAA03815.1; ...
InterPro; IPR004365; Cyclin.
InterPro; IPR004365; Cyclin.
InterPro; IPR004365; Cyclin.
Pfam; PF00134; cyclin_C; 1.
SWART; SW00385; CYCLIN; 1.
PROSTE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene. CONFLICT 68 68 1 68 E -> G (IN REF. 2).
CONFLICT 104 104 C -> V (IN REF. 2).
GONFLICT 232 232 T -> A (IN REF. 2).
GONFLICT 232 232 T -> A (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiong Y., Menninger J., Beach D., Ward D.C.; Molecular cloning and chromosomal mapping of CCND genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=92347850; PubMed=1386335;
Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
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Pred. No. 44;
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                                                                                                                                                             EMBL; L09752; AAA41010.1; -.
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hes 6; Conservative
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Matches
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                                                                    -:- SUBUNIT: INTEREACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-:- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
-i - FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
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01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Interpro; IPR004367; Cyclin_Cterm.
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MEDLINE=92196134; PubMed=1372445;
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EMBL; M88080; AAA51928.1; JOINED.
EMBL; M88081; AAA51928.1; JOINED.
EMBL; M88082; AAA51928.1; JOINED.
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Pfam; pr00384; cyclin; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
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EMBL; X68452; CAA48493.1; -.
EMBL; D13639; BAA02802.1; -.
EMBL; BC010958; AAH10958.1; -
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Best Local Similarity 60.0
Matches 6; Conservative
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PIR; S26580; S26580.
Genew; HGNC:1583; CCND2.
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P30280;
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                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and rhis statement is along as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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           -1-FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                    SUBJURY: TRANSITION.

SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLDENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.

SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: INVERSACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1264:257-260(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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"Zebrafish cyclin D1 is differentially expressed during early
embryogenesis.";
                                                                                                                                                                                                                                         | PIR; B40035; B40035. | PIR; A41984; A41984. | MGD; MGI: 88134; Ccnd2. | InterPro; IPR004366; Cyclin. | InterPro; IPR004366; Cyclin. | InterPro; IPR004367; Cyclin. | Ffam; PF00134; Cyclin; 1. | Ffam; PF00284; Cyclin; 1. | Ffam; PF00284; Cyclin; 1. | PR0SITE; PS00292; CYCLIN; 1. | PROSITE; PS00292; CYCLINS; 1. | PROSITE; PS00292; CYCLINS; 1. | Cyclin; Call Gycle; Call division; Multigene family. | SEQUENCE 289 AA; 32897 WW; 58P32277IDDIDA3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; Length 289;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
G1/S.specific cyclin D1.
                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96138542; PubMed-8547308;
                                                                                                                                                                                                                  EMBL; M86182; AAA37519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               57.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 60.0
hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMHY 10
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Cell 65:701-713(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 EEVFPLAMNY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGD1_BRARE
Q90459;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mphibla; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
NGBL_TaxID=835;
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                                                                                                                                                                                                                                                                                                                                           57.1%; Score 32; DB 1; Length 291; 60.0%; Pred. No. 44; 1: Mismatches 3; Indels
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                                          EMBL; X87581; CAA60885.1; -.
ZFIN; ZDB-GENE-980526-176; cycd1.
InterPro; IPR00436; Cyclin.
InterPro; IPR00445; Cyclin.
Pfam; PF00134; cyclin; 1.
Pfam; PF02944; cyclin, 2.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division.
SEQUENCE 291 AA; 33067 MW; FAS274CB1B46D5EF CRC64;
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E 291 AA; 32953 MW; A4747C5BD1679087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
G1/S.specific cyclin D1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 AA.
or send an email to license@isb-sib.ch).
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InterPro; IPR004367; Cyclin_Cterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X89475; CAA61664.1; -.
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Pfam; PF02984; cyclin_C; 1.
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                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 60.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGD1_XENLA
P50755;
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us-09-909-164-11.rsp

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CGD1_CHICK
P55169;
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                                                                                                                                                                                                                                                                     - SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.

- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                     Gene 167:341-342(1995).
-1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE GL/S
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.1%; Score 32; DB 1; Length 291; 60.0%; Pred. No. 44; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Cockerill M.J., Hunt T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF02984; cyclin_C; 1.
SMART: SM0385; CYCLIN: 1.
PROSITE: PS00292; CYCLINS: 1.
CYCLIN: Cell cycle: Cell division; Multigene family.
SEQUENCE 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;
                                                                                                                                                                                                                            'Structure and gene expression of avian cyclin D2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GL/S-specific cyclin D2.
CCND2.
                                                                    (Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
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                                 291 AA
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InterPro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                    MEDLINE=96144302; PubMed=8566807;
L1 H., Grenet J., Kidd V.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
                                                         01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U28980; AAA96955.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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                                   STANDARD;
                                                                                           G1/S-specific cyclin D2.
                                                                                                                    Gallus gallus (Chicken).
                                                                                                                                                                                                                                                               (START) TRANSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMHY 10
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                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                  NCBI_TaxID=9031;
                                                                      01-OCT-1996
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P53782;
                                                                                 16-OCT-2001
                                 CGD2_CHICK
P49706;
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                       CGD2_CHICK
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           RESULT 21
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                 early development.";
Biol. Cell 88:99-111(1996).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
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-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                      MEDLINE=97380591; PubMed=9237366;
Taleb F., Jessus C.;
"Xenopus cyclin D2: cloning and expression in oocytes and during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 291;
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PROSTTE: PS00292; CYCLINS; 1.
CYCLIN; Cell Cycle; Cell division; Multigene family.
SEQUERCE 291 AA; 32959 MW; 9A290F04F1531E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 1;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X89476; CAA61665.1; -.
EMBL; X83503; CAA58493.1; -.
InterPro; IPR004366; Cyclin_Cterm.
InterPro; IPR004367; Cyclin_Cterm.
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60.0%;
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Pfam; PF02984; cyclin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60...
Best 6; Conservative
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                                                                                                                                                                                                            (START) TRANSITION.
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SEQUENCE FROM N.A.
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NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression of human cyclin D genes.";
Genomics 13:565-574(1992).
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                    Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92347851; PubMed=1386336; Xiong Y., Menninger J., Beach D., Ward D.C.; Molecular cloning and chromosomal mapping of CCND genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93015922; PubMed-1383201;
Motokura T., Keyomarsi K., Kronenberg H.M., Arnold A.;
"Cloning and characterization of human cyclin D3, a cDNA closely
related in sequence to the PRADI/cyclin D1 proto-oncogene.";
J. Biol. Chem. 267:20412-20415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
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                                                                                                                                                                                DB 1; Length 292;
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EMBL; U40844; AAA83271.1; -.
InterPro: IPR004365; Cyclin.
InterPro: IPR004367; Cyclin.
Pfam; PF02194; Cyclin.1: 1.
Pfam; PF02984; Cyclin.2; 1.
SMART: SM00392; CYCLIN: 1.
PROSTIE: PS00292; CYCLIN: 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 292 AA; 33263 MW; 7B543029DB45A67D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R ;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                  CGD3_HUMAN STANDARD; PRT; 292 AA. P30281, Q95649, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) CCND3.
                                                                                                                                                                                            Pred. No. 44;
1; Mismatches
                                                                                                                                                                              Score 32;
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60.0%;
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Genomics 13:575-584(1992).
                                                                                                                                                                                                              6; Conservative
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Best Local
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Gaps
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MEDLINE=92005671; PubMed=1833066;
Lew D.J., Dulic V., Reed S.I.;
"Isolation of three novel human cyclins by rescue of G1 cyclin (Cln)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nature 350:512-515(1991).
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Kronenberg H.M., Arnold A.;
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MEDLINE-92017758; PubMed-1833629;
Withers D.A., Harvey R.C., Faust J.B., Melnyk O., Carey K.,
                                                                                                                                                                                                                                                                                                                               57.1%; Score 32; DB 1; Length 292; 60.0%; Pred. No. 44; 1; Mismatches 3; Indels
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01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1092 (Rel. 41, Last annotation update)
61/S-specific eyclin D1 (PRAD1 oncogene) (BCL-1 oncogene).
CCND1 OR PRAD1 OR BCL1.
                                                                                                                                                                                                                                                                                      S -> A (IN REF. 1).
; 16E7B1604FEB0029 CRC64;
                                                                                                                                                                                                             pfam; pF00134; cyclin; 1.
Pfam; PF0284; cyclin; 1.
PRANT; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLIN; 1.
CYCLIN; Cell cycle; Cell division; Multigene family.
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Mol. Cell. Biol. 11:4846-4853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91235304; Pubmed-1827756;
Xiong Y., Connolly T., Futcher B., Beach D.;
"Human D-type cyclin.";
or send an email to license@isb-sib.ch)
                                                                                                                                                                                  InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
                                                                      EMBL; M88087; AAA51929.1; -. EMBL; M88084; AAA51929.1; JOINED. EMBL; M88085; AAA51929.1; JOINED. MBL; M88086; AAA51929.1; JOINED. PIR; B42822; B42822.
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MEDLINE=91194766; Pubmed=1826542;
                                                        BC011616; AAH11616.1; -.
                                                                                                                                                                                                                                                                                                    292 AA; 32519 MW;
                            EMBL; M90814; AAA51927.1; -. EMBL; M92287; AAA52137.1; -.
                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                           Genew; HGNC:1585; CCND3.
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Best Local Similarity
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P24385;
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- : USTALA, TATANASTALOW.

- SUBGNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
INPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
- IDISEASE: INVOLVED IN B-LYMPHOCYTIC MALIGNANCY (PARTICULARLY
MANTLE-CELL LYMPHOMA (MCL)) BY A CHROMOSOMAL TRANSLOCATION
C REGIONS (BCL1 ONCOGENE). ACTIVATION OF CONDI MRY BE ONCOGENIC BY
C REGIONS (BCL1 ONCOGENE). ACTIVATION OF CONDI MRY BE ONCOGENIC BY
C DIRECTLY ALTERING PROGRESSION THROUGH THE CELL CYCLE.
- IDISEASE: INVOLVED IN A SUBSET OF PARATHYROID ADENOMAS BY A
C CHROMOSOMAL TRANSLOCATION T(11:11) (Q13:P15) THAT INVOLVES CCNDI
C CHROMOSOMAL TRANSLOCATION T(11:11) (Q13:P15) THAT INVOLVES CCNDI
C CHROMOSOMAL TRANSLOCATION T(11:11) (Q13:P15) THAT INVOLVES CCNDI
C CHROMOSOMAL TRANSLOCATION T(11:11) (Q13:P15) THAT INVOLVES
C - I SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
C - I DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
C WWW-"http://www.infoblogen.fr/services/chromosnoger/Genes/BCL1.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                      "CDK6 (PLSTIRE) and CDK4 (PSK-J3) are a distinct subset of the cyclin-dependent kinases that associate with cyclin D1."; Oncogene 9:71-79(1994).
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PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene;
SEQUENCE FROM N.A.
MEDLINE=9420433; PubMed=8204893;
REDINE=94204373; PubMed=8204893;
Rimokh R., Berger F., Bastard C., Klein B., French M., Archimbaud E.,
Rouault J.-P., Santa Lucia B., Duret L., Vuillaume M.;
Rearrangement of CCND1 (BCL1/PRAD1) 3' untranslated region in
mantle-cell lymphomas and t(11q13) associated leukemias.";
Blood 83:3689-3696(1994).
                                                                                                                                                                                                                                                                                     Bates S., Bonetta L., McAllan D., Parry D., Holder A., Dickson C.,
                                                                                                                                                                                             Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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MP -> IA (IN REF. 2).
L -> S (IN REF. 3).
; 3CC00C9905F58D3A CRC64;
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EMBL; M64349; AAA52136.1; -
EMBL; 23022; CAA8058.1; -
EMBL; BC00076; AAH00076.1; -
EMBL; BC001501; AAH01076.1; -
EMBL; BC01501; AAH14078.1; -
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Interpro; IPR004367; Cyclin_Cterm.
                                                                                                                                                                                                                                                 INTERACTION WITH CDK4 AND CDK6.
MEDLINE-94134440; PubMed=8302605;
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295 AA;
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A40034; A40034
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Query Match 57.1%; Score 32; DB 1; Length 295; Best Local Similarity 60.0%; Pred. No. 45; Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps
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Qy 1 EEVVPXGMHY 10 | | | | | | | | | Db 75 EEVFPLAMNY 84 Search completed: June 10, 2003, 13:40:21 Job time: 5.5 secs

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June 10, 2003, 13:30:25 ; Search time 25.7857 Seconds (without alignments) 87.898 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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56
1 EEVVPXGMHYS 11
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Sequence:
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13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archea:*
sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_novertebrate:*
sp_mammal:*
sp_mc:*
sp_organelle:*

sp_plant:* sp_rodent:*

sp_phage:*

sp_virus:*

### STIMMARTES

		Description	Q8rg86 fusobacteri	Q9x2e2 thermotoga	Q9hlh8 thermoplasm	Q99ur5 staphylococ	Q46486 corynebacte	Q8ywp1 anabaena sp	Q9avk4 pisum sativ	Q57489 bacteroides	Q9pc35 xylella fas	Q40479 nicotiana t	Q91w50 nicotiana s	Q38317 lactobacill	Q9xvk4 caenorhabdi	Q9sa71 arabidopsis	Q8tz07 methanopyru	027902 methanobact
SUMMARIES		ID	Q8RG86	Q9X2E2	8нгн6	Q99UR5	046486	Q8YWP1	Q9AVK4	057489	Q9PC35	040479	Q9LW50	038317	Q9XVK4	09SA71	Q8TZ07	027902
		DB	16	16	17	16	7	16	10	7	16	10	10	σ	2	10	17	17
		Juery Match Length DB	1063	308	322	1057	208	252	819	139	156	233	237	317	425	510	2042	264
	æ	Query Match	67.9	66.1	66.1	66.1	64.3	64.3	64.3	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	60.7
		Score	38	37	37	37	36	36	36	35	35	35	35	35	35	35	35	34
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# ALIGNMENTS

	PRT; 1063 AA.		1, Created)	<ol> <li>Last sequence update)</li> </ol>	21, Last annotation update)	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).	
	PRELIMINARY;		01-JUN-2002 (TrEMBLrel. 21, Created)	(TrEMBLrel. 2)	(TrEMBLrel. 2	osphate synth	
RESULT 1 Q8RG86	Q8RG86	Q8RG86;	01-JUN-2002	01-JUN-2002 (TrEMBLrel	01-JUN-2002 (TrEMBLrel.	Carbamoyl-ph	FN0422.
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STRAIN-WSBB (J. DSM 3109;
STRAIN-WSBB (J. DSM 3109;
MEDDLINE-99287316; PubMed-10360571;
Nelson K.E., Claytor R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nather B.H., Hikkey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linhner K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Mature 399:323-329(1999).
                                                                                                                                               MEDLINE-21886394; Pubmed=11889109; Reznik G., Los T., Lykidis A., Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain Arc 2586 ", J. Bacteriol. 184:2005-2018(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Ligase; Complete proteome.
SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease; Complete proteome.
SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FTSH protease activity modulator HFLK.
Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 308 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 48;
3; Mismatches
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InterPro; IPR0013190; GED.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00721; STOMATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 75.0 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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195 EIVPNGLNYS 204
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SMART; SM00244; PHB; 1.
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Best Local Similarity
6; Conserva
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41 VVPSGIHY 48
                                                                                                   SEQUENCE FROM N.A. STRAIN=ATCC 25586;
                                                         NCBI_TaxID=76856;
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SECUENCE FROM N.A.
SPECIES=S.aureus (strain MU50), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-DSM 1728; MEDLINE-20479972; PubMed=11029001; REUEPP A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophiluc scavenger Thermoplasma acidophilum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.1%; Score 37; DB 17; Length 322; 75.0%; Pred. No. 22; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                     Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
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                                                                                                                                                                                         01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Glucose-fructose oxidoreductase related protein.
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1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Carbamogl-phosphate synthase large chain.
PYRAB OR SAV1203 OR SA1046.
                                                                                  322 AA.
                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
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01-JUN-2001 (TrEMBLrel. 17, Last seq
                                                                                      PRT;
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EMBL: AL445063; CACAL1395.1; -.
InterPro: IPP000683; GFO_IDH_MOCA.
Pfam; PF01408; GFO_IDH_MOCA.
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InterPro; IPR004362; MGS_like.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00289; CPsase_L_chhain; 2.
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EMBL; AP003361; BAB57365.1; -.
EMBL; AP003132; BAB42298.1; -.
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NCBI_TaxID=158878, 158879;
                                                                              PRELIMINARY;
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Best Local Similarity
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66 VVPDGLHY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE 322 AA
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RESULT 3
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Q57489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES=C.xerosis; STRAIN=M82B;
MEDLINE=96117603; PubMed=8559800;
MEDLINE-96117603; F. Kalinowski J., Puhler A.;
Tauch A.; Rassing F., Kalinowski J., Puhler A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated IS1249, flanking the earythromycin resistance gene ermcX.";
Plasmid 34:119-131(1995).
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                                                                                                                            Score 37; DB 16; Length 1057; Pred. No. 77;
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                                                                                                                                                            2; Indels
                                                                                                       1057 AA; 117171 MW; E3E179EF0591F0F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Plasmid.
SEQUENCE 208 AA; 23012 MW; F1504BE1ECDE85A6 CRC64;
                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                    PRINTS: PROD098; CPSASE.
PROSITE; PSO0866; CPSASE_1; 2.
PROSITE; PSO0867; CPSASE_2; UNKNOWN_2.
PROSITE; PSO0639; THIOL_PROTEASE_HIS; UNKNOWN_1.
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                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last seq
(TrEMBLrel. 16, Last ann
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                                                                                                                                                                                                                                                                                                                                                  Hypothetical 23.0 kDa protein (GcrA)
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MEDLINE-20194806; PubMed-10732668;
                                                                                                                                                                                                                                                                                  PRT;
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Pfam; PF0278; CPSase_L_D3; 2. Pfam; PF0278; CPSase_L_D3; 1. Pfam; PF02142; MGS; 1.
                                                                                                                                66.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium xerosis, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium striatum
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                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium.
NCBI_TaxID=1725, 43770;
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                                                                                                                                                                                                                 190 EIVSNGLHYS 199
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Les 5; Conserv
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                          Complete proteome.
SEQUENCE 1057 AA
                                                                                                                                                                                                                                                                                                           01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                     01-MAR-2001
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Q8YWP1;
                                                                                                                                                                                                                                                                                  046486
                                                                                                                                                            Matches
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Pisum sativum (Garden pea).
Eukaryopts, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papllionoideae; Vicleae; Pisum.
NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sassa N., Matsushita Y., Nakamura T., Nyunoya H.; "The Molecular Characterization and in situ Expression Pattern of Pea SCARECROW Gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                             MEDLINE-2159281; PubMed-11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Katanaba A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yamada M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; PMBL; AP003586; BAB779291; --
Hypothetical protein; Complete proteome. SEQUENCE 252 AA; 28831 MW; 925572DA5DICA519 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                     Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Cell Physiol. 42:385-394(2001).
EMBL, AB048713; BAB39155.1; -.
InterPro: IPR00144; Flag_bb_rod.
InterPro: IPR005202; GRAS.
Pfam; PF03514; GRAS; I.
PROSTIE; PS00588; FLAGELIA_BB_ROD; UNKNOWN 1.
SEQUENCE 819 AA; 90372 MW; 41867Bb6Dc72ADFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
01-MAR-2002 (TIEMBLrel. 20, Last annotation update)
Hypothetical protein Alr1563..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB
Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. ALASKA;
MEDLINE-21231727; PubMed-11333309;
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Best Local Similarity
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                                                                                                                          NCBI_TaxID=103690;
                                                                                                                                                                             SEQUENCE FROM N.A.
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01-JUN-2001 (
01-JUN-2002 (
SCARECROW.
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us-09-909-164-11.rspt

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NCBI_TaxID=4097;
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Q40479
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                                                                                                                                                                                                                         "A multiple site-specific DNA-inversion model for the control of Ompl phase and antigenic variation in Dichelobacter nodosus."; MOI. Microbiol. 17:183-196(1995).
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                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-96020672; PubMed-7476204;
Moses E.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
                                                                                                                                                                                                                                                                                                                 MEDLINE-96257263; PubMed-8654969;
Billington S.J., Sinistaj M., Cheetham B.F., Ayres A., Moses E.K.,
Katz M.E., Rood J.I.; anative Dichelobacter nodosus plasmid and
implications for the evolution of the vap regions.";
EMBL, U02462; AABL2366.1; -.
InterPro: IPR001337; BRCT.
Family PR00533; BRCT.
SMART; SM00292; BRCT; 1.
                                                        Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
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139 AA; 15052 MW; E0E110AA4B7D4708 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09PC35;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf1950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 55.6 les 5; Conservative
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21 IVPAGVHWS 29
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                NCBI_TaxID=870;
                                                                                             Dichelobacter
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SEQUENCE
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Mon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Mani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira K.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
R. Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
R. Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
R. Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
R. da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
R. da Silva A.C.R., da Silva M.M., Verjovski-Almada H.J., de Souza A.A.,
R. Janada H., Van Sluys M.A., Verjovski-Almeda S., Vettore A.L.,
R. Aulada H., Van Sluys M.A., Setubal J.C.;
R. Menca 406:151-159(2000).
R. Mature 406:151-159(2000).
R. MEL; AEO04014; AAR84752.1; -.
R. MEL; AEO0260; CheW.
R. Mypothelical protein; Complete proteome.
SEQUENCE 156 AA; 17144 MW; D8358619C6671A5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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"Ethylene-inducible DNA binding proteins that interact with an ethylene responsive element.";
Plant Cell 7:173-182(1995).
EMBL; D38126; BAAC7324.1; -.
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Pred. No. 27;
3; Mismatches 1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2000 (TrEMBLrel, 15, Created)
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STRAIN-BY4; TISSUE-LEAF;
MEDLINE-95276459; PubMed-7756828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%;
55.6%;
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Best Local Similarity 55.0.
Best Local Si Conservative
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119 EEILPQGVH 127
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90 QAVVPKGRHY 99
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SEQUENCE FROM N.A.
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Matches
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Fremmaux C., De Antoni G., Raya R., Klaenhammer T.;
"Genetic organization and sequence of the region encoding integrative
functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                      MEDLINE-20399450; PubMed=10945353; Kitajina S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.; "Characterization of gene expression of NSERFs, transcription factors of basic PR genes from Nicotiana sylvestris."; Plant Cell Physiol. 41:817-824(2000). EMBI; AB016264; BAA97122.1; HSSP; O80337; 2GCC.
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                                                                                                Entrotains syrvestis (wood tobacco).
Entraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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Henrich B., Binishofer B., Blaesi U.;
Herrich S. tructure and functional analysis of the lysis genes of
Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26243 MW; 01BC3EEB51E46298 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Ethylene-responsive element binding factor.
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Last annotation update)
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Pred. No. 41;
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                                                                                       Nicotiana sylvestris (Wood tobacco)
                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001471; TF_ERF.
Pfam; PF00847; APZ-domain; 1.
PRINTS; PR00367; ETHRSPELENNT.
PLODOM; PD001423; TF_APZ; 1.
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60.0%;
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94 QAVVPKGRHY 103
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[5]
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01-NOV-1996 (
01-JUN-2002 (
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Engel G., Altermann E., Klein J., Henrich B.;
Engel G., Altermann E., Klein J., Henrich B.;

"Structure of a genome region of the Lactobacillus gasseri temperate phage phi adh covering a repressor gene and cognate promoters.";

Gene 210:67-70(1998).

EMBL, AJ13119; CAB52540.1; -.

EMBL, AJ13119; CAB52540.1; -.

InterPro; IPR002053; GH_25.

InterPro; IPR00346; SH3_bac.

Prodom; P001183; Glyco_hydro_25; 1.

Prodom; P0004620; GH_25; 1.

SMART; SM00287; SH3D; 1.

SMART; SM00287; SH3D; 1.
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NCBL_TaxID=6239;
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Pred. No. 76;
                                                                                                                                                                                                                                                      Length 317;
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Pred. No. 56;
1; Mismatches
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InterPro, IPR000719; Euk_pkinase.
Prom. PD00001; Buk_pkinase; 1.
PRODM: PD000001; Euk_pkinase; 1.
PROSITE, PS50011; PROTEIN_RINASE_DOM; 1.
ATP-binding; Transferase.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-JUN-2002 (TrEMBLrel. 21, Last annota
7518.1 protein.
Arabidopsis thaliana (Mouse-ear cress).
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MEDLINE=99069613; Pubmed=9851916;
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50.0%;
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Science 282:2012-2018(1998).
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Best Local Similarity bo...
6; Conservative
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R10D12.10.
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SEQUENCE FROM N.A.
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4 VPXGMHYS 11
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                    STRAIN-CV. COLUMBIA,
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Kremenerskala I., Luros J., Ngan I., Gonzalez A., Altafi H.,
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Pavis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC T518 sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
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STRAIN-AV19 / DSM 6324 / JCM 9639;

STRAIN-AV19 / DSM 6324 / JCM 9639;

STRAIN-AV19 / DSM 6324 / JCM 9639;

SLESAREY A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Halykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
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                                                                                                                                                                                                        510 AA; 55089 MW; 0DC63CC41F4712F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Predicted protein of the Cobn/Mg-chelatase family.
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Last annotation update)
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nes 6; Conservative
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                                                            SEQUENCE FROM N.A
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                                       NCBI_TaxID=3702;
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                                                                                                                                                                                              Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
NCBL_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                             Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%; Score 34; DB 17; Length 264; 62.5%; Pred. No. 74; 1; Indels tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 75.0%; Pred. No. 79; 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 AA; 28858 MW; 366BAE4E4D992C21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCEA100E0AEE8831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein DR0271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                              Methanobacteriaceae; Methanothermobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000940; AAB86340.1;
InterPro; IPR000878; Cor/por_Metransf.
InterPro; IPR004551; Dphthn_synthase.
Pfam; PF00590; TP_methylase; 1.
TIGRFAMS; TIGR00522; dph5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 protein; Complete proteome.
279 AA; 31140 MW; DCEA100E(
Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20036896; PubMed-10567266;
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EMBL; AE001889; AAF09867.1; -
TIGR; DR0271; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.50,
-20 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 VVPAGLHF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 264 AA;
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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Hopwood D.A.;
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                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                        Q9XAM3
                                                                                                                                                      Matches
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MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; Standar T., Sahikawa C., Kahikawa C., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
Michardi Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphille W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \mathrm{Rl.}^+;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.7%; Score 34; DB 16; Length 285; 55.6%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 AA; 30961 MW; 31D9CDE2711747EE CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
3-dehydroquinate synthase.
                                                                                                                01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.6%; Pred. No.
                                                                                    285 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS: PROJECT: CYCOCHROMECT: 1.
PRINTS: PROJEG3; CYTOCHROMECT.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003000; BAB49770.1; -.
Interpro; IPR000345; Cytc_heme_bind.
Interpro; IPR002326; Cyt_C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| | ||:
194 VIPEGTHYN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMHYS 11
100 VPLGRHYS 107
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                      NCBI_TaxID=381;
                                                                                                                                                              Cytochrome c1.
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Q9RW92
                                                          RESULT 18
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Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
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STRAIN-A3(2) / MI45.
STRAIN-A3(2) / MI45.
STRAIN-A3(2) / MI45.
STRAIN-A3(2) / MI45.
Thomson N.C., Chater K.E., Cerdeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,
Harrper D., Batenann A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Batenann A., Brown S., Cholber J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Ollver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:41-147(2002).
EMBL; AL079355; CAB45581.1;
InterPro; IPR000977; DNA_ligase.
Pfam; PF01068; DNA_ligase.
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                                                                                                                                                                                                                                                          60.7%; Score 34; DB 16; Length 350; 60.0%; Pred. No. le+02;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seeger S., Harris D.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         James K.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7A995A55116077B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor.
Bacteria, Firmicutes, Actinobacteria, Actinobacteridae;
                                                                                                                                                                                              350 AA; 37121 MW; 37601D08B2FB6116 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                   Interpro; IPR002658; DHQ_synthase.
Pfam; PF01761; DHQ_synthase; 1.
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Science 286:1571-1577(1999).
EMBL; AE001932; AAF10353.1; -
HSSP; P07547; 1DQS.
TIGR; DR0777; -.
                                                                                                                                                                                                                                                                                               60.08;
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 EAVAYGMHYA 261
                                                                                                                                                                                                                                                                                                                                                                                       2 EVVPXGMHYS 11
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SCO6707 OR SC4C6.17C
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                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                               Complete proteome. SEQUENCE 350 AA;
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ANTALANDELIA H;

A MICHAGH TO. BURNITA H;

A Madredge T., Bashizadeh R., Blakely D., COOK R., Gilbert K.,

A Andredge T., Bashizadeh R., Blakely D., COOK R., Gilbert K.,

RA Harrison D., Hoang L., Kagle P., Lumm W., Pothier B., Olu D.,

RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

A Juwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

RA Daniels C.J., Mao J.-I. Rice P., Noelling J., Reeve J.N.;

RA Daniels C.J., Mao J.-I. Rice P., Noelling J., Reeve J.N.;

R. Complete genome sequence of Methanobacterium thermoautotrophicum

R. J. Bacteriol. 179:7135-7155 (1997).

R. Rabi., PRO050323 AAB86115.1;

DR InterPro; IPR005141; eRFL_J.

DR InterPro; IPR005142; eRFL_J.

DR InterPro; IPR005142; eRFL_J.

DR Ffam; PF03465; eRFL_J.

DR Ffam; PF03465; eRFL_J:

DR Ffam; PF03465; eRFL_J:

DR Ffam; PF03465; eRFL_J:

R. TGRRAMS; TICRRO111; pelA.

SEQUENCE 360 AA; 40814 WW; 2A000CB4B3CEF469 CRC64;
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                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanobacterium thermoautotrophicum,
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
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NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.7%; Score 34; DB 17; Length 360;
45.5%; Pred. No. 1e+02;
Live 4; Mismatches 2; Indels
                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BH2027.
                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
ilarity 71.4%; Pred. No. 1e+02;
Conservative 1; Mismatches
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID-187420;
                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                          PRT;
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STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.38,
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |::|| | |::
98 EDLVPMGSHHT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell division protein.
                                                                                          4 VPXGMHY 10
                                                                                                                         :| |||||
20 IPPGMHY 26
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus halodurans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-DELTA H;
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Q9KBA1
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Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Horis Friji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.; "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL, APO01514; BAB05746.1; -RMBL, APO01514; -RMBL, APO01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson R., Ainscoud R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fullton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latraille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudnin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2. Mo of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Cenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                          Length 425;
                                                                                                                                                                                                                                                                   60.7%; Score 34; DB 16; Length 42:
60.0%; Pred. No. 1.2e+02;
Mismatches 2; Indels
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Graves T., Wohldmann P., Gillam B.;
Graves T., Wohldmann P., Gillam B.;
"The sequence of C. elegans cosmid F10D2.";
Submitted (SEP) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022972; AAC48234.1; -...
InterPro; IPR004151; Sre.
Pfam; PF03125; Sre; 1.
SEQUENCE 495 AA; 58190 MW; OC61139C138EEE4C CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                         Local Similarity 60.0
nes 6; Conservative
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218 ENIVPIGKHH 227
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016912;
01-JAN-1
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Q9Y0Y6;
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Matches
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MARINE-ZUIND-UGUE, PUNDAG-TU/J112;

RA Adams M.D. / Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D. / Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D. / Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA GAGGE R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Beace P.V., Baxendale J., Bayrattaroglu L., Beasley E.M.,
RA Burtis R.C., Busam D.A., Bultler H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Bultler H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Bultler H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Gabrielian A.E., Garg N.S., Glabart W.M., Glasser K.,
RA Burtis R., Gong F. Gorrell J.H., Gu Z., Genbart W.M., Glasser K.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Glan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Weil M.-H., Ibeywam C.,
RA Jalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Merlson D.L.,
Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefl A.,
Rushon D., Lei Y., Levitsky A.A., Li J., Li J., Mill Y.,
Raken D., Lei Y., McIntosh T.C., McLeodo M.P., McPherson D.L.,
RA Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefl A.,
Rabenor K.M., Wellen B., Wellen B., Mannel B.F.,
Rayer E., Spradling A.C., Stapleton M., Strong R., Sun B.,
Rylakas R., Tector C., Turnen R., Wenter E., Wang A.H., Wang Z.-Y., Wassamma D.L., Whork Weller E., Wang Z.-Y., Wassamma D.L., Whork Weller E., Wang Z.-Y., Wassamma D.L., Stapleton M., Strong K., Shu B., Shu B.C., Stapleton C., Stap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M., Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celniker S.E.,
                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AE003(APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF145690; AAD38665.1; ...
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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InterPro; IPR000719; Euk_pkinase.
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MEDLINE-20196006; PubMed=10731132;
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                                                                        BCDNA: LD28657 protein.
BCDNA: LD28657 OR CG1098.
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                          01-NOV-1999
01-JUN-2002
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SEQUENCE

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Pred. No. 2e+02;
   Score 34; DB 5; Length 637;
Pred. No. 1.9e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                               Cercopithecine herpesvirus 7.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 75.9 kDa protein.
                                                                                                                       678 AA.
                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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                                                                                                                        PRT;
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        60.78;
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Query Match
Best Local Similarity 60...
6, Conservative
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                                                                     263 VVPDAVHYS 271
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nes 5; Conserv
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Q9E1X6;
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June 10, 2003, 13:24:45; Search time 31.3571 Seconds (without alignments) 46.744 Million cell updates/sec
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/SIDS2/gcgdata/geneseqy-emb1/AA1984.DAT:*
/SIDS2/gcgdata/geneseqy-emb1/AA1985.DAT:*
/SIDS2/gcgdata/geneseqy-emb1/AA1985.DAT:*
/SIDS2/gcgdata/geneseqy-emb1/AA1987.DAT:*
/SIDS2/gcgdata/geneseqy-emb1/AA1987.DAT:*
/SIDS2/gcgdata/geneseqy-emb1/AA1989.DAT:*
/SIDS2/gcgdata/geneseqy/geneseqp-emb1/AA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
Listing first 75 summaries
                                                                                                                                           OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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54
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                                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description	Hepatitis C virus									
COLUMN		£ £	ABB80524	ABB80528	ABB80529	ABB80561	ABB80562	ABB80538	ABB80542	ABB80543	ABB80521	ABB80522
		DB	23	23	23	23	23	23	23	23	23	23
		Query e Match Length DB 1	11	11	11	11	11	11	11	11	11	11
	æ	Query Match	96.3	96.3	96.3	96.3	96.3	87.0	87.0	87.0	85.2	85.2
		Score	52	52	52	52	52	47	47	47	46	46
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ALIGNMENTS

RESULT 1 ABB80524 ID ABB8

ABB80524 standard; peptide; 11 AA.

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Modified-site
        virucide.
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                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a peptide compound of the invention having . hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-Ketoamide peptide analogues. The peptides have invention are are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 23; Length LL:
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.3%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                        /note≈ "N-terminal acetyl"
                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                                   /note= "D-form residue"
                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                           Brunck TK;
                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80528 standard; peptide; 11 AA.
                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                       21-JUL-2000; 2000US-220101P
                         08-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                         Levy OE,
                                                                                                                                                                                                                                                                                                         WPI; 2002-361643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AA;
                                                                                                                                                        Misc-difference
                                                                                                                                                                                                   WO200208251-A2
                                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                       Lim-wilby M,
                                                                                                                                                                                                                     31-JAN-2002
                                                                                      Synthetic
        ABB80524;
                                                                     virucide
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"Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have, virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 52; DB 23; Length 11
100.0%; Pred. No. 0.0015;
                                                                                        'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ...
                                                                                                                                                                                                                                                 /note= "C-terminal amide"
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                                                                                                                                                                                                      /note= "D-form residue"
                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001; 2001WO-US23169
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                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORV-) CORVAS INT INC
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                                                              Modified-site
                                                                                                           Modified-site
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Synthetic
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virus protease
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                                                                                                                                                                                                                                                                                                                                          The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
/note= "Norvaly1 carbony1 forming keto-amide linkage with residue ?"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
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                                                                                   /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                      "D-form residue"
                                                             /note= "D-form residue"
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                                                                                                                                                                                                                             Brunck TK;
                                                                                                                                                                                                                                                                                                                         Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pritive 0;
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Matches 11; Conservative
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                                       /note=
                                                                                                                                                                                                                             Levy OE,
                                                                                                                                                                                                      (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA;
                           Misc-difference
                                                  Misc-difference
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                                                                                                                                 31-JAN-2002
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 23; Length 11;
Pred. No. 0.0015;
0; Mismatches 0; Indels
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/note= "C-terminal amide"
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100.0%; Pre
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Best Local Similarity 100.
Matches 11; Conservative
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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Pred. No. 0.014;
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Pred. No. 0.014;
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                Claim 17; Page 65; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                       DB 23; Length 11,
                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                       Score 47; DB 23;
Pred. No. 0.014;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB80521 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 64; 69pp; English.
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                                                                                                                                                                                         87.0%;
90.9%;
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                                                                                                                                                                                         Query Match 87.0
Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                               EEVPXGQDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                   1 EEVVPXGMDYS 11
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Best Local Similarity
                                                                                                                                          11 AA;
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(first entry)

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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
ABB80525 standard; peptide; 11 AA.
                                       08-OCT-2002
                    ABB80525
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                                                                                                                                                                                                                                      "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have invented activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           oride compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
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Pred. No. 0.022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus
                                                                                                                                                                                                                  /note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                 Location/Qualifiers
                                                                    ABB80522 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.2%;
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                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-220101P
                                                                                                            (first entry)
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              EEVVPXGMSYS 11
     EEVVPXGMDYS 11
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                                                                                                            08-OCT-2002
                                                                                                                                                                            Synthetic
                                                                                        ABB80522;
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Best Local S:
Matches 10,
                                                                                                                                                            virucide.
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'Norvaly1 carbony1 forming keto-amide linkage with residue 7\,\mathrm{m}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis \mathsf{C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
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Pred. No. 0.022;
0; Mismatches 1; Indels
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                                                                                  note= "N-terminal acetyl"
                                                                                                                                                                                                                            "C-terminal amide"
                                                                                                                                                                                       'note= "D-form residue"
                                           Location/Qualifiers
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                                                                                                                        "Norvalyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-361643/39.
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Best Local Similarity
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                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus protease
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                                                            Modified-site
                                                                                                   Modified-site
                                                                                                                                                                                                        Modified-site
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Synthetic
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ABB80526
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RESULT 11 ABB80525

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Modified-site
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Modified-site
                   Modified-site
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                                                                                                 31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                      "Norvaly1 carbonyl forming keto-amide linkage with residue 7\,\mathrm{m}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                        peptide compound having hepatitis C virus protease inhibitory
ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 2
Pred, No. 0.022
0; Mismatches
                                                                     'note= "N-terminal acetyl"
                                                                                                                                                             /note= "C-terminal amide"
                                                                                                                       "D-form residue"
                                                                                                                                          'note= "D-form residue"
                                                 Location/Qualifiers
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90.9%;
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                                                                                                                                                                                                                                                                                   Lim-wilby M, Levy OE,
                                                                                                                       'note≕
                                                                                                                                                                                                                                                                (CORV-) CORVAS INT INC.
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nes 10; Conserv
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                                                                                                             Misc-difference
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                               /note- "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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/note= "N-terminal acetyl"
                                                                                               "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 65; 69pp; English.
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90.9%;
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/note=
                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AA;
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(CORV-) CORVAS INT INC
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                                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have inventide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\sf C}
                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                            Score 46; DB 23; Length 11;
Pred. No. 0.022;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
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                                                                                      Brunck TK;
                                                                                                                                                                                                                                                                                                                                                     ABB80551 standard; peptide; 11 AA.
                                                                                                                                                    Claim 17; Page 65; 69pp; English.
                                19-JUL-2001; 2001WO-US23169
                                                 21-JUL-2000; 2000US-220101P
                                                                                                                                                                                                                                                           85.2%;
90.9%;
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                                                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
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                                                                                    Lim-wilby M, Levy OE,
                                                                  (CORV-) CORVAS INT INC
                                                                                                    WPI; 2002-361643/39
                                                                                                                                                                                                                                           11 AA;
WO200208251-A2.
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                                                                                                                                       virus protease
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                  31-JAN-2002
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                                                                                                                                                                                                                                           Sequence
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis \mathsf{C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.
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90.9%; Pred. No. 0.022;
iive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C-terminal amide"
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     Brunck TK;
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                                                                                                                                                                                                        Claim 17; Page 65; 69pp; English.
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Lim-wilby M, Levy OE,
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                                                 WPI; 2002-361643/39
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es 10; Conserv
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                                                                                                                                                            virus protease
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Modified-site
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Matches
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residue 7"
                                                                  hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                              Gaps
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                                                        sequence represents a peptide compound of the invention having
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Pred. No. 0.022;
0; Mismatches
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                               Claim 17; Page 65; 69pp; English
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90.9%;
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Best Local Similarity
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       virus protease
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat alsorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Pred. No. 0.022;
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90.9%;
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(first entry)

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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
                                     ABB80564 standard; peptide; 11 AA.
                                                                               08-OCT-2002
                                                                                                                                                     Synthetic.
                                                          ABB80564;
                                                                                                                                 virucide,
                 RESULT 20
                             ABB80564
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                                                                                                                                                                                                                                                                                                               "Valy1 carbonyl forming keto-amide linkage with residue 7"
                                             Gaps
                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a peptide compound of the invention having
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                        DB 23; Length 11;
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                                           1; Indels
                      Score 46; DB 23
Pred. No. 0.022;
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                      85.2%;
90.9%;
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                                          Conservative
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Matches 10; Conservative
                                                             1 EEVVPXGMDYS 11
                                                                                1 EEVVPXGMSYS 11
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/note= '
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                    Query Match
Best Local Similarity
Matches 10; Conserv
 11 AA;
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 Sequence
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                                                                                      "Leucyl carbonyl forming keto-amide linkage with
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                                             "N-terminal acetyl"
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/note= "C-terminal amide"
Location/Qualifiers
                                                                                                                 residue 7'
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Matches 10; Conservative
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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/note= "2-aminoisobutyryl carbonyl residue forming a keto-amide linkage with residue 7"
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Pred. No. 0.022;
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90.9%;
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Best Local Similarity
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                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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90.9%;
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to traat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
        activity useful for treating disorders associated with hepatitis C
                                                                    sequence represents a peptide compound of the invention having
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                                                                                                                                                                                                    85.2%; Score 46; DB 23; Length 11; 90.9%; Pred. No. 0.022;
                                                                                                                                                                                                                              0; Mismatches
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                                             Claim 17; Page 65; 69pp; English
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                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
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             21-JUL-2000; 2000US-220101P.
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                                                             Lim-wilby M, Levy OE,
                                     (CORV-) CORVAS INT INC
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have
Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease.
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OM protein - protein search, using sw model

June 10, 2003, 13:31:45 ; Search time 9.64286 Seconds Run on:

(without alignments)
33.564 Million cell updates/sec

US-09-909-164-12 54 1 EEVVPXGMDYS 11 Perfect score:

Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

Issued_Patents_AA:*

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/AB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 4, Appli	Ŋ,	• •	11,	7,	7,	76,	82,	14,	8, 7	ш	9		Sequence 23, Appl	4	Sequence 4, Appli	4	7, A	21,	21,	21,	21,	Sequence 20, Appl	C	22,	22,	22,
SUMMARIES	ID	US-08-853-948B-4	US-08-853-948B-5	US-09-697-367-24	US-08-429-054A-11	US-08-718-777-7	US-09-051-341-7	US-08-569-147-76	US-08-569-147-82	US-08-963-851-14	US-08-070-165F-8	US-08-885-418-8	US-06-383-630-6	5177197-51	US-08-580-988A-23	US-08-460-694-4	US-08-460-744-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	US-08-246-361A-21	US-08-463-772-21	PCT-US93-05000-21	US-08-926-842B-20	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22
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S-08-926 S-08-926 S-08-463 S-08-246 CT-US93- CT-US93- S-08-2464 S-08-2466 S-08-2466 S-08-2466	77-947-120-8 78-47-120-8 78-472-93A- 78-464-517-1 78-464-517-1 78-46-517-1 78-78-78-78-78-78-1 78-78-78-78-1 78-78-78-78-1 78-78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-1 78-78-	
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## ALIGNMENTS

GENERAL INFORMATION:
APPLICANT: AKIHAMA, TOYOGA
APPLICANT: AKIHAMA, TOYOGA
APPLICANT: AKIHAMA, TOYOGA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 0049-0235-0
CURRENT APPLICATION NUMBER: 05/09/853,948B
CURRENT FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10
SSOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 341 OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, Asn, Asp, OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Sequence 4, Application US/08853948B Patent No. 6210943 ORGANISM: Citrus unshiu US-08-853-948B-4 TYPE: PRT FEATURE RESULT 1

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10016
                                  US-08-429-054A-11
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                                                                                                                                                                                                                                                            CITY:
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TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 0049-0235-0
CORRENT APPLICATION NUMBER: US/08/853,948B
CURRENT FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10
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                                                  Score 36; DB 4; Length 341;
Pred. No. 14;
2; Mismatches 1; Indels
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Pred. No. 15;
2; Mismatches 1; Indels
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Pred. No. 16;
2; Mismatches 1; Indels
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OCOCO Jr., Emil M.
APPLICANT: OCOCO Jr., Emil M.
APPLICANT: Caimi, Perry G.
APPLICANT: Caimi, Perry G.
APPLICANT: Tarczynski, Mitchell
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: BB1166 US NA
CURRENT APPLICATION NUMBER: US/09/697,367
CURRENT FILING DATE: 2000-10-26
PRIOR FILING DATE: 1998-MAY-07
PRIOR FILING DATE: 1999-MAY-06
NUMBER OF SEQ ID NOSS: 24
NUMBER OF SEQ ID NOSS: 24
NUMBER OF SEQ ID NOSS: 24
                                                                                                                                                                                                                                    Sequence 5, Application US/08853948B Patent No. 6210943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09697367
Patent No. 6323015
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                                                  66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Ver. 2.1
                                 Query Match
Best Local Similarity 66.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.7
Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conservative
                                                                                                                                      ; ORGANISM: Citrus unshiu US-08-853-948B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patr
SEQ ID NO 5
LENGTH: 348
TYPE: PRT
                                                                                                                                                                                                                    US-08-853-948B-5
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GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: JEAN: VOELKER, TONI: GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYMPHETASE (SPS),
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 53;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: French 90402094.9
TING DATE: 20-July-1990
                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1995
26-APR-1995
26-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 842,337
FILLING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILLING DATE: 18-July-1991
                                                                                                                                                          NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,05
Sequence 11, Application US/08429054A
Patent No. 5917126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08718777
Patent No. 5981852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 20-July-1990
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Charles A. Muserlian
RECISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.
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TELEPHONE: (212) 661-8000
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bruneau, J. M.
Voelker, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.77
Pest Similarity 65.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Unknown MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: Single
Unknown
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                                                                                                                                                                                                                                                         NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26 CLASSIFICATION:
                                                                                                                                                                                                                                         NEW YORK
                                                                                                                                                                                                                                                                              USA
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APPLICANT:
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APPLICANT:
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63.0%;
75.0%;
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LENGTH: 140 amino acids
TYPE: amino acid
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-569-147-76
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
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435 VIPPGMDFS 443
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGMDYS 11
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US-08-569-147-76
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                                                                                                                                                                                                                                                                                                                                                                                                US-09-051-341-7
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Patent No. 6124528
GENERAL INFORMATION:
APPLICANT: Shewmaker, C. K.
TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 36; DB 2; Length 1068; 66.7%; Pred. No. 53; 1; Indels tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: R-LOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SUFRREM: APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPELICATION NUMBER: US/08/718,777 FILING DATE: NOT YET ASSIGNED CLASSIFICATION: 800
                                                                                          ADDRESSEE: Law Offices of Barbara Rae-Venter STREET: 260 Sheridan Avenue, Suite 440 CITY: Palo Alto STATE: California
    MODIFICATION OF SUCROSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Rae-Venter Law Group, P.C. STREET: 260 Sheridan Avenue, Suite 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGNE.072.02US
                                         SYNTHASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGN
TELECOMMUNICATION:
TELEPHONE: (415)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 VIPPGMDFS 443
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CITY: Palo Alto
STATE: California
    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                COUNTRY: USA ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-051-341-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76, Application US/08569147

Patent No. 6180377

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: One Liberty Place - 46th Floor
                                                                   FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-JAN-1995
ATORNEY/AGENT INFORMATION:
NAME: BATDARA RAS-VENTER: Ph.D.,
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.110.02US
TELEPHONE: (415)328-4400
TELEPHONE: (415)328-4477
INFORMATION FOR EQUID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
PCT/US96/17351
             AFFLING DATE: 25-OCT-1990
APPLICATION NUMBER: US 08/549,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERRACE/DOCKET NUMBER: CARP-C
TELECOMMUNICATION INFORMATION:
TELEPHAN: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 76:
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Gaps

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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43210
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                                                                                                                                                                                                                                                                 US-08-070-165F-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-885-418-8
        LENGTH: 59
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       Gaps
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Pred. No. 13;
0; Mismatches 2; Indels
       Indels
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Fatent No. 6300116
GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BAUDITZ, PETER
APPLICANT: BAUDITZ, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-018
CURRENT APPLICATION NUMBER: US/08/963,851
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
     ;
;
 0; Mismatches
                                                                                                                                                                                                                      HUMANISED ANTIBODIES 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
RECISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/569,147
25-March-1996
                                                                                                                                                    Sequence 82, Application US/08569147 Patent No. 6180377 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
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TELEPHONE: (215) 568-3410
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 140 amino acids
amino acid
6; Conservative
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                    TITLE OF INVENTION: HUM
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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122 VVPTGFDY 129
                                 3 VVPXGMDY 10
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                        19103
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                                                                                                                                  US-08-569-147-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-569-147-82
                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Matches
                                                                                                                  RESULT 8
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Gaps
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chiu, Ing-Ming
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: 82052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08885418
Patent No. 5925528
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: 9th Avenue
STREET: 9th Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 378;
                                                                                  Score 33; DB 4; Length 59;
Pred. No. 7.5;
                                                                                                                            2; Indels
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                                                                                                                          4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08070165F
Patent No. 5750365
GENERAL INFORMATION:
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-08-963-851-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.1%;
85.7%;
                                                                              Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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38 EKHIPGGLEYS 48
                                                                                                                                                                1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-070-165F-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |||||
| 139 PPGMDYS 145
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Best Local Similarity
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; SEQ ID NO:51:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: AVNER YAYON et al.
IITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
FACTOR RECEPTOR ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER RELABBLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* $1imnote*890TX
COPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
to an ASCI file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2; Length 378;
Pred. No. 64;
                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/383,630A FILING DATE: 26-Aug-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUBBER: 33,883
REFERENCE/DOCKET NUMBER: 1402/2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHONDRODYSPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09383630A Patent No. 6265632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                  : 378 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 PPGMDYS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PXGMDYS 11
Columbus
                                        USA
                       Ohio
                                                                                                                                                                                                                          FILING DATE:
                                                         43210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-08-383-630-e
                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-885-418-8
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Sequence 23, Application US/08580988A

Sequence 23, Application US/08580988A

Patent No. 5856161

GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                          RESULT 13
5177197-51
; Patent No. 5177197
; PAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER, HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
                                                                                                                                                                                                                                                                                                                                                                                                                                           LEWA; HELDIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORTING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                         Score 33; DB 4; Length 801; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 6; Length 65;
Pred. No. 13;
3; Mismatches 3; Indels
                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Benjamin Aaron Adler, Ph.D., J.D.
                                     TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/580,988A FILING DATE: January 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PE: 1.44 Mb floppy disk
Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Dr. Benjamin A. Adler
8011 Candle Lane
                                                                                                                                                           61.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.3%;
SEQUENCE CHARACTERISTICS:
LENGTH: 801
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                                                                                                                                           Query Match
Best Local Similarity 85...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.3
Best Local Similarity 45.5
Matches 5; Conservative
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 KEICPGGMGYT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 MD
                                                                                                                                                                                                                                                                                   566 PPGMDYS 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 65
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                                                                                                                     US-09-383-630-6
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20 EEVFPLAMNY 29
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                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-460-744-4
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STATE:
                                                                                                                                                                                                                                                                                                  STATE:
                                                                                   RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Arnold, Andrew TITLE OF INVENTION: PRAD1 Cyclin and its cDNA NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
SORTWARY APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                           59.3%; Score 32; DB 2; Ilarity 60.0%; Pred. No. 22; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0609.4070002
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MCCONALTHY, EVELYN H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08460694
Patent No. 5858655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                     TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 amino acids
                                                                                                                                                                                                                                                    ); ANTI-SENSE: no
; FRGAMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-580-9888-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.3
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                              TOPOLOGA..
MOLECULE TYPE:
DESCRIPTION: protein
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Best Local Similarity
'-hea 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                             STRANDEDNESS:
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59.3%; Score 32; DB 3; Length 152;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 3; Indels
762-08-460-744-4
7 Sequence 4, Application US/08460744
7 Sequence 4, Application US/08460744
7 Fatent No. 6107541
7 GENERAL INFORMATION:
7 APPLICANT: Arnold, Andrew
7 TITLE OF INVENTION: PRADI Cyclin and its CDNA
7 NUMBER OF SEQUENCES: 8
7 CARRESPONDENCE ADDRESS:
7 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
7 STREET: 1100 New York Avenue, N.W., Suite 600
7 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. R. 1100 NEW YORK AVE., NW, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ralease #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
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Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MCCOMATRY, 25,279
REFERENCE/DOCKET NUMBER: 35,279
TELECOMMUNICATION INFORMATION:
TELEPPHONE: 202-371-2600
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 amino acids
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
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STRANDEDNESS: not
TOPOLOGY: linear
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Gaps ö

Indels

3,

1; Mismatches

60.08;

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1 EEVVPXGMDY

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Best Local Similarity 60.0 Matches 6; Conservative

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APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND
TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
TITLE OF INVENTION: P34LDCMAVIRUS E7 ONCOPROTEIN
NUMBER OF SEQUENCES: 34
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Pred. No. 35;
1; Mismatches 3; Indels
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COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
                                                                             ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFRENCE/DOCKET NUMBER: 35,811
REFRENCE/COCKET NUMBER: 0609.4070000
TELECOMMINICATION INFORMATION:
TELEPHONE: (202) 371.2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 5998-0016
REFERENCE/DOCKET NUMBER: 5998-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08193977
Patent No. 5625031
                                                                                                                                                                                                                                                                                                                                                                                                                                       59.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 635 BRYANT STREET
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REED & ROBINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 173 amino acids
                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: not relevant; MOLECULE TYPE: peptide US-07-667-711B-4
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity bv..
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: sin
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-193-977-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-193-977-7
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59.3%; Score 32; DB 1; Length 173;

Query Match

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Gaps
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Patent No. 5998582

GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
                                       Sequence 21, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INFORMICS: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.3%; Score 32; DB 2; Length 189; 60.0%; Pred. No. 46; 3; Indels tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSILICATION DATA:

APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: 36,709
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATCHEW P. VINCENT
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.3
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | | | :|
74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                     COUNTRY: USA ZIP: 02109
                                                                                                                                                                                                                                                         Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-246-361A-21
                      US-08-464-517-21
                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 20
RESULT 19
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D-Type Cyclin and Uses Related Thereto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
GLASSIFICATION:
PRIOR APPLICATION DATE: 19930525
GLASSIFICATION UNBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 616-861-6540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 3
Pred. No. 46;
1; Mismatches
                          PRIOR APPLICATION 1473.

APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATE: 36-MAY-1991
ATTORNEY-AGENT INFORMATION:
NAME: MATCHEW-AGENT INCOMARTION:
NAME: MATCHEW-CFDCOKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
FELECOMMUNICATION INFORMATION:
TELECHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARRATERISTICS:
LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application PC/TUS9305000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 189 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.3
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Militia D
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-463-772-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MITOTIX
TITLE OF INVENTION: D-'
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               кк: US
02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US93-05000-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB;
Pred. No. 46;
1; Mismatches
                                                                                                                                                                                                                                                             CURKENY APPLICATION LOTA'S

APPLICATION NUMBER: US/08/246,361A

FILING DATE: 19-MAY-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308

FILING DAME: 16-OCT-1992

PRIOR APPLICATION DATA: 1992

APPLICATION NUMBER: US 07/01,514

FILING DAME: 16-MAY-1991

APPLICATION NUMBER: US 07/701,514

FILING APPLICATION NUMBER: US 07/701,514

FILING APPLICATION NUMBER: 36,709

RECISTRATION NUMBER: 36,709

RECISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: 36,709

REFERENCE/TOCKET NUMBER: MII-004C

TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400

TELEFAX: (617) 227-7401

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/08463772 Patent No. 6066501
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 189 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                   SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                          USA
                                                                 Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 60 St
CITY: Boston
                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                 CITY: BOST
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-246-361A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-463-772-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
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Gaps

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Matches
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                                                                                                                                                                                                       Sequence 20, Application US/08926842B
Patent No. 6030807
GENERAL INFORMATION:
APPLICANT: Sa-No. 6030807ueira, Isabel
APPLICANT: de Lencastre, Herminia
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                    Gaps
                                                                   ;
0
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Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH,
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 3; Length 231;
Pred. No. 58;
                                 Length 189;
                                                                   3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER TO A COMPUTE TO A COMPUTER TEACHABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,842B
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
ATTOKNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET NUMBER: 26,742
RELECOMMULATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELEFAK: 201 343-1684
                                 DB 5;
46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                   Mismatches
                                 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.3%;
                                 59.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                   1 EEVVPXGMDY 10
                                                                                                                                  74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                               STREET: 411 m.c.
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | |:|||
41 IKPSGVDYS 49
               Ouery Match
Best Local Similarity
6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: ESC
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-926-842B-20
PCT-US93-05000-21
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US-08-464-517-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Patent No. 5998582
GENERAL INCRMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION:
TUTLE OF INVENTION:
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                    SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                     ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-464-517-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIÚM TYPE: Floppy
                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 EEVFPLAMNY 29
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 60 Sta
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                     USA
                                                                             Boston
                                                                                                                                 ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-246-361A-22
                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                     COUNTRY:
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

June 10, 2003, 13:46:50; Search time 15 Seconds

(without alignments)
75.710 Million cell updates/sec

Title:

Perfect score:
54

Sequence:
1 EEVVPXGMDYS 11

Scoring table:
Gapop 10.0, Gapext 0.5

Searched:
392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters:
392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Published Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 14, Appl. Sequence 4881, Ap Sequence 10697, A Sequence 526, App Sequence 526, App Sequence 526, App Sequence 10, Appl Sequence 8, Appli Sequence 11, Appl Sequence 9, Appli Sequence 27, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 526, Sequence 526, Sequence 420, Description 0.92.09.738-626-4811 0.02.09-738-626-4811 0.02.09-778-528-526 05-09-978-697-526 05-09-978-192A-526 05-09-978-182A-526 05-09-978-189-526 05-09-978-189-526 05-10-174-590-420 US-09-815-242-5111 US-10-027-806-4 US-10-217-700-10
US-10-217-700-8
US-10-217-700-4
US-10-217-700-11
US-10-217-700-11
US-10-217-700-9 US-09-948-080-14 US-10-034-623-4 US-10-027-801-4 SUMMARIES 9 10 Query Match Length DB 440 1062 3472 3472 3472 1081 1083 1084 283 299 299 736 736 736 736 Score Result Š

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76 - 758 - 4 775 - 737 - 4 775 - 737 - 4 775 - 737 - 4 775 - 737 - 4 776 - 942 - 4 80 - 552 - 4 80 - 562 - 4 80 - 502 - 4 80 - 502 - 4 80 - 502 - 4 80 - 502 - 4 80 - 6 80 - 7 80	180-549 180-555 181-000-1 183-010-1 184-614-1
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## ALIGNMENTS

US-10-217-700-10

Sequence 10, Application US/10217700

Sequence 10, Application No. US20030070191A1

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Holaday A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

CURRENT APPLICATION NUMBER: US/10/217,700

CURRENT FILING DATE: 2002-08-12

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RESULT 6
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Sequence 8, Application US/10217700

Publication No. US20030070191A1

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Holdady, A. Scott

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/10/217,700

CURRENT PELLING DATE: 1090-09-10

EARLIER FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFFWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                         Score 36; DB 9; Length 1049;
Pred. No. 96;
2; Mismatches 1; Indels
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Pred. No.
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1049
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT : ORGANISM: Craterostigma plantagineum US-10-217-700-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10217700 Publication No. US20030070191A1 GENERAL INFORMATION:
                                                                                                                                                                                                         66.78;
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66.7%;
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Matches 6; Conservative
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                              436 VIPPGMDFS 444
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435 VIPPGMDFS 443
                                                                                                                                          ; ORGANISM: Oryza sativa
US-10-217-700-10
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LENGTH: 1081
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66.7%; Score 36; DB 9; Length 1081;

Query Match

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Publication No. US20030070191A1
GENERAL INFORMATION:
APPLICANT: Holadac H.
APPLICANT: Holadac, A. Scott
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
CURRENT APPLICATION UNMBER: US/10/217,700
CURRENT APPLICATION NUMBER: 09/394,272
EARLIER RPILING DATE: 2002-08-12
SEALIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOTUTANE PLICH OF INVENTION VET: 2.0
SED ID NO 11
LENGTH: 1083
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| Publication No. US20030070191a1
| GENERAL INFORMATION:
| APPLICAMY: Haigler, Candace H. APPLICAMY: Holaday, A. Scott
| TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| FILE REFERENCE: 201304/1000
| CURRENT APPLICATION NUMBER: US/10/217,700
| EARLIER APPLICATION NUMBER: 09/394,272
| EARLIER FILING DATE: 2002-08-12
| EARLIER FILING DATE: 199-09-10
| NUMBER OF SEQ ID NOS: 194
| SOFTWARE: Patentin Ver. 2.0
                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; 'Score 36; DB 9; Length 1084; 66.7%; Pred. No. 1e+02;
                         Indels
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                      1;
66.7%; Pred. No. 1e+02;
tive 2; Mismatches
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ORGANISM: Arabidopsis thaliana
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                      445 VIPPGMDFS 453
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483 VIPPGMDFS 491
                                                             3 VVPXGMDYS 11
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453 VIPPGMDFS 461
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US-10-217-700-9
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Best Local Similarity
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SWAINSON, Ronald V.
APPLICANT: SCHIEBER: Chiesta
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/034,623
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
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Pred. No. 9.1e+02;
4; Mismatches 2; Indels
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Pred. No. 9.1e+02;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/10034623; Publication No. US20020198365A1; GENERAL INFORMATION: APPLICANT: Swanson, Ronald V.
                                                                                ; Sequence 4, Application US/10027806
; Patent No. US20020160476A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Cenarchaeum symbiosum US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
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2294 EDVIPRGISFS 2304
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Best Local Similarity 45.37
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2294 EDVIPRGISFS 2304
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Best Local Similarity 45.5
Matches 5; Conservative
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                                                         US-10-027-806-4
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Publication No. US20030049619A1
GENERAL INFORMATION:
APPLICANT: Delagrave, Simon
APPLICANT: Delagrave, Simon
APPLICANT: Delagrave, Simon
APPLICANT: Marrs, Barry
ITLE OF INVENTION: Of Polynucleotides
FITLE OF INVENTION: Of Polynucleotides
FITLE OF INVENTION: Of Polynucleotides
FILE REFERENCE: HRR0041
CURRENT APPLICATION NUMBER: US/09/813,408
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEO ID NOS: 85
SOFTWARE: Patentin version 3.0
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 440;
58;
                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FELING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                           Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5111, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%;
85.7%;
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66.7%;
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7.
6, Conservative
                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Aeropyrum pernix US-09-813-408-27
                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EVVPXGMDY 10
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SOFTWARE: FASTS.
SEQ ID NO 5111
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                                                                                                                                                                                                                                             SEQ ID NO 27
LENGTH: 440
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APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.0029.
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 9.1e+02;
4; Mismatches 2; Indels
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45.5%; Pred. No. 15;
Live 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BANDERS.
APPLICANT: BANDERS.
APPLICANT: BANDER, PETER
APPLICANT: BANDEN, PETER KAMP
TILLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/09/948,080
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SEQ ID NOS: 35
LENGTH: 59
LENGTH: 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4881, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09948080 Patent No. US20020102702A1 GENERAL INFORMATION:
                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Enterococcus faecalis
US-09-948-080-14
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                               63.0%;
45.5%;
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.5.
For 5; Conservative
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2294 EDVIPRGISFS 2304
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPXGMDYS 11
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                                                                                                                                                                        SEQ ID NO 4
LENGTH: 3472
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APPLICANT:
APPLICANT:
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APPLICANT:
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Pred. No. 94;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 9; Length 283;
Pred. No. 88;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GASELDELY, NUCELL
APPLICANT: Syskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITLE OF INVENTION: Identification of Essential Genes in TILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: 60/204
PRIOR APPLICATION NUMBER: 60/204
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/205, 848
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/205, 848
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PILING DATE: 2000-112-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR RILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PEALENTIN VET: 3.0
SOFTWARE: PEALENTIN VET: 3.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10697
LENGTH: 299
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; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.1%;
75.0%;
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40.0%;
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.1
Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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| 218 EQITPTGIEY 227
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US-09-815-242-10697
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07978
PRIOR PELING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR PLING DATE: 1998-03-30
PRIOR PLING DATE: 1998-03-31
PRIOR PLING DATE: 1998-04-01
PRIOR PLING DATE: 1998-04-15
PRIOR PRING DATE: 1998-04-22
P
                          R FILING DATE: 1998-03-27
R PAPLICATION NUMBER: 60/079689
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079663
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/07928
R FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/083392
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APPLICATION NUMBER: 60/083495
APPLICATION NUMBER: 60/079664
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                                                                                                                             Sequence 526, Application US/09978295A Patent No. US20020156006A1
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APPLICATION NUMBER: 60/079656
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FILING DATE: 1998-03-20
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Gao, Wei-Qiang
Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                                                                         Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                                                          APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                 Desnoyers, Luc
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                                                                     RESULT 14
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APPLICANT: Paon1, Unicholas F.
APPLICANT: Paon1, Unicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, David L.
APPLICANT: Tumas, David L.
APPLICANT: Williams. P. Mickey
APPLICANT: Williams.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane
FILE REFERENCE: P5030PL027
CURRENT APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066344
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077631
PRIOR APPLICATION NUMBER: 60/077631
PRIOR APPLICATION NUMBER: 60/077631
PRIOR APPLICATION NUMBER: 60/077631
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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R FILING DATE: 1998-03-20
R FILING DATE: 1998-03-20
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/078939
R FILING DATE: 1998-03-20
R FILING DATE: 1998-03-20
R FILING DATE: 1998-03-20
R FILING DATE: 1998-03-25
R APPLICATION NUMBER: 60/079294
R FILING DATE: 1998-03-25
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FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077791
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FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/078004
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Filvaroff, Ellen
Fong, Sherman
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Kuo, Sophia S.
                                                                                     Botstein, David
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                                                                                                                  Desnoyers, Luc
Eaton, Dan
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                                                     Baker Kevin P
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                                                                                     R APPLICATION NUMBER: 60/083499
R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083545
R RILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083554
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083559
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/08359
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/08366
R APPLICATION NUMBER: 60/08366
R APPLICATION NUMBER: 60/08414
R FILING DATE: 1998-04-30
R APPLICATION NUMBER: 60/084414
R FILING DATE: 1998-05-05
R APPLICATION NUMBER: 60/084637
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084641
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084640
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084539
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084538
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/085339
R FILING DATE: 1998-05-03
R APPLICATION NUMBER: 60/085339
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R APPLICATION NUMBER: 60/085689
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/08559
R FILING DATE: 1998-05-15
R FILING DATE: 1998-05-15
R FILING DATE: 1998-05-18
R FILING DATE: 1998-05-18
R APPLICATION NUMBER: 60/085573
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/085573
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Patent No. US20020169284A1.
GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/079728

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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1998-03-31
PRIOR PELING DATE: 1998-03-31
PRIOR PELING DATE: 1998-03-31
PRIOR PELING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-22
PRIOR PILING DATE: 1998-04-29
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Gaps
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US-09-978-192A-526
US-09-978-192A-526
Sequence 526, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Bankenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Beton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08358
PRIOR APPLICATION NUMBER: 60/08359
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR PAPLICATION NUMBER: 60/08342
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-30
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-06
PRIOR PELING DATE: 1998-05-06
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PRIOR PELING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084639
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08460
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PRIOR APPLICATION NUMBER: 60/08463
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08463
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08533
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08530
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08550
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08550
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PELING DATE: 1998-05-15
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Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
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Best Local Similarity 70.0'
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APPLICANT:

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PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR FILING DATE: 1998-04-08
PRIOR PELING DATE: 1998-04-08
PRIOR PELING DATE: 1998-04-08
PRIOR PEPLICATION NUMBER: 60/081195
PRIOR PELING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
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PRIOR PELING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/08197
PRIOR APPLICATION NUMBER: 60/08197
PRIOR APPLICATION NUMBER: 60/08197
PRIOR APPLICATION NUMBER: 60/081817
PRIOR APPLICATION NUMBER: 60/081817
PRIOR APPLICATION NUMBER: 60/081817
                                      R APPLICATION NUMBER: 60/080107
R APPLICATION NUMBER: 60/080107
R APPLICATION NUMBER: 60/080165
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080194
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080327
R FILING DATE: 1998-04-01
R FILING DATE: 1998-04-01
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080328
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080333
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R APPLICATION NUMBER: 60/080334

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R APPLICATION NUMBER: 60/081070

R FILING DATE: 1998-04-08

R APPLICATION NUMBER: 60/081049

R APPLICATION NUMBER: 60/081049

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R APPLICATION NUMBER: 60/081195
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PRIOR
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                                                   Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kuo, Sophia S.
Napier, Mary A.
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RR FILING DATE: 1998-03-13
RAPPLICATION NUMBER: 60/07886
RR FILING DATE: 1998-03-20
RR APPLICATION NUMBER: 60/078936
RR FILING DATE: 1998-03-20
RR APPLICATION NUMBER: 60/078910
RR FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923
FILING DATE: 1998-03-30
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
Fong, Snermann, Cao, Wei-Qiang
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPRENCE: B6509PC63 COURSENT PERDICATION: Secreted and Transmembrane Polypeptides and Nucleic CHRENT PEDICATION: Acids Encoding the Same FILE REPRENCE: B6509PC63 COURSENT PEDICATION: Acids Encoding the Same CURRENT PEDICATION NUMBER: 05/04/249 PRIOR PEDICATION NUMBER: 05/06250 PRIOR PEDICATION NUMBER: 05/06511 PRIOR PEDICATION NUMBER: 05/06511 PRIOR PEDICATION NUMBER: 05/06511 PRIOR PEDICATION NUMBER: 05/06511 PRIOR PEDICATION NUMBER: 05/07/32 PRIOR PEDICATIO
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Pan, James;
Paoni, Nicholas F.
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PRIOR FILING DATE: 1986.05-07
PRIOR PELING DATE: 1986.05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR PELING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084640
R APPLICATION NUMBER: 60/084598
R APPLICATION NUMBER: 60/084598
R FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
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APPLICATION NUMBER: 60/084637
FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085697
        FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
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Filvaroff, Ellen
Fong, Sherman
Gao, Wai-Qiang
Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
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Matches 7; Conservative
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RESULT 17

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Query Match

Gaps ö Length 736; 61.1%; Score 33; DB 9; Length 736 70.0%; Pred. No. 2.6e+02; Live 0; Mismatches 3; Indels NE FILING DATE: 1998-05-06

NA APPLICATION NUMBER: 60/084637

NE FILING DATE: 1998-05-07

NE PLING DATE: 1998-05-07

OR APPLICATION NUMBER: 60/084640

OR FILING DATE: 1998-05-07

OR PILING DATE: 1998-05-07

OR PILING DATE: 1998-05-07

OR PILING DATE: 1998-05-07

OR PILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR PRILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR APPLICATION NUMBER: 60/08559 THING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084627

R APPLICATION NUMBER: 60/084627

R APPLICATION NUMBER: 60/084643

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085338

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085338

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085582 Sequence 526, Application US/09978189 Publication No. US20030004102A1 GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085700 Godowski, Paul J.
Grimaldi, J. Christopher PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION UNDBER: 60/085704 PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085697 Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A. Ferrara, Napoleon Filvaroff, Ellen Fong, Sherman Gao, Wel-Qiang Gerber, Hanspeter Gerritsen, Mary E Goddard, Audrey Query Match
Best Local Similarity 70.0
Matches 7; Conservative Botstein, David Desnoyers, Luc Eaton, Dan 331 EPVVVYGMDY 340 1 EEVVPXGMDY 10 US-09-978-189-526 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT δ Dp

Pan, James; Paoni, Nicholas F

APPLICANT: APPLICANT:

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PRIOR APPLICATION NUMBER: 60/081049
PRIOR APPLICATION NUMBER: 60/081049
PRIOR APPLICATION NUMBER: 60/081041
PRIOR PLING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-20
PRIOR PRICATION NUMBER: 60/083559
PRIOR PRILICATION NUMBER: 60/083559
PRIOR PRILICATION NUMBER: 60/083559
PRIOR PRILICATION NUMBER: 60/083559
PRIOR PLING DATE: 1998-04-20
PRIOR PRILICATION NUMBER: 60/083550
PRIOR PRILICATION NUMBER: 60/083550
PRIOR PLING DATE: 1998-04-20
PRIOR 
                     FILLING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
                                                                      APPLICANT: SLOWER ALLIANA: MARILLANA: MACHILLANA: 
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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APPLICANT: Goddward, Audrey,
APPLICANT: Goddward, Audrey,
APPLICANT: Goddward, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT APPLICATION NUMBER: US/10/176,758
FILE REPERENCE: P3430R1C104
CURRENT APPLICATION TEMOVEd - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
EENGTH: 736
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 420
LENGTH: 736
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                                                                                                                                                                    ; Sequence 420, Application US/10176758; Publication No. US20030008353Al; GENERAL INFORMATION:
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Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 70.0
Matches 7, Conservative
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Smith, Victoria
                                                      331 EPVVVYGMDY 340
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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; ORGANISM: Homo Sapien
US-10-176-758-420
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US-10-175-737-420
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CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
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                                                                                    R FILING DATE: 1998-5-07

R APPLICATION NUMBER: 60/084627

RR FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084643

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/085339

R APPLICATION NUMBER: 60/085339

R APPLICATION NUMBER: 60/08538

R FILING DATE: 1998-05-13
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R FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/085689

R FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/085579

R APPLICATION NUMBER: 60/085580

R FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/085580

R FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/085573

R APPLICATION NUMBER: 60/085573

R APPLICATION NUMBER: 60/085573

R APPLICATION NUMBER: 60/085573

R FILING DATE: 1998-05-15
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Publication No. US20030008352A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                    APPLICATION NUMBER: 60/084600
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
FILING DATE: 1998-05-15
                         60/084598
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
FILING DATE: 1998-05-07
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Wood, William I.
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Smith, Victoria
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US-10-174-590-420
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LENGTH: 736
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